

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 22:15:05 ; Search time 2159 Seconds
(without alignments)
1079.473 Million cell updates/sec

Title: US-09-904-968a-1_n3336_COPY_3300_3340
Perfect score: 41
Sequence: 1 aagctccggatgccagtc.....tcatcggtgcccgcgncgcg 41

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_slc:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hg:*
15: gb_pl:*

prior ant dbs
Seq 1, "N" at 3336
searched nt 3300-3340
using "identity-nucdx" matrix.
(Matches to 'N' are marked with a colon [:]; N in query seq considered a match to anything in db seq)

Pred. No. is the number of
score greater than or equal
and is derived by analysis

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	41	100.0	164	10	HSA248385
C 2	41	100.0	31571	6	I59642
C 3	41	100.0	34934	14	AC141442
C 4	41	100.0	37244	14	AC140806
C 5	41	100.0	37279	14	AC140702
C 6	41	100.0	38849	8	AC005346
C 7	41	100.0	39322	14	AC140703
C 8	41	100.0	40673	14	AC140704
C 9	41	100.0	41489	14	AC142549
C 10	41	100.0	47934	8	HS024498
C 11	41	100.0	53522	8	AX440497
C 12	41	100.0	53522	8	HUMPKD1GEN
C 13	41	100.0	53526	6	AR097326
C 14	41	100.0	53526	6	BD128573
C 15	41	100.0	53577	6	AR097325
C 16	41	100.0	53577	6	BD128572
C 17	41	100.0	53577	6	AR643858
C 18	41	100.0	84562	14	AC140700

C 19	41	100.0	84928	14	AC141231
C 20	41	100.0	89599	14	AC138966
C 21	41	100.0	109340	8	AC010488
C 22	41	100.0	127485	8	HUAC002039
C 23	41	100.0	131353	14	AC137642
C 24	41	100.0	145971	8	AC136427
C 25	41	100.0	147573	14	AC133566
C 26	41	100.0	148930	14	AC138949
C 27	41	100.0	152171	14	AC138892
C 28	41	100.0	162264	14	AC139266
C 29	41	100.0	167184	14	AC138888
C 30	41	100.0	168230	14	AC138901
C 31	41	100.0	168408	14	AC139265
C 32	41	100.0	172474	14	AC142081
C 33	41	100.0	173775	14	AC141410
C 34	41	100.0	177920	14	AC137806
C 35	41	100.0	179399	14	AC141465
C 36	41	100.0	179399	14	AC141465
C 37	41	100.0	179754	14	AC141616
C 38	41	100.0	180798	8	AC138932
C 39	41	100.0	181231	14	AC138903
C 40	41	100.0	183215	14	AC142195
C 41	41	100.0	183537	14	AC141266
C 42	41	100.0	187226	14	AC139258
C 43	41	100.0	188734	14	AC141304
C 44	41	100.0	194670	14	AC141613
C 45	41	100.0	199759	8	AC009065
C 46	41	100.0	202656	14	AC141468
C 47	41	100.0	202882	14	AC141411
C 48	41	100.0	204500	14	AC141267
C 49	41	100.0	204638	14	AC141253
C 50	41	100.0	215974	14	AC141607
C 51	41	100.0	216759	8	AC138969
C 52	41	100.0	223432	8	AC126755
C 53	39.4	96.1	865	8	HS323057
C 54	39.4	96.1	38848	14	AC141236
C 55	39.4	96.1	129473	14	AC040158
C 56	39.4	96.1	144161	14	AC141602
C 57	39.4	96.1	183396	14	AC154112
C 58	39.4	96.1	184891	8	AC092137
C 59	39.4	96.1	187721	8	AC126763
C 60	39.4	96.1	189770	14	AC139281
C 61	39.4	96.1	196687	14	AC136442
C 62	39.4	96.1	215222	14	AC141467
C 63	39.4	96.1	215960	14	AC144881
C 64	39.4	96.1	218593	14	AC141303
C 65	37.8	92.2	192549	14	AC141401
C 66	36.4	88.8	131818	14	AC138872
C 67	36.2	88.3	51437	14	AC140805
C 68	36.2	88.3	162696	14	AC148537
C 69	36.2	88.3	166278	14	AC141276
C 70	35.4	86.3	198295	14	AC141080
C 71	34.6	84.4	202023	14	AC141270
C 72	30.4	74.1	159468	14	AC140888
C 73	29.8	72.7	6423	6	AX281458
C 74	29.8	72.7	6423	6	AX348742
C 75	29	70.7	187328	14	AC150732
C 76	28.4	69.3	110000	1	AY596297_27
C 77	25.2	61.5	173370	14	AC116286
C 78	25.2	61.5	192405	14	AC126160
C 79	25	61.0	371	3	AY574424
C 80	24.6	60.0	1424	6	AR621724
C 81	24.6	60.0	15268	6	AR619747
C 82	24.2	59.0	2202	6	C0615018
C 83	24.2	59.0	5083	6	C0615017
C 84	24.2	59.0	12393	1	AE012414
C 85	24.2	59.0	33483	14	AC020333
C 86	24.2	59.0	110000	1	BA000040_71
C 87	24.2	59.0	110000	1	CP000050_13
C 88	24.2	59.0	167344	2	AC093438
C 89	24.2	59.0	170988	2	AC091223
C 90	24.2	59.0	254095	14	AC108990
C 91	24.2	59.0	265524	2	AE003541

AC141231	Homo sapi
AC138966	Homo sapi
AC010488	Homo sapi
AC002039	Homo sapi
AC137642	Homo sapi
AC136427	Homo sapi
AC133566	Homo sapi
AC138949	Homo sapi
AC138892	Homo sapi
AC139266	Homo sapi
AC138888	Homo sapi
AC138901	Homo sapi
AC139265	Homo sapi
AC142081	Homo sapi
AC141410	Homo sapi
AC137806	Homo sapi
AC141465	Homo sapi
AC141465	Homo sapi
AC141616	Homo sapi
AC138932	Homo sapi
AC138903	Homo sapi
AC142195	Homo sapi
AC141266	Homo sapi
AC139258	Homo sapi
AC141304	Homo sapi
AC141613	Homo sapi
AC009065	Homo sapi
AC141468	Homo sapi
AC141411	Homo sapi
AC141267	Homo sapi
AC141253	Homo sapi
AC141607	Homo sapi
AC138969	Homo sapi
AC126755	Homo sapi
AJ323057	Homo sapi
AC141236	Homo sapi
AC040158	Homo sapi
AC141602	Homo sapi
AC154112	Pan trogl
AC092137	Homo sapi
AC126763	Homo sapi
AC139281	Homo sapi
AC136442	Homo sapi
AC141467	Homo sapi
AC144881	Gorilla g
AC141303	Homo sapi
AC141401	Homo sapi
AC138872	Homo sapi
AC140805	Homo sapi
AC148537	Pan trogl
AC141276	Homo sapi
AC141080	Homo sapi
AC141270	Homo sapi
AC140888	Homo sapi
AX281458	Sequence
AX348742	Sequence
AC150732	Papio anu
Continuation (28 o	
AC116286	Rattus no
AY574424	Rattus no
AR621724	Sequence
AR619747	Sequence
C0615018	Sequence
CQ615017	Sequence
AE012414	Xanthomon
AC020333	Drosophil
Continuation (72 o	
CP000050_13	Continuation (14 o
AC093438	Drosophil
AC091223	Drosophil
AC108990	Rattus no
AE003541	Drosophil

238	22	53.7	139961	15	AP004668	Oryza sat	AP004668	Oryza sat	C 311	21.8	53.2	138819	14	AC155467	Zea mays
C 239	22	53.7	141649	15	AP004097	Oryza sat	AP004097	Oryza sat	312	21.8	53.2	141394	14	AC155221	Dromaius
240	22	53.7	147890	15	AP004395	Oryza sat	AP004395	Oryza sat	C 313	21.8	53.2	141511	14	AC155475	Zea mays
C 241	22	53.7	158798	15	AP005308	Oryza sat	AP005308	Oryza sat	C 314	21.8	53.2	143192	8	AL954247	Pan trogl
C 242	22	53.7	165122	8	AC011448	Homo sapi	AC011448	Homo sapi	C 315	21.8	53.2	144601	15	AC104709	Oryza sat
243	22	53.7	165369	14	AL353609	Homo sapi	AL353609	Homo sapi	C 316	21.8	53.2	145050	1	AL627275	Salmonell
244	22	53.7	166054	8	CNS06671	Human chr	AL389895	Human chr	C 317	21.8	53.2	153921	15	AP004570	Oryza sat
C 245	22	53.7	169511	8	AC146026	Pan trogl	AC146026	Pan trogl	C 318	21.8	53.2	153921	15	AP004570	Oryza sat
C 246	22	53.7	173213	14	AC073865	Homo sapi	AC073865	Homo sapi	C 319	21.8	53.2	153921	15	AP004570	Oryza sat
C 247	22	53.7	180035	14	AC125819	Rattus no	AC125819	Rattus no	C 320	21.8	53.2	162839	8	AL137846	Human DNA
C 248	22	53.7	189729	14	AC073930	Homo sapi	AC073930	Homo sapi	C 321	21.8	53.2	162839	8	AL137846	Human DNA
C 249	22	53.7	189884	14	AC024440	Homo sapi	AC024440	Homo sapi	C 322	21.8	53.2	169627	14	AC155528	Zea mays
C 250	22	53.7	198427	15	ATCHRIV52	Arabidops	AL161552	Arabidops	C 323	21.8	53.2	170072	14	AC155589	Zea mays
C 251	22	53.7	217841	14	AC095995	Rattus no	AC095995	Rattus no	C 324	21.8	53.2	174864	14	AC155530	Zea mays
C 252	22	53.7	241206	14	AC120484	Rattus no	AC120484	Rattus no	C 325	21.8	53.2	184752	14	AC155597	Zea mays
C 253	22	53.7	241627	14	AC128374	Rattus no	AC128374	Rattus no	C 326	21.8	53.2	185534	14	AC145481	Zea mays
C 254	22	53.7	244292	14	AC098749	Rattus no	AC098749	Rattus no	C 327	21.8	53.2	195859	13	AP281817	Tupaia he
C 255	22	53.7	264270	14	AC156048	Bos tauru	AC156048	Bos tauru	C 328	21.8	53.2	196249	14	AC154418	Mus muscu
C 256	22	53.7	289308	1	AE017242	Mycobacte	AE017242	Mycobacte	C 329	21.8	53.2	197030	14	AY542797	Zea mays
C 257	22	53.7	300100	1	SC093123	Streptomy	AE017242	Mycobacte	C 330	21.8	53.2	201041	14	AC154139	Zea mays
C 258	22	53.7	300242	1	AE016790	Pseudomob	AE016790	Pseudomob	C 331	21.8	53.2	203498	2	AC011697	Drosophil
C 259	22	53.7	301617	1	AE016911	Chromobac	AE016911	Chromobac	C 332	21.8	53.2	238578	14	AC110968	Rattus no
C 260	22	53.7	304282	1	AE016910	Chromobac	AE016910	Chromobac	C 333	21.8	53.2	239030	9	AC131323	Mus muscu
C 261	21.8	53.2	289	6	AE249266	Sequence	AE249266	Sequence	C 334	21.8	53.2	300431	1	AE016835	Salmonell
C 262	21.8	53.2	371	3	AY574505	Unculture	AY574505	Unculture	C 335	21.8	53.2	303855	1	AE017230	Mycobacte
C 263	21.8	53.2	500	3	AJ812177	Unculture	AJ812177	Unculture	C 336	21.8	53.2	304450	1	EX294134	Pirellula
C 264	21.8	53.2	676	3	AY343244	Unculture	AY343244	Unculture	C 337	21.8	53.2	314743	2	AE003495	Drosophil
C 265	21.8	53.2	684	15											

C 384	21.6	52.7	226640	14	AC097833	AC097833 Rattus no	457	21.4	52.2	110000	1	CP000076_33	Continuation (34 o
C 385	21.6	52.7	228864	14	AC155755	AC155755 Bos tauru	458	21.4	52.2	110000	1	CP000076_39	Continuation (40 o
C 386	21.6	52.7	234949	5	BX936288	BX936288 Zebrafish	459	21.4	52.2	110000	1	CP000076_40	Continuation (41 o
C 387	21.6	52.7	271034	14	AC102996	AC102996 Rattus no	460	21.4	52.2	110000	1	CP000076_61	Continuation (62 o
C 388	21.6	52.7	277307	14	AC105149	AC105149 Rattus no	461	21.4	52.2	110000	2	CP000078_2	Continuation (3 of
C 389	21.6	52.7	302007	1	SC0939132	AL939132 Streptomy	462	21.4	52.2	110000	1	AC125991_3	Continuation (4 of
C 390	21.6	52.7	349980	6	AX492784	AX492784 Sequence	463	21.4	52.2	110000	14	BX255276_13	Continuation (14 o
C 391	21.6	52.7	349980	6	AX553951	AX553951 Sequence	464	21.4	52.2	110000	14	CHY105E8_0	AL022594 Caenorhab
C 392	21.4	52.2	409	6	AR623837	AR623837 Sequence	465	21.4	52.2	110000	14	CHY54213_1	Continuation (2 of
C 393	21.4	52.2	438	9	MMFGF6E1	X51552 Mouse FGF-6	466	21.4	52.2	110000	15	AP008214_097	Continuation (98 o
C 394	21.4	52.2	447	15	BT009578	BT009578 Triflicum	467	21.4	52.2	110000	15	AP008218_093	Continuation (94 o
C 395	21.4	52.2	572	6	CQ178247	CQ178247 Sequence	468	21.4	52.2	110000	15	AP008209_168	Continuation (169
C 396	21.4	52.2	572	6	CQ138404	CQ138404 Sequence	469	21.4	52.2	110000	15	AP008210_171	Continuation (172
C 397	21.4	52.2	627	9	AB079674	AB079674 Rattus no	470	21.4	52.2	110000	15	AP008211_251	Continuation (252
C 398	21.4	52.2	630	6	E26527	E26527 Sugar chain	471	21.4	52.2	110000	15	AP008212_050	Continuation (51 o
C 399	21.4	52.2	642	11	AY657572	AY657572 Synthetic	472	21.4	52.2	112351	8	AC011484	AC011484 Homo sapi
C 400	21.4	52.2	670	10	BV218271	BV218271 S23P626R	473	21.4	52.2	113266	15	AC092262	AC092262 Oryza sat
C 401	21.4	52.2	747	6	CQ740186	CQ740186 Sequence	474	21.4	52.2	113266	15	AC163683	AC163683 Mus muscu
C 402	21.4	52.2	1038	15	AY659123	AY659123 Oryza sat	475	21.4	52.2	130712	14	AC141789	AC141789 Apis mell
C 403	21.4	52.2	1098	11	AY659060	AY659060 Synthetic	476	21.4	52.2	130748	14	AP005906	AP005906 Oryza sat
C 404	21.4	52.2	1182	9	AB035383	AB035383 Mus muscu	477	21.4	52.2	131141	14	AC153085	AC153085 Ornithorh
C 405	21.4	52.2	1224	9	BC063748	BC063748 Mus muscu	478	21.4	52.2	132781	14	AC141265	AC141265 Homo sapi
C 406	21.4	52.2	1305	6	AX659744	AX659744 Sequence	479	21.4	52.2	132830	14	AC148864	AC148864 Canis fam
C 407	21.4	52.2	1532	6	AR507090	AR507090 Sequence	480	21.4	52.2	134059	14	AC016284	AC016284 Homo sapi
C 408	21.4	52.2	1578	15	AY570713	AY570713 Ostreococ	481	21.4	52.2	134184	14	AC150028	AC150028 Canis fam
C 409	21.4	52.2	1602	15	BT017987	BT017987 Zea mays	482	21.4	52.2	143427	8	AC002432	AC002432 Homo sapi
C 410	21.4	52.2	1719	1	CSU16275	UI6275 Comamonas s	483	21.4	52.2	146712	15	AC130604	AC130604 Oryza sat
C 411	21.4	52.2	1739	1	AF031149	AF031149 Chromatiu	484	21.4	52.2	152945	14	AC130606	AC130606 Oryza sat
C 412	21.4	52.2	1861	6	CQ598842	CQ598842 Sequence	485	21.4	52.2	154440	14	AC108176	AC108176 Bos tauru
C 413	21.4	52.2	2069	9	BC025585	BC025585 Mus muscu	486	21.4	52.2	155649	14	AC015874	AC015874 Homo sapi
C 414	21.4	52.2	2113	1	AB000508	AB000508 Comamonas	487	21.4	52.2	157493	14	AC022175	AC022175 Homo sapi
C 415	21.4	52.2	2266	6	CQ573282	CQ573282 Sequence	488	21.4	52.2	158892	14	AC108175	AC108175 Bos tauru
C 416	21.4	52.2	2303	2	AF145614	AF145614 Drosophila	489	21.4	52.2	162727	8	HS467L1	Z98884 Human DNA s
C 417	21.4	52.2	2303	15	AK071363	AK071363 Oryza sat	490	21.4	52.2	162772	15	AC108873	AC108873 Oryza sat
C 418	21.4	52.2	2328	2	AF342986	AF342986 Caenorhab	491	21.4	52.2	163162	14	AC139311	AC139311 Bos tauru
C 419	21.4	52.2	2328	2	BT009935	BT009935 Drosophila	492	21.4	52.2	163741	2	AC007821	AC007821 Drosophila
C 420	21.4	52.2	4236	6	AR623966	AR623966 Sequence	493	21.4	52.2	164632	14	AC025624	AC025624 Homo sapi
C 421	21.4	52.2	4339	15	AY081008	AY081008 Aspergill	494	21.4	52.2	165902	8	AC106763	AC106763 Homo sapi
C 422	21.4	52.2	4607	9	MUSFGFAB	M92416 Mus musculu	495	21.4	52.2	168076	14	AC013304	AC013304 Homo sapi
C 423	21.4	52.2	5888	1	AF038578	AF038578 Pseudomon	496	21.4	52.2	168243	14	AC011269	AC011269 Homo sapi
C 424	21.4	52.2	5998	1	AB032524	AB032524 Streptomy	497	21.4	52.2	169509	14	AC150713	AC150713 Bos tauru
C 425	21.4	52.2	6037	6	CQ573281	CQ573281 Streptomy	498	21.4	52.2	169559	15	OSJN00159	AL662956 Oryza sat
C 426	21.4	52.2	6323	6	CQ598841	CQ598841 Sequence	499	21.4	52.2	170453	15	AP005095	AP005095 Oryza sat
C 427	21.4	52.2	6683	9	RNU24070	U24070 Rattus norv	500	21.4	52.2	170453	15	AC092934	AC092934 Homo sapi
C 428	21.4	52.2	10647	1	AE004518	AE004518 Pseudomon							
C 429	21.4	52.2	10773	1	AE012272	AE012272 Xanthomon							
C 430	21.4	52.2	10965	1	AE004740	AE004740 Pseudomon							
C 431	21.4	52.2	11854	6	AR619642	AR619642 Sequence							
C 432	21.4	52.2	20776	2	CEK03D10	Z81561 Caenorhabdi							
C 433	21.4	52.2	34662	6	AR619866	AR619866 Sequence							
C 434	21.4	52.2	39200	8	AC024584	AC024584 Homo sapi							
C 435	21.4	52.2	39263	3	AY281354	AY281354 Unculture							
C 436	21.4	52.2	39360	1	AY943953	AY943953 Streptomy							
C 437	21.4	52.2	44567	6	AX695371	AX695371 Sequence							
C 438	21.4	52.2	47618	14	AC166904	AC166904 Bos tauru							
C 439	21.4	52.2	55578	1	PPS304453	PPS304453 Plasmid p							
C 440	21.4	52.2	66093	14	AC125991_4	Continuation (5 of							
C 441	21.4	52.2	76345	14	AC165120	AC165120 Homo sapi							
C 442	21.4	52.2	78065	8	AC005355	AC005355 Bos tauru							
C 443	21.4	52.2	91170	14	AC014779	AC014779 Drosophila							
C 444	21.4	52.2	104561	1	AE017282_32	Continuation (33 o							
C 445	21.4	52.2	110000	1	AE006470_07	Continuation (8 of							
C 446	21.4	52.2	110000	1	AP006618_21	Continuation (22 o							
C 447	21.4	52.2	110000	1	AP006618_25	Continuation (26 o							
C 448	21.4	52.2	110000	1	AP006618_36	Continuation (37 o							
C 449	21.4	52.2	110000	1	BA000030_11	Continuation (12 o							
C 450	21.4	52.2	110000	1	BA000030_27	Continuation (28 o							
C 451	21.4	52.2	110000	1	BA000030_27	Continuation (28 o							
C 452	21.4	52.2	110000	1	BA000030_28	Continuation (29 o							
C 453	21.4	52.2	110000	1	BA000030_77	Continuation (78 o							
C 454	21.4	52.2	110000	1	BA000030_85	Continuation (86 o							
C 455	21.4	52.2	110000	1	CP000050_30	Continuation (31 o							
C 456	21.4	52.2	110000	1	CP000058_45	Continuation (46 o							

ALIGNMENTS

RESULT 1	HSA248385/c	HSA248385	164 bp	DNA	linear	STS 08-MAR-2000
LOCUS	Homo sapiens STS J-210R, sequence tagged site.					
DEFINITION	AJ248385					
ACCESSION	AJ248385.1	GI:5514773				
VERSION						
KEYWORDS	STS.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 164)					
AUTHORS	Sulimova,G.E., Udina,I.G., Kunizheva,S.S. and Kompaniytzev,A.A.					
TITLE	Creating NotI-STS Markers for Human Chromosome 3					
JOURNAL	Mol. Biol. 33, 698-703 (1999)					
REFERENCE	2 (bases 1 to 164)					
AUTHORS	Sulimova,G.E.					
TITLE	Direct Submission					
JOURNAL	Submitted (23-JUN-1999) Sulimova G.E., Laboratory of Comparative Animal Genetics, N.I.Vavilov Institute of General Genetics RAS, Gubkin str. 3, Moscow B-333, 117809 GSP-1, RUSSIA					
COMMENT	The STS markers registered were developed to clones from NotI library of human chromosome					

3 received by E.R. Zabarovsky (Karolinska Institute, Sweden) as a result of collaborative research work with Engelhardt Molecular Biology Institute of the Russian Academy of Sciences. The NotI clones were used to construct NotI map of human chromosome 3 by FISH and mapping by a somatic cell hybrid panel.

FEATURES

source

1. .164
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/cell_line="MCH903.1"
/clone_lib="mouse/human microcell hybrid lines"
/clone_lib="NotI-linking library"

primer_bind

1. .20
/notes="J-210R forward primer"
/PCR_conditions="96deg. 0.8min, 65deg. 0.8min, 72deg. 1.0min"

STS

21. .143
/standard_name="J-210R"
/notes="STS PCR product"

primer_bind

complement(144. .164)
/notes="J-210R reverse primer"
/PCR_conditions="96deg. 0.8min, 65deg. 0.8min, 72deg. 1.0min"

ORIGIN

Query Match 100.0%; Score 41; DB 10; Length 164;
Best Local Similarity 97.6%; Pred. No. 0.046;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGCCGCGCG 41
|||||
Db 131 AAGCTCCGGATGCCAGTCCCTCATCGTCGCCGCGCG 91
|||||

RESULT 2

159642/c

LOCUS 159642 Sequence 1 from patent US 5654170. linear PAT 07-OCT-1997

DEFINITION

ACCESSION 159642

VERSION 159642.1 GI:2478274

KEYWORDS

SOURCE

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 31571)

Authors Klingner, K.W., Landes, G.M., Burn, T.C., Connors, T.D., Dackowski, W.,

Germino, G., and Qian, F.

TITLE Polycystic kidney disease gene

JOURNAL Patent: US 5654170-A 1 05-AUG-1997;

FEATURES

source

1. .31571
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 41; DB 6; Length 31571;
Best Local Similarity 97.6%; Pred. No. 0.017;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGCCGCGCG 41
|||||
Db 3633 AAGCTCCGGATGCCAGTCCCTCATCGTCGCCGCGCG 3593
|||||

RESULT 3

AC141442/c

LOCUS

DEFINITION

HTG 16-MAR-2003

Homo sapiens chromosome 16 clone LA16C-371H10, WORKING DRAFT

SEQUENCE, 4 unordered pieces.

ACCESSION

AC141442

VERSION AC141442.1 GI:28974995

KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 34934)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 16

JOURNAL

REFERENCE

2 (bases 1 to 34934)

DOE Joint Genome Institute.

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (16-MAR-2003) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

-----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: http://www.jgi.doe.gov

Project Information

Center Project Name: 1222782

Center clone name: LANL-16C_371H10

Summary Statistics

Consensus quality: 3315 bases at least Q40

Consensus quality: 33242 bases at least Q30

Consensus quality: 33298 bases at least Q20

Estimated insert size: 40000; agarose-fp estimation

Estimated insert size: 34634; sum-of-contigs estimation

Quality coverage: 15.87 in Q20 bases; agarose-fp estimation

Quality coverage: 18.32 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1026: contig of 1026 bp in length

* 1027 1126: gap of unknown length

* 1127 2407: contig of 1281 bp in length

* 2408 2507: gap of unknown length

* 2508 7632: contig of 5125 bp in length

* 7633 7732: gap of unknown length

* 7733 34934: contig of 27202 bp in length.

Location/Qualifiers

1. .34934

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="16"

/clone_lib="LA16C-371H10"

/libraries="LA16C01 and LA16C02"

1027. .1126

/estimated_length=unknown

2408. .2507

/estimated_length=unknown

7633. .7732

/estimated_length=unknown

FEATURES

source

gap

gap

gap

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 34934;
Best Local Similarity 97.6%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGCCGCGCG 41
|||||
Db 24319 AAGCTCCGGATGCCAGTCCCTCATCGTCGCCGCGCG 24279
|||||

RESULT 4
AC140806
LOCUS
DEFINITION
AC140806 Homo sapiens chromosome 16 clone LA16C-379A4, WORKING DRAFT
SEQUENCE, 2 unordered pieces.
ACCESSION
AC140806
VERSION
AC140806.1 GI:28631187
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 37244)
DOE Joint Genome Institute.
TITLE
Sequencing of Human Chromosome 16
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 37244)
DOE Joint Genome Institute.
AUTHORS
Direct Submission
TITLE
Submitted (03-MAR-2003) Production Sequencing Facility, DOE Joint
JOURNAL
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1223460
Center clone name: LANL-16C_379A4

Summary Statistics
Consensus quality: 36406 bases at least Q40
Consensus quality: 36465 bases at least Q30
Consensus quality: 36556 bases at least Q20
Estimated insert size: 4000; agarose-fp estimation
Estimated insert size: 37144; sum-of-contigs estimation
Quality coverage: 9.59 in Q20 bases; agarose-fp estimation
Quality coverage: 10.33 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 17558: contig of 17558 bp in length
* 17559 17658: gap of unknown length
* 17859 37244: contig of 19586 bp in length.

FEATURES
source
1..37244
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16C-379A4"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
17559..17658
/estimated_length=unknown
gap
17559..17658
/estimated_length=unknown
ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 37244;
Best Local Similarity 97.6%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 0; Gaps 0;
QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCG 41
|||||
DB 16992 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCG 17032
|||||

RESULT 5
AC140702
LOCUS
DEFINITION
AC140702 Homo sapiens chromosome 16 clone LA16C-317A11, WORKING DRAFT
SEQUENCE, 2 unordered pieces.
ACCESSION
AC140702
VERSION
AC140702.1 GI:28603918
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 37279)
DOE Joint Genome Institute.
TITLE
Sequencing of Human Chromosome 16
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 37279)
DOE Joint Genome Institute.
AUTHORS
Direct Submission
TITLE
Submitted (28-FEB-2003) Production Sequencing Facility, DOE Joint
JOURNAL
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1217515
Center clone name: LANL-16C_317A11

Summary Statistics
Consensus quality: 36867 bases at least Q40
Consensus quality: 37083 bases at least Q30
Consensus quality: 37153 bases at least Q20
Estimated insert size: 4000; agarose-fp estimation
Estimated insert size: 37179; sum-of-contigs estimation
Quality coverage: 15.56 in Q20 bases; agarose-fp estimation
Quality coverage: 16.74 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2057: contig of 2057 bp in length
* 2058 2157: gap of unknown length
* 2158 37279: contig of 35122 bp in length.

FEATURES
source
1..37279
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16C-317A11"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
2058..2157
/estimated_length=unknown
gap
2058..2157
/estimated_length=unknown
ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 37279;
Best Local Similarity 97.6%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 0; Gaps 0;
QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCG 41
|||||
DB 37099 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCG 37139
|||||

```

RESULT 6
AC005346      38849 bp      DNA      linear      PRI 31-JUL-1998
LOCUS      Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete
DEFINITION      sequence.
AC005346
VERSION      AC005346.1 GI:3366566
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Ricke,D.O.
TITLE      1 (bases 1 to 38849)
JOURNAL      Large Scale Sequence Analysis and Annotation with the Sequence
REFERENCE      Comparison Analysis (SCAN) System
AUTHORS      Unpublished
2 (bases 1 to 38849)
Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E.,
Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S.,
Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J.,
White,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M.,
Misra,M. and Deaven,L.
Sequencing of Human Chromosome 16p13.3
Unpublished
3 (bases 1 to 38849)
Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E.,
Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S.,
Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J.,
White,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M.,
Misra,M. and Deaven,L.
Direct Submission
Submitted (31-JUL-1998) Center for Human Genome Studies, DOE Joint
Genome Institute, Los Alamos National Laboratory, MS M888, Los
Alamos, NM 87545, USA
FEATURES
Source
1..38849
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.3"
/clone="2H2"
complement(join(544..637,2772..2834,4702..4832))
/notes="100% identity EST zt53d08.s1"
/db_xref="dbEST:AA399469"
complement(join(544..637,2772..2834,4719..4823))
/notes="85% identity mouse EST mj33h06.r1"
/db_xref="dbEST:AA048697"
complement(544..635)
/notes="GRAIL 2 excellent exon, frame 2"
repeat_region
2023..2291
/rpt_family="Alu"
complement(2776..2833)
/notes="GRAIL 2 excellent exon, frame 0"
misc_feature
join(2868..3015,3611..3712,3884..3999,4552..4795)
/notes="9% identity dbEST:H86633 & H86545 yt04f02"
misc_feature
complement(5954..6098)
/notes="GRAIL 2 excellent exon, frame 0"
repeat_region
12312..12503
/rpt_family="MER20"
join(13385..13572,13788..13910)
/notes="96% identity dbEST:W60179 & W60180 zd28b11"
repeat_region
complement(14071..14338)
/rpt_family="Alu"
repeat_region
14071..14090
/notes="(T)20"
/rpt_type=tandem
/rpt_unit="c"
misc_feature
complement(14995..15137)
misc_feature
complement(15261..15398)

```

```

/notes="83% identity me96a10.r1"
/db_xref="dbEST:W82874"
complement(join(15275..15398,15492..15587,18689..18805))
/standard_names="Rab26 (Rat homolog)"
complement(join(15301..15398,15512..15571,15826..15898))
/notes="97%, 100%, & 100% identity EST AA984064 am76b10.s1"
complement(15493..15601)
/notes="GRAIL 2 excellent exon, frame 0"
complement(15786..15895)
/notes="GRAIL 2 excellent exon, frame 1"
15995..16022
/notes="(T)24"
/rpt_type=tandem
/rpt_unit="c"
complement(16005..16528)
/rpt_family="Alu"
misc_feature
complement(16808..16860)
/notes="GRAIL 2 excellent exon, frame 1"
misc_feature
complement(17106..17147)
/notes="GRAIL 2 excellent exon, frame 0"
repeat_region
17508..17576
/rpt_family="Alu"
complement(18689..18799)
/notes="100% identity I48770 (clone exon trap 44.2)"
complement(18689..18799)
/notes="GRAIL 2 excellent exon, frame 1"
19415..19436
/notes="(A)22"
/rpt_type=tandem
/rpt_unit="a"
complement(19762..19956)
/notes="GRAIL 2 excellent exon, frame 2"
20058..20093
/notes="(G)C12"
/rpt_type=tandem
/rpt_unit="ggc"
22264..22545
/rpt_family="Alu"
23195..23760
/rpt_family="Alu"
25104..25127
/notes="GRAIL 2 excellent exon, frame 2"
complement(25572..26174)
/rpt_family="Alu"
25875..25898
/notes="(T)24"
/rpt_type=tandem
/rpt_unit="t"
26184..26205
/notes="(T)22"
/rpt_type=tandem
/rpt_unit="t"
complement(26188..26461)
/rpt_family="Alu"
complement(27153..27447)
/rpt_family="Alu"
complement(27494..27773)
/rpt_family="Alu"
complement(28010..28315)
/rpt_family="Alu"
28478..28777
/rpt_family="Alu"
complement(28795..28971)
/rpt_family="Alu"
28995..29301
/rpt_family="Alu"
complement(29325..29382)
/rpt_family="Alu"
complement(29421..29487)
/rpt_family="Alu"
complement(29647..29950)
/rpt_family="Alu"
30100..30123

```

```

/notes="(T)24"
/rpt_type=tandem
/rpt_unit="t"
repeat_region complement(30106..30688)
repeat_region /rpt_family="Alu"
repeat_region complement(30881..31183)
repeat_region /rpt_family="Alu"
repeat_region complement(31488..31754)
repeat_region /rpt_family="Alu"
misc_feature complement(31673..38849)
repeat_region /notes="L39891 overlap"
repeat_region complement(31787..32068)
repeat_region /rpt_family="Alu"
repeat_region 35647..35670
repeat_region /notes="(T)24"
repeat_region /rpt_type=tandem
repeat_region /rpt_unit="t"
repeat_region complement(35653..35942)
repeat_region /rpt_family="Alu"
repeat_region complement(36161..36779)
repeat_region /rpt_family="Alu"
repeat_region complement(36922..37194)
repeat_region /rpt_family="Alu"
repeat_region 37212..37235
repeat_region /notes="(ATT)6"
repeat_region /rpt_type=tandem
repeat_region /rpt_unit="attc"
repeat_region complement(37242..37514)
repeat_region /rpt_family="Alu"

ORIGIN
Query Match 100.0%; Score 41; DB 8; Length 38849;
Best Local Similarity 97.6%; Pred. No. 0.017; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
|||||
Db 32714 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCGCGCG 32754
|||||

RESULT 7
AC140703/c
LOCUS AC140703 39322 bp DNA linear HTG 28-FEB-2003
DEFINITION Homo sapiens chromosome 16 clone LA16c-320A3, WORKING DRAFT
SEQUENCE, 2 unordered pieces.
ACCESSION AC140703
VERSION AC140703.1 GI:28603919
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 39322)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 39322)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1217795
Center clone name: LANL-16c_320A3
-----
Summary Statistics
Consensus quality: 38784 bases at least Q40

Consensus quality: 38986 bases at least Q30
Consensus quality: 39072 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Quality coverage: 16.68 in Q20 bases; agarose-fp estimation
Quality coverage: 17.02 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 10022: contig of 10022 bp in length
* 10023 10122: gap of unknown length
* 10123 39322: contig of 29200 bp in length.
FEATURES
Location/Qualifiers
1..39322
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
10023..10122
/estimated_length=unknown

gap
estimated_length=unknown

ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 39322;
Best Local Similarity 97.6%; Pred. No. 0.016;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
|||||
Db 10416 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCGCGCG 10376
|||||

RESULT 8
AC140704
LOCUS AC140704 40673 bp DNA linear HTG 28-FEB-2003
DEFINITION Homo sapiens chromosome 16 clone LA16c-326B6, WORKING DRAFT
SEQUENCE, 2 unordered pieces.
ACCESSION AC140704
VERSION AC140704.1 GI:28603920
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 40673)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 40673)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1218386
Center clone name: LANL-16c_326B6
-----
Summary Statistics
Consensus quality: 38913 bases at least Q40
Consensus quality: 39592 bases at least Q30

```

Consensus quality: 3957 bases at least Q20
 Estimated insert size: 4000; agarose-fp estimation
 Estimated insert size: 40573; sum-of-contigs estimation
 Quality coverage: 15.02 in Q20 bases; agarose-fp estimation
 Quality coverage: 14.8 in Q20 bases; sum-of-contigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

1 14666: contig of 14666 bp in length
 * 14667 14766: gap of unknown length
 * 14767 40673: contig of 25907 bp in length.

FEATURES
 source
 1..40673
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="LA16C-326B6"
 /library="Los Alamos human chromosome 16 cosmid
 libraries; LA16NC01 and LA16NC02"
 14667..14766
 /estimated_length=unknown

gap

ORIGIN
 Query Match 100.0%; Score 41; DB 14; Length 40673;
 Best Local Similarity 97.6%; Pred. No. 0.016;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCG 41
 |||||
 Db 24348 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCG 24388

RESULT 9
 AC142549 41489 bp DNA linear HTG 04-APR-2003
 LOCUS
 DEFINITION Homo sapiens chromosome 16 clone XXfos-81795G9, WORKING DRAFT
 SEQUENCE, 5 unordered pieces.
 AC142549
 AC142549.1 GI:29540584
 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 41489)
 DOE Joint Genome Institute.
 Sequencing of Human Chromosome 16
 Unpublished
 2 (bases 1 to 41489)
 DOE Joint Genome Institute.
 Direct Submission
 TITLE
 JOURNAL
 Submitted (04-APR-2003) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: http://www.jgi.doe.gov

 Project Information
 Center Project Name: 3436195
 Center clone name: WF-81795G9

 Summary Statistics
 Consensus quality: 39376 bases at least Q40
 Consensus quality: 39697 bases at least Q30
 Consensus quality: 39943 bases at least Q20

Estimated insert size: 40000; agarose-fp estimation
 Estimated insert size: 41089; sum-of-contigs estimation
 Quality coverage: 8.2 in Q20 bases; agarose-fp estimation
 Quality coverage: 7.98 in Q20 bases; sum-of-contigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

1 1669: contig of 1669 bp in length
 * 1670 1769: gap of unknown length
 * 1770 4523: contig of 2754 bp in length
 * 4524 4623: gap of unknown length
 * 4624 17325: contig of 12702 bp in length
 * 17326 17425: gap of unknown length
 * 17426 24658: contig of 7233 bp in length
 * 24659 24758: gap of unknown length
 * 24759 41489: contig of 16731 bp in length.

FEATURES
 Location/Qualifiers
 1..41489
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="XXfos-81795G9"
 1670..1769
 /estimated_length=unknown
 4524..4623
 /estimated_length=unknown
 17326..17425
 /estimated_length=unknown
 24659..24758
 /estimated_length=unknown

ORIGIN
 Query Match 100.0%; Score 41; DB 14; Length 41489;
 Best Local Similarity 97.6%; Pred. No. 0.016;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCG 41
 |||||
 Db 24485 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCG 24525

RESULT 10
 HSU24498 47934 bp DNA linear PRI 09-MAY-2002
 LOCUS
 DEFINITION Human autosomal dominant polycystic kidney disease protein 1 (PKD1)
 Gene.
 U24498
 U24498.1 GI:794297
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 47934)
 The International Polycystic Kidney Disease Consortium.
 Polycystic kidney disease: the complete structure of the PKD1 gene
 and its protein
 Cell 81 (2), 289-298 (1995)
 JOURNAL
 PUBLISHED 7736581
 REFERENCE
 2 (bases 1 to 47934)
 Glucksmann-Kuis, M.A.
 DIRECT SUBMISSION
 TITLE
 JOURNAL
 Submitted (10-APR-1995) M. Alexandra Glucksmann-Kuis, Genomics,
 Millennium Pharmaceuticals, 640 Memorial Drive, Cambridge, MA
 02139, USA
 Location/Qualifiers

source	1. .47934 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="16" /map="16p13.3"									
ORIGIN										
Query Match	100.0%; Score 41; DB 8; Length 47934;									
Best Local Similarity	97.6%; Pred. No. 0.016;									
Matches	40;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
QY	1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCG 41 									
Db	724 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCG 764 									
RESULT 11										
AX440497										
LOCUS	AX440497 53522 bp DNA linear PAT 28-JUN-2002									
DEFINITION	Sequence 1 from Patent WO0206529.									
ACCESSION	AX440497									
VERSION	AX440497.1 GI:21665301									
KEYWORDS	Homo sapiens (human)									
SOURCE	Homo sapiens									
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE	1									
AUTHORS	Germino,G.G., Watnick,T.J. and Phakdeekitcharoen,B.									
TITLE	Detection and treatment of polycystic kidney disease									
JOURNAL	Patent: WO 0206529-A 1 24-JAN-2002;									
FEATURES	The Johns Hopkins University School of Medicine (US)									
source	Location/Qualifiers									
1. .53522	/organism="Homo sapiens"									
/mol_type="genomic DNA"	/db_xref="taxon:9606"									
ORIGIN										
Query Match	100.0%; Score 41; DB 6; Length 53522;									
Best Local Similarity	97.6%; Pred. No. 0.016;									
Matches	40;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
QY	1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCG 41 									
Db	3300 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCG 3340 									
RESULT 12										
HUMPKD1GEN										
LOCUS	HUMPKD1GEN 53522 bp DNA linear PRI 10-MAY-2002									
DEFINITION	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds.									
ACCESSION	L39891									
VERSION	L39891.1 GI:790818									
KEYWORDS	polycystic kidney disease.									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	1									
AUTHORS	Ward,C.J., Peral,B., Hughes,J., Thomas,S., Gamble,V., MacCarthy,A.B., Sloane-Stanley,J., Buckle,V.J., Kearney,L., Higgs,D.R., Ratcliffe,P.J., Harris,P.C., Roelfsema,J.H., Spruit,L.L., Saris,J.J., Dauwerse,H.G., Peters,D.J.M., Breuning,M.H., Nellist,M., Brook-Carter,P.T., Maheshwar,M.M., Cordeiro,I., Santos,H., Cabral,P., Sampson,J.R., Janssen,B., Hesseling-Janssen,A.L.W., van den Ouweland,A.M.W., Eussen,B., Verhoeve,S., Lindhout,D. and Halley,D.J.J.									
TITLE	The polycystic kidney disease 1 gene encodes a 14 kb transcript and									

[illegible]

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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 41; DB 6; Length 53577;
Best Local Similarity 97.6%; Pred.No. 0.016;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATCCAGTCCCTCATCGTGGCCGCGCG 41
|||||
Db 3300 AAGCCTCCGGATCCAGTCCCTCATCGTGGCCGCGCG 3340

RESULT 18
AC140700      84562 bp      DNA      linear      HTG 28-FEB-2003
LOCUS      Homo sapiens chromosome 16 clone LA16C-304D8, WORKING DRAFT
DEFINITION      SEQUENCE, 5 unordered pieces.
ACCESSION      AC140700
VERSION      AC140700.1 GI:28603916
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 84562)
AUTHORS      DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 16
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 84562)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Submitted (28-FEB-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1216300
Center clone name: LANL-16C_304D8
-----
Summary Statistics
Consensus quality: 83255 bases at least Q40
Consensus quality: 83860 bases at least Q30
Consensus quality: 84027 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Estimated insert size: 84162; sum-of-contigs estimation
Quality coverage: 15.89 in Q20 bases; agarose-fp estimation
Quality coverage: 7.55 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 3092: contig of 3092 bp in length.
* 3093 3192: gap of unknown length
* 3193 19478: contig of 16286 bp in length
* 19479 36789: gap of unknown length
* 36790 36889: contig of 17211 bp in length
* 36890 57552: gap of unknown length
* 57553 84562: contig of 20663 bp in length
* 84562: gap of unknown length
* 84562: contig of 26910 bp in length.
* 84562
1. 84562
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"

FEATURES
source
1. 84562

/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16C-304D8"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
3093..3192
/estimated_length=unknown
19479..19578
/estimated_length=unknown
36790..36889
/estimated_length=unknown
57553..57652
/estimated_length=unknown

ORIGIN
Query Match      100.0%; Score 41; DB 14; Length 84562;
Best Local Similarity 97.6%; Pred.No. 0.014;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATCCAGTCCCTCATCGTGGCCGCGCG 41
|||||
Db 84456 AAGCCTCCGGATCCAGTCCCTCATCGTGGCCGCGCG 84496

RESULT 19
AC141231/c
LOCUS      AC141231
DEFINITION      Homo sapiens chromosome 16 clone LA16C-339B10, WORKING DRAFT
ACCESSION      AC141231
VERSION      AC141231.1 GI:28913011
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 84928)
AUTHORS      DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 16
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 84928)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1219638
Center clone name: LANL-16C_339B10
-----
Summary Statistics
Consensus quality: 83944 bases at least Q40
Consensus quality: 84247 bases at least Q30
Consensus quality: 84389 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Estimated insert size: 84628; sum-of-contigs estimation
Quality coverage: 18.18 in Q20 bases; agarose-fp estimation
Quality coverage: 8.59 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2589: contig of 2589 bp in length
* 2590 2689: gap of unknown length
```

```
* 2690 19595: contig of 16906 bp in length
* 19596 19695: gap of unknown length
* 19696 46734: contig of 27039 bp in length
* 46735 46834: gap of unknown length
* 46835 84928: contig of 38094 bp in length.
FEATURES
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    1..84928
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        /chromosome="16"
        /clone="LA16C-339B10"
        /clone_lib="Los Alamos human chromosome 16 cosmid
        libraries: LA16NC01 and LA16NC02"
        2590..2689
            /estimated_length=unknown
        gap
        19596..19695
            /estimated_length=unknown
        gap
        46735..46834
            /estimated_length=unknown
    ORIGIN
        Query Match      100.0%; Score 41; DB 14; Length 84928;
        Best Local Similarity 97.6%; Pred.No.0.014;
        Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCG 41
|||||
Db 19931 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCG 19891

RESULT 20
AC138966 89599 bp DNA linear HTG 21-JAN-2003
LOCUS Homo sapiens chromosome 16 clone RP11-921M23, WORKING DRAFT
DEFINITION SEQUENCE, 9 unordered pieces.
ACCESSION AC138966
VERSION AC138966.1 GI:27805378
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1648479
Center clone name: RPCI-11_921M23
-----
Summary Statistics
Consensus quality: 85343 bases at least Q40
Consensus quality: 86141 bases at least Q30
Consensus quality: 86639 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 89793; sum-of-contigs estimation
Quality coverage: 8.26 in Q20 bases; agarose-fp estimation
Quality coverage: 16.74 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
```

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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* this record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1131: contig of 1131 bp in length
* 1132 1231: gap of unknown length
* 1232 3226: contig of 1995 bp in length
* 3227 3326: gap of unknown length
* 3327 7532: contig of 4206 bp in length
* 7533 7632: gap of unknown length
* 7633 19088: contig of 11456 bp in length
* 19089 19188: gap of unknown length
* 19189 35501: contig of 16313 bp in length
* 35502 35601: gap of unknown length
* 35602 44326: contig of 8724 bp in length
* 44326 44426: gap of unknown length
* 44426 52314: contig of 7789 bp in length
* 52315 52315: gap of unknown length
* 52315 70547: contig of 18232 bp in length
* 70547 89599: gap of unknown length
* 70647 89599: contig of 18953 bp in length.
FEATURES
    Location/Qualifiers
    1..89599
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        /chromosome="16"
        /clone="RP11-921M23"
        /clone_lib="RPCI human BAC library 11"
        1132..1231
            /estimated_length=unknown
        gap
        3227..3326
            /estimated_length=unknown
        gap
        7533..7632
            /estimated_length=unknown
        gap
        19089..19188
            /estimated_length=unknown
        gap
        35502..35601
            /estimated_length=unknown
        gap
        44326..44426
            /estimated_length=unknown
        gap
        52315..52314
            /estimated_length=unknown
        gap
        70547..70646
            /estimated_length=unknown
    ORIGIN
        Query Match      100.0%; Score 41; DB 14; Length 89599;
        Best Local Similarity 97.6%; Pred.No.0.014;
        Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCG 41
|||||
Db 7144 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCG 7184

RESULT 21
AC010488/c 109340 bp DNA linear PRI 07-APR-2003
LOCUS Homo sapiens chromosome 16 clone CTD-2332D4, complete sequence.
DEFINITION AC010488
ACCESSION AC010488
VERSION AC010488.7 GI:28973804
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
```

```

JOURNAL      Unpublished
REFERENCE     2 (bases 1 to 109340)
AUTHORS       DOE Joint Genome Institute.
TITLE         Direct Submission
JOURNAL      Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
REFERENCE     Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
AUTHORS       3 (bases 1 to 109340)
TITLE         DOE Joint Genome Institute, Stanford Human Genome Center and Los
JOURNAL      Alamos National Laboratory.
REFERENCE     Direct Submission
AUTHORS       Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
TITLE         Drive, Walnut Creek, CA 94598, USA
JOURNAL      4 (bases 1 to 109340)
REFERENCE     DOE Joint Genome Institute, Stanford Human Genome Center and Los
AUTHORS       Alamos National Laboratory.
TITLE         Direct Submission
JOURNAL      Submitted (07-APR-2003) DOE Joint Genome Institute, 2800 Mitchell
REFERENCE     Drive, Walnut Creek, CA 94598, USA
AUTHORS       On Mar 15, 2003 this sequence version replaced gi:16924086.
TITLE         Draft Sequence Produced by DOE Joint Genome Institute
JOURNAL      Finishing Completed at Stanford Human Genome Center and Los Alamos
REFERENCE     National Laboratory
AUTHORS       www.sngc.stanford.edu
TITLE         Quality: Phrap Quality >=40 99.8% of Sequence;
JOURNAL      Estimated Total Number of Errors is 0.3.
REFERENCE     NOTE: Unsure number of dinucleotide repeats from 25789 to 26208.
AUTHORS       Forced join at 26030. The number of missing bases by PCR is 100.
TITLE         Location/Qualifiers
JOURNAL      1. .109340
REFERENCE     /organism="Homo sapiens"
AUTHORS       /mol_type="genomic DNA"
TITLE         /db_xref="taxon:9606"
JOURNAL      /chromosome="16"
REFERENCE     /clone="CTD-2332D4"
AUTHORS       25789..26208
TITLE         /note="NOTE: Unsure number of dinucleotide repeats from
JOURNAL      25789 to 26208. Forced join at 26030. The number of
REFERENCE     missing bases by PCR is 100."
AUTHORS
TITLE
JOURNAL
SOURCE
Query Match 100.0%; Score 41; DB 8; Length 109340;
Best Local Similarity 97.6%; Pred. No. 0.014;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCTCATCGTGGCCGCGCG 41
Db 42483 AAGCCTCCGATGCCAGTCCTCATCGTGGCCGCGCG 42443

RESULT 22
HUAC002039 127485 bp DNA linear PRI 30-OCT-2002
LOCUS Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 -complete
DEFINITION genomic sequence, complete sequence.
ACCESSION AC002039
VERSION AC002039.1 GI:2342716
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 127485)
AUTHORS Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,P., Brandon,R.,
Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,
Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S.,
Bichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.
TITLE Genome duplications and other features in 12 Mb of DNA sequence
JOURNAL from human chromosome 16p and 16q
PUBMED Genomics 60 (3), 295-308 (1999)
REFERENCE 10493829
2 (bases 1 to 127485)
AUTHORS Adams,M.D., Loftus,B.J., Zhou,L., LaBombard,M., Fuhrmann,J.,
Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
TITLE Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 #complete
JOURNAL genomic sequence
REFERENCE Unpublished
AUTHORS 3 (bases 1 to 127485)
TITLE Direct Submission
JOURNAL Submitted (29-APR-1997) The Institute for Genomic Research, 9712
REFERENCE Medical Center Dr., Rockville, MD 20850, USA
AUTHORS 4 (bases 1 to 127485)
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1997) The Institute for Genomic Research, 9712
REFERENCE Medical Center Dr., Rockville, MD 20850, USA
AUTHORS On Aug 26, 1997 this sequence version replaced gi:2341053.
TITLE Address all correspondence to:
JOURNAL Mark Adams
REFERENCE The Institute for Genomic Research
AUTHORS 9712 Medical Center Dr.
TITLE Rockville, MD 20850,USAe-mail address: mdadams@tigr.org. The bac
JOURNAL location is on chromosome BAC clone is located on human chromosome
REFERENCE 16p13.11. The orientation of the sequence is from SP6 end to T7
AUTHORS end.Genes were identified by a combination of five methods
JOURNAL including: XGRAIL (available by anonymous ftp from
REFERENCE arthur.epm.ornl.gov), Genefinder (Phil Green, University of
AUTHORS Washington), Genscan (Chris Burge,
JOURNAL http://genome.stanford.edu/~chris/GENSCANW.html
REFERENCE )
TITLE searches of the complete sequence against a peptide database, and
JOURNAL the Human gene Index database at TIGR
REFERENCE (http://www.tigr.org/tdb/hgi/hgi.html). A gene with homology to
AUTHORS another protein is annotated as the isolog of that protein. Genes
JOURNAL without peptide homology having spliced EST hits are termed
REFERENCE 'unknown protein'. Genes encoding tRNAs are predicted by
AUTHORS tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
TITLE Location/Qualifiers
JOURNAL 1. .127485
REFERENCE /organism="Homo sapiens"
AUTHORS /mol_type="genomic DNA"
TITLE /db_xref="taxon:9606"
JOURNAL /chromosome="16"
REFERENCE /map="16p13.11"
AUTHORS /clone="A-13F4"
JOURNAL 847..1095
REFERENCE /note="GB|G19453|G19453"
AUTHORS complement(945..967)
TITLE /rpt_family="AT_rich"
JOURNAL 1022..1156
REFERENCE /note="GB|G15446|G15446"
AUTHORS complement(2687..2979)
TITLE /rpt_family="AluSq"
JOURNAL repeat_region
REFERENCE complement(3206..3337)
AUTHORS /rpt_family="FLAM_C"
JOURNAL repeat_region
REFERENCE complement(3428..3480)
AUTHORS /rpt_family="(CA)n"
JOURNAL repeat_region
REFERENCE complement(3620..3827)
AUTHORS /rpt_family="MIR"
JOURNAL repeat_region
REFERENCE 4270..4672
AUTHORS /rpt_family="MLT1F"
JOURNAL repeat_region
REFERENCE 4840..4932
AUTHORS /rpt_family="MLT1F"
JOURNAL repeat_region
REFERENCE 5688..5977
AUTHORS /rpt_family="AluSc"
JOURNAL repeat_region
REFERENCE complement(6249..6556)
AUTHORS /rpt_family="AluJo"
JOURNAL repeat_region
REFERENCE complement(7173..7355)
AUTHORS /rpt_family="MER58A"
JOURNAL repeat_region
REFERENCE complement(7358..7658)
AUTHORS /rpt_family="AluSx"
JOURNAL repeat_region
REFERENCE complement(7725..8865)
AUTHORS /rpt_family="LINE2"
JOURNAL repeat_region
REFERENCE 8892..8946

```

```
repeat_region /rpt_family="L1" (TGA)n"
repeat_region 9149..9249
repeat_region /rpt_family="LMC3"
repeat_region 9318..9749
repeat_region /rpt_family="LMC3"
repeat_region complement(9750..10056)
repeat_region /rpt_family="AluSx"
repeat_region 10058..10491
repeat_region /rpt_family="LMC3"
repeat_region 10494..10797
repeat_region /rpt_family="AluJb"
repeat_region 10798..10967
repeat_region /rpt_family="AluJo"
repeat_region 11014..11078
repeat_region /rpt_family="LMC3"
repeat_region complement(11370..11574)
repeat_region /rpt_family="MERS5A"
repeat_region complement(11668..11970)
repeat_region /rpt_family="AluSx"
repeat_region complement(13440..13559)
repeat_region /rpt_family="CA)n"
repeat_region complement(14144..14572)
repeat_region /rpt_family="MERS7A"
repeat_region complement(14676..14832)
repeat_region /rpt_family="MIR"
repeat_region complement(15113..15410)
repeat_region /rpt_family="AluSx"
repeat_region complement(15426..15723)
repeat_region /rpt_family="AluJb"
repeat_region 15725..15822
repeat_region /rpt_family="MIR"
repeat_region complement(15865..15950)
repeat_region /rpt_family="GA)n"
repeat_region complement(16406..16663)
repeat_region /rpt_family="GC_rich"
misc_feature 16535..16595
note="Unresolved region of approximately 1000bp
containing GC repeat"
repeat_region 16845..16870
repeat_region /rpt_family="GC_rich"
repeat_region complement(17362..17470)
repeat_region /rpt_family="MIR"
repeat_region complement(19001..19299)
repeat_region /rpt_family="AluSp"
repeat_region complement(19504..19810)
repeat_region /rpt_family="AluSc"
repeat_region complement(19833..20130)
repeat_region /rpt_family="AluSp"
STS 19926..20043
repeat_region /note="GB|G02122|G02122"
repeat_region complement(20155..20251)
repeat_region /rpt_family="HY3"
repeat_region complement(20261..20551)
repeat_region /rpt_family="AluSx"
repeat_region complement(20576..20872)
repeat_region /rpt_family="AluY"
repeat_region complement(20889..21164)
misc_feature 21000..59000
note="Large duplication of approximately 38kb also
occurring between positions 60,000 and 102,000"
STS 21323..21422
repeat_region /note="GB|G25306|G25306"
repeat_region complement(21385..21678)
repeat_region /rpt_family="AluJo"
repeat_region 24433..24502
repeat_region /rpt_family="MIR"
repeat_region complement(28098..28134)
repeat_region /rpt_family="MIR"
repeat_region complement(31832..31890)
repeat_region /rpt_family="CAGG)n"
repeat_region complement(32323..32447)
repeat_region /rpt_family="GGGA)n"
```

```
misc_feature 32358..32408
note="region containing unresolved CT-repeat of
approximately 400bp"
repeat_region complement(32451..32573)
repeat_region /rpt_family="GGA)n"
repeat_region complement(32958..33010)
repeat_region /rpt_family="GC_rich"
misc_feature 33055..33105
note="Unresolved region of approximately 200 bp
containing CT repeat"
repeat_region complement(33120..33410)
repeat_region /rpt_family="GAA)n"
repeat_region complement(35689..35960)
repeat_region /rpt_family="AluSx"
repeat_region 36043..36343
repeat_region /rpt_family="AluY"
repeat_region 37805..37919
repeat_region /rpt_family="L1"
repeat_region 38065..38194
repeat_region /rpt_family="AluJo/FLAM"
repeat_region 38196..38496
repeat_region /rpt_family="AluSx"
repeat_region 38498..38621
repeat_region /rpt_family="L1"
repeat_region complement(38772..38812)
repeat_region /rpt_family="MER3"
repeat_region 38817..39122
repeat_region /rpt_family="AluSx"
repeat_region complement(39961..40264)
repeat_region /rpt_family="AluSg"
repeat_region complement(40350..40642)
repeat_region /rpt_family="AluSg"
repeat_region complement(42188..42346)

Query Match 100.0%; Score 41; DB 8; Length 127485;
Best Local Similarity 97.6%; Pred. No. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
Db 16355 AAGCTTCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 16395

RESULT 23
AC137642/c
LOCUS AC137642 131353 bp DNA linear HTG 03-DEC-2002
DEFINITION Homo sapiens chromosome 16 clone RP11-624C8, WORKING DRAFT
SEQUENCE, 10 unordered pieces.
ACCESSION AC137642
VERSION AC137642.2 GI:26006509
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 131353)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 131353)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (27-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 131353)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 3, 2002 this sequence version replaced gi:25698531.
-----Genome Center
Center: Joint Genome Institute
```

Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1534176
Center clone name: RPCI-11_624C8

Summary Statistics
Consensus quality: 127527 bases at least Q40
Consensus quality: 128577 bases at least Q30
Consensus quality: 129224 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Quality coverage: 8.79 in Q20 bases; agarose-fp estimation
Quality coverage: 10.78 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1566: contig of 1566 bp in length
1567 1666: gap of unknown length
1667 4256: contig of 2590 bp in length
4257 4356: gap of unknown length
4357 7659: contig of 3303 bp in length
7660 7759: gap of unknown length
7760 14250: contig of 6491 bp in length
14251 14350: gap of unknown length
14351 20962: contig of 6612 bp in length
20963 21062: gap of unknown length
21063 31690: contig of 10628 bp in length
31691 31790: gap of unknown length
31791 50658: contig of 18868 bp in length
50659 50758: gap of unknown length
50759 85243: contig of 34485 bp in length
85244 85344: gap of unknown length
85344 103268: contig of 17925 bp in length
103269 103369: gap of unknown length
103369 131353: contig of 27985 bp in length.

FEATURES
source

1. .131353
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone_lib="RPCI human BAC library 11"
1567. .1666
/estimated_length=unknown
4257. .4356
/estimated_length=unknown
7660. .7759
/estimated_length=unknown
14251. .14350
/estimated_length=unknown
20963. .21062
/estimated_length=unknown
31691. .31790
/estimated_length=unknown
50659. .50758
/estimated_length=unknown
85244. .85343
/estimated_length=unknown
103269. .103368
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 131353;
Best Local Similarity 97.6%; Pred.No. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGCGCG 41
|||||
Db 51077 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGCG 51037
|||||

RESULT 24
AC136427/c

LOCUS AC136427 145971 bp DNA linear PRI 18-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-103G5, complete sequence.
ACCESSION AC136427
VERSION AC136427.3 GI:29029243
KEYWORDS HTG.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE

1 (bases 1 to 145971)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission

TITLE

Unpublished

REFERENCE

2 (bases 1 to 145971)
DOE Joint Genome Institute.

AUTHORS

Direct Submission

TITLE

Submitted (01-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE

3 (bases 1 to 145971)
DOE Joint Genome Institute.

AUTHORS

Direct Submission

TITLE

Submitted (12-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE

4 (bases 1 to 145971)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.

AUTHORS

Direct Submission

TITLE

Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA

JOURNAL

On Mar 18, 2003 this sequence version replaced gi:24899410.

COMMENT

Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.ehgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
NOTE: Shatter libraries failed to verify the dinucleotide repeat
region 76038-76702. Unsure number of repeat copies 76038-76702.
Forced join at 76403.

FEATURES

Location/Qualifiers

source

1. .145971

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="16"

/clone="RP11-103G5"

76038. .76702

/note="NOTE: Shatter libraries failed to verify the
dinucleotide repeat region 76038-76702. Unsure number of
repeat copies 76038-76702. Forced join at 76403."

misc_feature

100.0%; Score 41; DB 8; Length 145971;

Best Local Similarity 97.6%; Pred.No. 0.013;

Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGCGCG 41
|||||

Db 93003 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGCGCG 92963
|||||

RESULT 25

```
AC133566/c
LOCUS          147573 bp      DNA      linear      HTG 14-SEP-2002
DEFINITION     Homo sapiens chromosome 16 clone RP11-93013, WORKING DRAFT
AC133566
AC133566
AC133566.1 GI:22857562
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1 (bases 1 to 147573)
AUTHORS        DOE Joint Genome Institute.
TITLE          Sequencing of Human Chromosome 16
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 147573)
AUTHORS        DOE Joint Genome Institute.
TITLE          Direct Submission
JOURNAL        Submitted (14-SEP-2002) Production Sequencing Facility, DOE Joint
               Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT        -----Genome Center
               Center: Joint Genome Institute
               Center Code: JGI
               Web site: http://www.jgi.doe.gov
               -----
Project Information
Center Project Name: 442426
Center clone name: RPCI-11_93013
               -----
Summary Statistics
Consensus quality: 139742 bases at least Q40
Consensus quality: 14376 bases at least Q30
Consensus quality: 145054 bases at least Q20
Estimated insert size: 145000; agarose-fp estimation
Estimated insert size: 146973; sum-of-contigs estimation
Quality coverage: 6.68 in Q20 bases; agarose-fp estimation
Quality coverage: 6.59 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1053: contig of 1053 bp in length
* 1054 1153: gap of unknown length
* 1154 2572: contig of 1419 bp in length
* 2573 2672: gap of unknown length
* 2673 12141: contig of 9469 bp in length
* 12142 12241: gap of unknown length
* 12242 20412: contig of 8171 bp in length
* 20413 20512: gap of unknown length
* 20513 33545: contig of 13033 bp in length
* 33546 33645: gap of unknown length
* 33646 68965: contig of 35320 bp in length
* 68966 69085: gap of unknown length
* 69086 147573: contig of 78508 bp in length.
               Location/Qualifiers
               1. .147573
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /chromosome="16"
               /clone="RP11-93013"
               /clone_lib="RPCI human BAC library 11"
               1054. _1153
               /estimated_length=unknown
               2573. .2672
               /estimated_length=unknown
               12142. .12241
               /estimated_length=unknown
```

```
20413. .20512
/estimated_length=unknown
33546. .33645
/estimated_length=unknown
68966. .69065
/estimated_length=unknown

ORIGIN
Query Match      100.0%; Score 41; DB 14; Length 147573;
Best Local Similarity 97.6%; Pred. No. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
    |||||
DB 34688 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 34648

RESULT 26
AC138949/c
LOCUS          148930 bp      DNA      linear      HTG 21-JAN-2003
DEFINITION     Homo sapiens chromosome 16 clone RP11-805F23, WORKING DRAFT
AC138949
AC138949.1 GI:27805361
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1 (bases 1 to 148930)
AUTHORS        DOE Joint Genome Institute.
TITLE          Sequencing of Human Chromosome 16
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 148930)
AUTHORS        DOE Joint Genome Institute.
TITLE          Direct Submission
JOURNAL        Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
               Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT        -----Genome Center
               Center: Joint Genome Institute
               Center Code: JGI
               Web site: http://www.jgi.doe.gov
               -----
Project Information
Center Project Name: 1603767
Center clone name: RPCI-11_805F23
               -----
Summary Statistics
Consensus quality: 143446 bases at least Q40
Consensus quality: 144466 bases at least Q30
Consensus quality: 145318 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 147730; sum-of-contigs estimation
Quality coverage: 9.82 in Q20 bases; agarose-fp estimation
Quality coverage: 11.97 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1211: contig of 1211 bp in length
* 1212 1311: gap of unknown length
* 1312 2482: contig of 1171 bp in length
* 2483 2583: gap of unknown length
* 2583 3798: contig of 1216 bp in length
* 3799 3899: gap of unknown length
* 3899 5487: contig of 1589 bp in length
* 5488 5588: gap of unknown length
* 5589 6870: contig of 1283 bp in length
```


* 6871 6970: gap of unknown length
 * 6971 10798: contig of 3828 bp in length
 * 10799 10898: gap of unknown length
 * 10899 13993: contig of 3095 bp in length
 * 13994 14093: gap of unknown length
 * 14094 22594: contig of 8501 bp in length
 * 22595 22694: gap of unknown length
 * 22695 28641: contig of 5947 bp in length
 * 28642 28741: gap of unknown length
 * 28742 40015: contig of 11274 bp in length
 * 40016 40115: gap of unknown length
 * 40116 58107: contig of 17992 bp in length
 * 58108 58207: gap of unknown length
 * 58208 79533: contig of 21326 bp in length
 * 79534 79634: gap of unknown length
 * 79634 148930: contig of 69297 bp in length.

FEATURES

source

1..148930
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-805F23"
 /clone_lib="RPCI human BAC library 11"
 1212..1311
 /estimated_length=unknown
 2483..2582
 /estimated_length=unknown
 3799..3898
 /estimated_length=unknown
 5488..5587
 /estimated_length=unknown
 6871..6970
 /estimated_length=unknown
 10799..10898
 /estimated_length=unknown
 13994..14093
 /estimated_length=unknown
 22595..22694
 /estimated_length=unknown
 28642..28741
 /estimated_length=unknown
 40016..40115
 /estimated_length=unknown
 58108..58207
 /estimated_length=unknown
 79534..79633
 /estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 148930;
 Best Local Similarity 97.6%; Pred. No. 0.013; Indels 0; Gaps 0;
 Matches 40; Conservative 1; Mismatches 0; Gaps 0;
 QY 1 AAGCCTCGGATCCGAGTCCTCATCGTGGCCGCGCG 41
 |||||
 Db 7189 AAGCCTCGGATCCGAGTCCTCATCGTGGCCGCGCG 7149

RESULT 27

AC138892

LOCUS

AC138892 Homo sapiens chromosome 16 clone RP11-43108, WORKING DRAFT
 SEQUENCE, 12 unordered pieces.

ACCESSION

AC138892

VERSION

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 152171)

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

DOE Joint Genome Institute.

Sequencing of Human Chromosome 16

Unpublished

2 (bases 1 to 152171)

DOE Joint Genome Institute.

Direct Submission

Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

-----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: http://www.jgi.doe.gov

Project Information

Center Project Name: 572213

Center clone name: RPCI-11_43108

Summary Statistics

Consensus quality: 147669 bases at least Q40

Consensus quality: 148410 bases at least Q30

Consensus quality: 149034 bases at least Q20

Estimated insert size: 180000; agarose-fp estimation

Quality coverage: 12.06 in Q20 bases; agarose-fp estimation

Quality coverage: 14.37 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 12 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1087: contig of 1087 bp in length

* 1088 1187: gap of unknown length

* 1188 2506: contig of 1319 bp in length

* 2507 2606: gap of unknown length

* 2607 4415: contig of 1809 bp in length

* 4416 4515: gap of unknown length

* 4516 6448: contig of 1933 bp in length

* 6449 6549: gap of unknown length

* 6549 7689: contig of 1140 bp in length

* 7689 9094: contig of 1306 bp in length

* 9095 9194: gap of unknown length

* 9195 11683: contig of 2489 bp in length

* 11684 11784: gap of unknown length

* 11784 14477: gap of unknown length

* 14477 23843: contig of 9266 bp in length

* 23843 23942: gap of unknown length

* 23943 34969: contig of 11026 bp in length

* 34969 72126: gap of unknown length

* 72127 72227: gap of unknown length

* 72227 152171: contig of 79945 bp in length.

* Location/Qualifiers

1..152171

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="16"

/clone="RP11-43108"

/clone_lib="RPCI human BAC library 11"

1088..1187

/estimated_length=unknown

2507..2606

/estimated_length=unknown

4416..4515

/estimated_length=unknown

6449..6548

/estimated_length=unknown

7689..7788

FEATURES

source

gap

gap

gap

gap

gap

gap

```

gap /estimated_length=unknown
9095..9194
/estimated_length=unknown
gap 11684..11783
/estimated_length=unknown
gap 14477..14576
/estimated_length=unknown
gap 23843..23942
/estimated_length=unknown
gap 34969..35068
/estimated_length=unknown
gap 72127..72226
/estimated_length=unknown

ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 152171;
Best Local Similarity 97.6%; Pred. NO. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCTCCGATGCCAGTCCTCATCGCTGGCCGCGCG 41
Db 53382 AAGCCTCCGATGCCAGTCCTCATCGCTGGCCGCGCG 53422

RESULT 28
AC139266 162264 bp DNA linear HTG 29-JAN-2003
LOCUS Homo sapiens chromosome 16 clone RP11-1438F19, WORKING DRAFT
DEFINITION AC139266
ACCESSION AC139266
VERSION AC139266.1 GI:28009412
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 162264)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 162264)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 2771965
Center clone name: RPCI-11_1438F19
-----
Summary Statistics
Consensus quality: 148324 bases at least Q40
Consensus quality: 150195 bases at least Q30
Consensus quality: 151673 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 159464; sum-of-contigs estimation
Quality coverage: 12.47 in Q20 bases; agarose-fp estimation
Quality coverage: 13.69 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1056: contig of 1056 bp in length
* 1057 1156: gap of unknown length

```

FEATURES

source

```

1..162264
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1438F19"
/clone_lib="RPCI human BAC library 11"
1057..1156
/estimated_length=unknown
2315..2414
/estimated_length=unknown
3609..3708
/estimated_length=unknown
4848..4947
/estimated_length=unknown
6079..6178
/estimated_length=unknown

```


gap /estimated_length=unknown
4465..4564
gap /estimated_length=unknown
6075..6174
gap /estimated_length=unknown
7742..7841
gap /estimated_length=unknown
8866..8965
gap /estimated_length=unknown
10251..10350
gap /estimated_length=unknown
11529..11628
gap /estimated_length=unknown
14062..14161
gap /estimated_length=unknown
17283..17382
gap /estimated_length=unknown
26903..27002
gap /estimated_length=unknown
42763..42862
gap /estimated_length=unknown
64562..64661
gap /estimated_length=unknown
89821..89920
gap /estimated_length=unknown
110576..110675
gap /estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 167184;
Best Local Similarity 97.6%; Pred.No.0.013; 0; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 41
|||||
Db 89670 AAGCTTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 89710
|||||

RESULT 30
AC138901
LOCUS
DEFINITION Homo sapiens chromosome 16 clone RP11-53114, *** SEQUENCING IN
PROGRESS ***, 5 ordered pieces.
AC138901
VERSION AC138901.3 GI:29336209
KEYWORDS HTG; HTGS_PHASE2; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 28, 2003 this sequence version replaced gi:28008527.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have

* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 53269: contig of 53269 bp in length
* 53270: gap of unknown length
* 53370: contig of 16422 bp in length
* 69791: gap of unknown length
* 69891: contig of 773 bp in length
* 69892: gap of unknown length
* 70665: contig of 89735 bp in length
* 70765: gap of unknown length
* 160500: contig of 7631 bp in length.
* 160600: 168230: contig of 7631 bp in length.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 610465
Center clone name: RP11-53114

Summary Statistics
Consensus quality: 166501 bases at least Q40
Consensus quality: 166789 bases at least Q30
Consensus quality: 166959 bases at least Q20
Estimated insert size: 167825; agarose-fp estimation
Estimated insert size: 167130; sum-of-contigs

estimation Quality coverage: 0.99 in Q20 bases; agarose-fp
estimation Quality coverage: 1 in Q20 bases; sum-of-contigs
estimation.

FEATURES
source

gap
gap
gap
gap

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 168230;
Best Local Similarity 97.6%; Pred.No.0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 41
|||||
Db 52969 AAGCTTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 53009
|||||

RESULT 31
AC139265
LOCUS
DEFINITION Homo sapiens chromosome 16 clone RP11-1428P22, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
AC139265
VERSION AC139265.1 GI:28009381
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 168408)

AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 168408)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 2768368
Center clone name: RPCI-11_1428P22

Summary Statistics
Consensus quality: 164984 bases at least Q40
Consensus quality: 165330 bases at least Q30
Consensus quality: 165596 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 167808; sum-of-contigs estimation
Quality coverage: 13.12 in Q20 bases; sum-of-contigs estimation
Quality coverage: 13.68 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1051: contig of 1051 bp in length
* 1052 1151: gap of unknown length
* 1152 2903: contig of 1752 bp in length
* 2904 3003: gap of unknown length
* 3004 5134: contig of 2131 bp in length
* 5135 5235: gap of unknown length
* 5236 21508: contig of 16274 bp in length
* 21509 39533: contig of 18045 bp in length
* 39534 39754: gap of unknown length
* 39755 78533: contig of 38780 bp in length
* 78534 78634: gap of unknown length
* 78635 168408: contig of 89775 bp in length.

FEATURES
source

1. .168408
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1428P22"
/clone_lib="RPCI human BAC library 11"
1052. .1151
/estimated_length=unknown
2904. .3003
/estimated_length=unknown
5135. .5234
/estimated_length=unknown
21509. .21608
/estimated_length=unknown
39654. .39753
/estimated_length=unknown
78534. .78633
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 168408;
Best Local Similarity 97.6%; Pred. No. 0.013; Gaps 0;
Matches 40; Conservative 1; Mismatches 0; Indels 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATGCTGGCCGCGCGC 41

Db 38926 AAGCCTCCGATGCCAGTCCCTCATGCTGGCCGCGCGC 38966
RESULT 32
AC142081/c
LOCUS
DEFINITION
AC142081 172474 bp DNA linear HTG 21-MAR-2003
SEQUENCE, 9 unordered pieces.
AC142081
AC142081.1 GI:29135556
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 172474)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 172474)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 2726990
Center clone name: RPCI-11_1321D20

Summary Statistics

Consensus quality: 169588 bases at least Q40
Consensus quality: 170176 bases at least Q30
Consensus quality: 170569 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 171674; sum-of-contigs estimation
Quality coverage: 13.27 in Q20 bases; agarose-fp estimation
Quality coverage: 13.61 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1068: contig of 1068 bp in length
* 1069 1168: gap of unknown length
* 1169 6747: contig of 5579 bp in length
* 6748 6847: gap of unknown length
* 6848 13485: contig of 6638 bp in length
* 13486 13585: gap of unknown length
* 13586 22941: contig of 9356 bp in length
* 22942 23041: gap of unknown length
* 23042 35439: contig of 12398 bp in length
* 35440 35539: gap of unknown length
* 35540 46853: contig of 11314 bp in length
* 46854 46953: gap of unknown length
* 46954 66628: contig of 19675 bp in length
* 66629 66729: gap of unknown length
* 66729 101269: contig of 34541 bp in length
* 101270 101369: gap of unknown length
* 101370 172474: contig of 71105 bp in length.

FEATURES
source

1. 172474
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

```
/chromosomes="16"
/clone="RP11-1321D20"
/clone_lib="RPCI human BAC library 11"
1069. .1168
gap /estimated_length=unknown
gap 6748. .6847
gap /estimated_length=unknown
gap 13486. .13585
gap /estimated_length=unknown
gap 22942. .23041
gap /estimated_length=unknown
gap 35440. .35539
gap /estimated_length=unknown
gap 46854. .46953
gap /estimated_length=unknown
gap 66629. .66728
gap /estimated_length=unknown
gap 101270. .101369
gap /estimated_length=unknown

ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 172474;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCGCGCGCG 41
|||||
Db 67062 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCGCGCGCG 67022
|||||

RESULT 33
AC141410/c
LOCUS AC141410 173775 bp DNA linear HTG 14-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-891N17, WORKING DRAFT
SEQUENCE 3 unordered pieces.
ACCESSION AC141410.1 GI:28951156
VERSION AC141410.1
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 173775)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
REFERENCE 2 (bases 1 to 173775)
DOE Joint Genome Institute.
Direct Submission
TITLE Submitted (14-MAR-2003) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
AUTHORS
CENTER: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1636977
Center clone name: RPCI-11_891N17
-----
Summary Statistics
Consensus quality: 172677 bases at least Q40
Consensus quality: 172933 bases at least Q30
Consensus quality: 173141 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 173575; sum-of-contigs estimation
Quality coverage: 16.15 in Q20 bases; agarose-fp estimation
Quality coverage: 16.74 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
* this record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1237: contig of 1237 bp in length
* 1238 1337: gap of unknown length
* 1338 78991: contig of 77654 bp in length
* 78992 173775: gap of unknown length
* 79092 173775: contig of 94684 bp in length.
Location/Qualifiers
FEATURES
1. 173775
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-891N17"
/clone_lib="RPCI human BAC library 11"
1238_1337
/estimated_length=unknown
78992..79091
/estimated_length=unknown

ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 173775;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCGCGCGCG 41
|||||
Db 95387 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCGCGCGCG 95347
|||||

RESULT 34
AC137806/c
LOCUS AC137806 177920 bp DNA linear HTG 03-DEC-2002
DEFINITION Homo sapiens chromosome 16 clone RP11-876J15, WORKING DRAFT
SEQUENCE 12 unordered pieces.
ACCESSION AC137806
VERSION AC137806.1 GI:26006548
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 177920)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
REFERENCE 2 (bases 1 to 177920)
DOE Joint Genome Institute.
Direct Submission
TITLE Submitted (03-DEC-2002) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
AUTHORS
CENTER: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1631119
Center clone name: RPCI-11_876J15
-----
Summary Statistics
Consensus quality: 173780 bases at least Q40
Consensus quality: 174683 bases at least Q30
Consensus quality: 175248 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 176820; sum-of-contigs estimation
Quality coverage: 11.17 in Q20 bases; agarose-fp estimation
Quality coverage: 10.1 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
```

* is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1 1526: contig of 1526 bp in length
1527 1626: gap of unknown length
1627 2737: contig of 1111 bp in length
2738 2837: gap of unknown length
2838 4892: contig of 2055 bp in length
4893 7232: gap of unknown length
7233 9840: contig of 2508 bp in length
9841 16612: contig of 6672 bp in length
16613 24572: contig of 7860 bp in length
24573 31339: contig of 6667 bp in length
31340 42416: contig of 10977 bp in length
42417 42516: gap of unknown length
42517 76997: contig of 34480 bp in length
76998 77097: gap of unknown length
77098 119504: contig of 42408 bp in length
119505 119604: gap of unknown length
119605 177920: contig of 58316 bp in length.

```

FEATURES

```

Source
1. .177920
  /organism="Homo sapiens"
  /mol_type="genomic DNA"
  /db_xref="taxon:9606"
  /chromosome="16"
  /clone="RP11-876J15"
  /clone_lib="RPC1 human BAC library 11"
1527. .1626
  /estimated_length=unknown
2738. .2837
  /estimated_length=unknown
4893. .4992
  /estimated_length=unknown
7233. .7332
  /estimated_length=unknown
9841. .9940
  /estimated_length=unknown
16613. .16712
  /estimated_length=unknown
24573. .24672
  /estimated_length=unknown
31340. .31439
  /estimated_length=unknown
42417. .42516
  /estimated_length=unknown
76997. .77096
  /estimated_length=unknown
119505. .119604
  /estimated_length=unknown

```

ORIGIN

```

Query Match      100.0%; Score 41; DB 14; Length 177920;
Best Local Similarity 97.6%; Pred. No. 0.012; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 0;

```

```

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 41
|||||
Db 42775 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 42735
|||||

```

```

RESULT 35
AC141465
LOCUS          AC141465          179399 bp    DNA    linear    HTG 27-MAR-2003

```

DEFINITION

Homo sapiens Chromosome 16 clone RP11-847E10, WORKING DRAFT
 SEQUENCE, 4 ordered pieces.

ACCESSION

AC141465

VERSION

AC141465.3 GI:29294006

KEYWORDS

HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

1 (bases 1 to 179399)
 DOE Joint Genome Institute.

AUTHORS

Sequencing of Human Chromosome 16

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 179399)
 DOE Joint Genome Institute.

AUTHORS

Direct Submission

JOURNAL

Submitted (16-MAR-2003) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE

3 (bases 1 to 179399)
 DOE Joint Genome Institute.

AUTHORS

Direct Submission

JOURNAL

Submitted (27-MAR-2003) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT

On Mar 27, 2003 this sequence version replaced gi:29171368.
 Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

```

-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 19943: contig of 19943 bp in length
* 19944 20443: gap of unknown length
* 20444 41569: contig of 21526 bp in length
* 41570 41669: gap of unknown length
* 41670 47815: contig of 6146 bp in length
* 47816 47915: gap of unknown length
* 47916 179399: contig of 131484 bp in length.

```

FEATURES

```

Location/Qualifiers
1. .179399
  /organism="Homo sapiens"
  /mol_type="genomic DNA"
  /db_xref="taxon:9606"
  /chromosome="16"
  /clone="RP11-847E10"
19944. .20043
  /estimated_length=unknown
41570. .41669
  /estimated_length=unknown
47816. .47915
  /estimated_length=unknown

```

ORIGIN

```

Query Match      100.0%; Score 41; DB 14; Length 179399;
Best Local Similarity 97.6%; Pred. No. 0.012; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 0;

```

```

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 41
|||||
Db 3639 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 3679
|||||

```

RESULT 36
AC141465/c
LOCUS
DEFINITION
AC141465 179399 bp DNA linear HTG 27-MAR-2003
Homo sapiens chromosome 16 clone RP11-847E10, WORKING DRAFT
SEQUENCE, 4 ordered pieces.
AC141465
AC141465.3 GI:29294006
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 179399)
DOE Joint Genome Institute.
TITLE
Sequencing of Human Chromosome 16
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 179399)
DOE Joint Genome Institute.
TITLE
Direct Submission
JOURNAL
Submitted (16-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 179399)
DOE Joint Genome Institute.
TITLE
Direct Submission
JOURNAL
Submitted (27-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 27, 2003 this sequence version replaced gi:29171368.
COMMENT
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 19943: contig of 19943 bp in length
* 19944 20043: gap of unknown length
* 20044 41569: contig of 21526 bp in length
* 41570 41659: gap of unknown length
* 41670 47815: contig of 6146 bp in length
* 47816 47915: gap of unknown length
* 47916 179399: contig of 131484 bp in length.
FEATURES
source
1. .179399
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-847E10"
19944..20043
/estimated_length=unknown
41570..41569
/estimated_length=unknown
47816..47915
/estimated_length=unknown
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 179399;
Best Local Similarity 97.6%; Pred. No. 0.012;

Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCTTCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|||||
Db 126482 AAGCTTCGGATGCCAGTCCCTCATCGTGGCCCGTGGCG 126442
|||||
RESULT 37
AC141616/c
LOCUS
DEFINITION
AC141616 179754 bp DNA linear HTG 18-MAR-2003
Homo sapiens chromosome 16 clone RP11-958M13, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
AC141616
AC141616.1 GI:29029201
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 179754)
DOE Joint Genome Institute.
TITLE
Sequencing of Human Chromosome 16
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 179754)
DOE Joint Genome Institute.
TITLE
Direct Submission
JOURNAL
Submitted (18-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1662677
Center clone name: RPCI-11_958M13

Summary Statistics
Consensus quality: 175245 bases at least Q40
Consensus quality: 176826 bases at least Q30
Consensus quality: 177518 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 179054; sum-of-contigs estimation
Quality coverage: 10.49 in Q20 bases; agarose-fp estimation
Quality coverage: 10.25 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 6779: contig of 6779 bp in length
* 6780 6879: gap of unknown length
* 6880 14927: contig of 8048 bp in length
* 14928 15027: gap of unknown length
* 15028 31236: contig of 16209 bp in length
* 31237 31336: gap of unknown length
* 31337 45749: contig of 14413 bp in length
* 45750 45849: gap of unknown length
* 45850 64995: contig of 19146 bp in length
* 64996 65095: gap of unknown length
* 65096 99462: contig of 34367 bp in length
* 99463 99562: gap of unknown length
* 99563 134459: contig of 34897 bp in length
* 134460 134559: gap of unknown length
* 134560 179754: contig of 45195 bp in length.
FEATURES
Location/Qualifiers
1. .179754
/organism="Homo sapiens"
/mol_type="genomic DNA"


```

/db_xref="taxon:9606"
/chromosome="16"
/clone_lib="RPCI human BAC library 11"
6780_-6879
/estimated_length=unknown
14928_.15027
/estimated_length=unknown
31237_.31336
/estimated_length=unknown
45750_.45849
/estimated_length=unknown
64996_.65095
/estimated_length=unknown
99463_.99562
/estimated_length=unknown
134460_.134559
/estimated_length=unknown

ORIGIN
Query Match          100.0%;   Score 41;   DB 14;   Length 179754;
Best Local Similarity 97.6%;   Pred. No. 0.012;   Indels 0;   Gaps 0;
Matches 40;   Conservative 1;   Mismatches 0;

QY 1 AAGCTCCGATGCCAGTCCCTCATCGTCGCGCCGCGCG 41
|||||
Db 65147 AAGCTCCGATGCCAGTCCCTCATCGTCGCGCCGCGCG 65107
|||||

RESULT 38
AC138932/c
LOCUS
DEFINITION
AC138932 Homo sapiens chromosome 16 clone RP11-680G24, linear PRI 07-APR-2003
AC138932.4 GI:29570376
HTG.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 180798)
DOE Joint Genome Institute.
DIRECT SUBMISSION
SUBMITTED (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 180798)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
DIRECT SUBMISSION
SUBMITTED (28-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 180798)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
DIRECT SUBMISSION
SUBMITTED (07-APR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Apr 7, 2003 this sequence version replaced gi:29336210.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
NOTE: Unresolved dinucleotide repeat region 111025-111533. Unsure
number of repeat copies 111025-111533. Forced join 111355.

/db_xref="taxon:9606"
/chromosome="16"
/clone_lib="RPCI human BAC library 11"
6780_-6879
/estimated_length=unknown
14928_.15027
/estimated_length=unknown
31237_.31336
/estimated_length=unknown
45750_.45849
/estimated_length=unknown
64996_.65095
/estimated_length=unknown
99463_.99562
/estimated_length=unknown
134460_.134559
/estimated_length=unknown

ORIGIN
Query Match          100.0%;   Score 41;   DB 8;   Length 180798;
Best Local Similarity 97.6%;   Pred. No. 0.012;   Indels 0;   Gaps 0;
Matches 40;   Conservative 1;   Mismatches 0;

QY 1 AAGCTCCGATGCCAGTCCCTCATCGTCGCGCCGCGCG 41
|||||
Db 127830 AAGCTCCGATGCCAGTCCCTCATCGTCGCGCCGCGCG 127790
|||||

RESULT 39
AC138903/c
LOCUS
DEFINITION
AC138903 Homo sapiens chromosome 16 clone RP11-566I3, WORKING DRAFT
AC138903.2 GI:29150348
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 181231)
DOE Joint Genome Institute.
DIRECT SUBMISSION
SUBMITTED (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 181231)
DOE Joint Genome Institute.
DIRECT SUBMISSION
SUBMITTED (22-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 22, 2003 this sequence version replaced gi:27805315.
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
-----
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces

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* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 41176: contig of 41176 bp in length
* 41177: gap of unknown length
* 41277 181231: contig of 139955 bp in length.
Location/Qualifiers
1. .181231
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-56613"
41177. .41276
/estimated_length=unknown
gap
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 181231;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGATGCCAGTCCTCATCGCTGCCGCCGCGCG 41
|||||
Db 57793 AAGCCTCCGATGCCAGTCCTCATCGCTGCCGCCGCGCG 57753
|||||
RESULT 40
AC142195/c
LOCUS AC142195.1 183215 bp DNA linear HTG 25-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-1006H4, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
ACCESSION AC142195.1 GI:29171371
VERSION AC142195
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 183215)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 183215)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1680980
Center clone name: RPCI-11_1006H4

Summary Statistics
Consensus quality: 181858 bases at least Q40
Consensus quality: 182021 bases at least Q30
Consensus quality: 182181 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 182915; sum-of-contigs estimation
Quality coverage: 15.08 in Q20 bases; agarose-fp estimation
Quality coverage: 14.84 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 16451: contig of 16451 bp in length
* 16452 16551: gap of unknown length
* 16552 51103: contig of 34552 bp in length
* 51104 51203: gap of unknown length
* 51204 107468: contig of 56265 bp in length
* 107469 107568: gap of unknown length
* 107569 183215: contig of 75647 bp in length.
Location/Qualifiers
1. .183215
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1006H4"
/clone_lib="RPCI human BAC library 11"
16452..16551
/estimated_length=unknown
51104..51203
/estimated_length=unknown
107469..107568
/estimated_length=unknown
gap
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 183215;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGATGCCAGTCCTCATCGCTGCCGCCGCGCG 41
|||||
Db 16793 AAGCCTCCGATGCCAGTCCTCATCGCTGCCGCCGCGCG 16753
|||||
RESULT 41
AC141266/c
LOCUS AC141266.1 183537 bp DNA linear HTG 11-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-1357B21, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
ACCESSION AC141266.1 GI:28913046
VERSION AC141266
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 183537)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 183537)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 2740767
Center clone name: RPCI-11_1357B21

Summary Statistics
Consensus quality: 178517 bases at least Q40
Consensus quality: 179942 bases at least Q30
Consensus quality: 180636 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 182837; sum-of-contigs estimation
Quality coverage: 10.29 in Q20 bases; agarose-fp estimation

Quality coverage: 9.9 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

* 1 1161: contig of 1161 bp in length
* 1162 1261: gap of unknown length
* 1262 2521: contig of 1260 bp in length
* 2522 2621: gap of unknown length
* 2622 5829: contig of 3208 bp in length
* 5830 5929: gap of unknown length
* 5930 9996: contig of 4067 bp in length
* 9997 10096: gap of unknown length
* 10097 15804: contig of 5708 bp in length
* 15805 15904: gap of unknown length
* 15905 27778: contig of 11874 bp in length
* 27779 70728: gap of unknown length
* 70729 70828: contig of 42850 bp in length
* 70829 183537: gap of unknown length
* 70830 183537: contig of 112709 bp in length.

```

FEATURES

source

```

1. .183537
   /organism="Homo sapiens"
   /mol_type="genomic DNA"
   /db_xref="taxon:9606"
   /chromosome="16"
   /clone_lib="RPCI human BAC library 11"
   /estimated_length=unknown
2522: .2621
   /estimated_length=unknown
5830: .5929
   /estimated_length=unknown
9997: .10096
   /estimated_length=unknown
15805: .15904
   /estimated_length=unknown
27779: .27878
   /estimated_length=unknown
70729: .70828
   /estimated_length=unknown

```

ORIGIN

```

Query Match      100.0%; Score 41; DB 14; Length 183537;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGCG 41
    |||||
Db 71080 AAGCCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGCG 71040
    |||||

RESULT 42
AC139258/c
LOCUS
DEFINITION
  Homo sapiens chromosome 16 clone RP11-1228E2, WORKING DRAFT
ACCESSION
  AC139258.2
VERSION
  HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1 (bases 1 to 187226)
  DOE Joint Genome Institute.
  Sequencing of Human Chromosome 16

```

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

2 (bases 1 to 187226)

DOE Joint Genome Institute.

Direct Submission

Submitted (29-JAN-2003) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

3 (bases 1 to 187226)

DOE Joint Genome Institute.

Direct Submission

Submitted (21-FEB-2003) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Feb 21, 2003 this sequence version replaced gi:28009167.

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

* NOTE: This is a 'working draft' sequence. It currently

consists of 3 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

been provided by the submitter.

* This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.

* 1 4513: contig of 4513 bp in length

* 4514 4613: gap of unknown length

* 4614 94503: contig of 89890 bp in length

* 94504 94603: gap of unknown length

* 94604 187226: contig of 92623 bp in length.

* Location/Qualifiers

1. .187226

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="16"

/clone="RP11-1228E2"

4514: .4613

/estimated_length=unknown

94504: .94603

/estimated_length=unknown

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 41; DB 14; Length 187226;

Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGCG 41

|||||

Db 111119 AAGCCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGCG 111079

|||||

RESULT 43

AC141304

LOCUS

DEFINITION

188734 bp DNA linear HTG 11-MAR-2003

Homo sapiens chromosome 16 clone RP11-800P6, WORKING DRAFT

SEQUENCE, 12 unordered pieces.

```
AC141304
AC141304.1 GI:28913084
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
REFERENCE
  1 (bases 1 to 188734)
  DOE Joint Genome Institute.
  Sequencing of Human Chromosome 16
  Unpublished
REFERENCE
  2 (bases 1 to 188734)
  DOE Joint Genome Institute.
  Direct Submission
  Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
  Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
  -----Genome Center
  Center: Joint Genome Institute
  Center Code: JGI
  Web site: http://www.jgi.doe.gov
  -----
Project Information
Center Project Name: 1602070
Center clone name: RPCI-11_800P6
-----
Summary Statistics
Consensus quality: 179991 bases at least Q40
Consensus quality: 182288 bases at least Q30
Consensus quality: 183598 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 187634; sum-of-contigs estimation
Quality coverage: 10.73 in Q20 bases; agarose-fp estimation
Quality coverage: 10.07 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1144: contig of 1144 bp in length
* 1145 1244: gap of unknown length
* 1245 2328: contig of 1084 bp in length
* 2329 3544: gap of unknown length
* 3545 3644: contig of 1116 bp in length
* 3645 4797: contig of unknown length
* 4798 4897: contig of 1153 bp in length
* 4898 6155: gap of unknown length
* 6156 6255: contig of 1258 bp in length
* 6256 7347: contig of unknown length
* 7347 7446: contig of 1091 bp in length
* 7447 8754: contig of 1308 bp in length
* 8755 8854: gap of unknown length
* 8855 9987: contig of 1132 bp in length
* 9988 10086: contig of unknown length
* 10087 25546: contig of 15460 bp in length
* 25547 25646: gap of unknown length
* 25647 43662: contig of 18016 bp in length
* 43663 43762: gap of unknown length
* 43763 106056: contig of 62294 bp in length
* 106057 106156: gap of unknown length
* 106157 188734: contig of 82578 bp in length.
  Location/Qualifiers
    1. .188734
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /chromosome="16"
      /clone_lib="RPCI-800P6"
      /clone_lib="RPCI human BAC library 11"
FEATURES
  source
```

```
gap
1145..1244
/estimated_length=unknown
gap
2329..2428
/estimated_length=unknown
gap
3545..3644
/estimated_length=unknown
gap
4798..4897
/estimated_length=unknown
gap
6156..6255
/estimated_length=unknown
gap
7347..7446
/estimated_length=unknown
gap
8755..8854
/estimated_length=unknown
gap
9987..10086
/estimated_length=unknown
gap
25547..25646
/estimated_length=unknown
gap
43663..43762
/estimated_length=unknown
gap
106057..106156
/estimated_length=unknown
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 188734;
Best Local Similarity 97.6%; Pred.No. 0.012; 0; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCGCG 41
|||||
Db 105107 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCGCG 105147
|||||
RESULT 44
AC141613/c
LOCUS
DEFINITION
  Homo sapiens chromosome 16 clone RP11-837F19, WORKING DRAFT
AC141613
ACCESSION
  AC141613.1 GI:29029198
VERSION
  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS
  Homo sapiens (human)
SOURCE
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  1 (bases 1 to 194670)
  DOE Joint Genome Institute.
  Sequencing of Human Chromosome 16
  Unpublished
  2 (bases 1 to 194670)
  DOE Joint Genome Institute.
  Direct Submission
  Submitted (18-MAR-2003) Production Sequencing Facility, DOE Joint
  Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
  -----Genome Center
  Center: Joint Genome Institute
  Center Code: JGI
  Web site: http://www.jgi.doe.gov
  -----
Project Information
Center Project Name: 1616051
Center clone name: RPCI-11_837F19
-----
Summary Statistics
Consensus quality: 191315 bases at least Q40
Consensus quality: 191814 bases at least Q30
Consensus quality: 192245 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 194070; sum-of-contigs estimation
Quality coverage: 13.92 in Q20 bases; agarose-fp estimation
Quality coverage: 12.63 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
```

* consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1 1051: contig of 1051 bp in length
* 1052 1151: gap of unknown length
* 1052 10992: contig of 9841 bp in length
* 10993 11092: gap of unknown length
* 11093 18333: contig of 7241 bp in length
* 18334 18433: gap of unknown length
* 18434 31888: contig of 13455 bp in length
* 31889 31988: gap of unknown length
* 31989 55558: contig of 23570 bp in length
* 55559 55658: gap of unknown length
* 55659 121024: contig of 65366 bp in length
* 121025 121124: gap of unknown length
* 121125 194670: contig of 73546 bp in length.

```

FEATURES

```

source
1. .194670
   /organism="Homo sapiens"
   /mol_type="genomic DNA"
   /db_xref="taxon:9606"
   /chromosome="16"
   /clone="RP11-837F19"
   /clone_lib="RPCI human BAC library 11"
1052..1151
   /estimated_length=unknown
10993..11092
   /estimated_length=unknown
18334..18433
   /estimated_length=unknown
31889..31988
   /estimated_length=unknown
55559..55658
   /estimated_length=unknown
121025..121124
   /estimated_length=unknown

```

ORIGIN

```

Query Match      100.0%; Score 41; DB 14; Length 194670;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AAGCTCCGATGCCAGTCCCTCATCGTCGCCGCGCG 41
    |||||
Db 48312 AAGCTCCGATGCCAGTCCCTCATCGTCGCCGCGCG 48272

```

RESULT 45

```

AC009065 AC009065 199759 bp DNA linear PRI 15-MAR-2003
LOCUS Homo sapiens chromosome 16 clone RP11-304L19, complete sequence.
DEFINITION
ACCESSION AC009065
VERSION AC009065.8 GI:28973803
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

```

```

1 (bases 1 to 199759)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Unpublished

```

REFERENCE

```

DOE Joint Genome Institute.
DOE Joint Genome Institute.
Direct Submission

```

AUTHORS

```

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

```

REFERENCE

```

3 (bases 1 to 199759)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 15, 2003 this sequence version replaced gi:13786295.
Draft Sequence produced by DOE Joint Genome Institute
www.jgi.doe.gov

```

COMMENT

```

Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.sngc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
NOTE: Unsure number of dinucleotide repeat copies from
172446-172529. Forced join at 172492.

```

FEATURES

```

source
1. .199759
   /organism="Homo sapiens"
   /mol_type="genomic DNA"
   /db_xref="taxon:9606"
   /chromosome="16"
   /clone="RP11-304L19"
   /clone_lib="RPCI human BAC library 11"
172446..172529
   /estimated_length=unknown
172446..172529
   /estimated_length=unknown
18334..18433
   /estimated_length=unknown
31889..31988
   /estimated_length=unknown
55559..55658
   /estimated_length=unknown
121025..121124
   /estimated_length=unknown

```

misc_feature

```

172446..172529
   /note="NOTE: Unsure number of dinucleotide repeat copies
from 172446-172529. Forced join at 172492."

```

ORIGIN

```

Query Match      100.0%; Score 41; DB 8; Length 199759;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AAGCTCCGATGCCAGTCCCTCATCGTCGCCGCGCG 41
    |||||
Db 141374 AAGCTCCGATGCCAGTCCCTCATCGTCGCCGCGCG 141414

```

RESULT 46

```

AC141468/c AC141468 202656 bp DNA linear HTG 16-MAR-2003
LOCUS Homo sapiens chromosome 16 clone RP11-954C1, WORKING DRAFT
DEFINITION
ACCESSION AC141468
VERSION AC141468.1 GI:28975021
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

```

```

1 (bases 1 to 202656)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished

```

REFERENCE

```

DOE Joint Genome Institute.
DOE Joint Genome Institute.
Direct Submission

```

AUTHORS

```

Submitted (16-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

```

COMMENT

```

-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

```

Project Information

```

Center Project Name: 1660899
Center clone name: RPCI-11_954C1

```

Summary Statistics

```

Consensus quality: 194148 bases at least Q40
Consensus quality: 196921 bases at least Q30
Consensus quality: 198190 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation

```

Estimated insert size: 201356; sum-of-contigs estimation
Quality coverage: 9.93 in Q20 bases; agarose-fp estimation
Quality coverage: 8.68 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1000: contig of 1000 bp in length
* 1001: gap of unknown length
* 1101: contig of 1360 bp in length
* 2460: gap of unknown length
* 2561: contig of 2360 bp in length
* 4921: gap of unknown length
* 5021: contig of 4589 bp in length
* 9609: gap of unknown length
* 9710: contig of 4786 bp in length
* 14495: gap of unknown length
* 14596: contig of 7237 bp in length
* 21832: gap of unknown length
* 32172: contig of 10240 bp in length
* 32272: gap of unknown length
* 49575: contig of 17303 bp in length
* 49675: gap of unknown length
* 64516: contig of 14841 bp in length
* 64616: gap of unknown length
* 85275: contig of 20659 bp in length
* 85375: gap of unknown length
* 106615: contig of 21240 bp in length
* 106715: gap of unknown length
* 126404: contig of 19689 bp in length
* 126405: gap of unknown length
* 126505: contig of 26372 bp in length
* 152877: gap of unknown length
* 152977: contig of 49680 bp in length.

FEATURES
source

1. .202656
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone_lib="RP11-954C1"
/clone_lib="RP11-954C1"
1001. .1100
/estimated_length=unknown
2461. .2560
/estimated_length=unknown
4921. .5020
/estimated_length=unknown
9610. .9709
/estimated_length=unknown
14496. .14595
/estimated_length=unknown
21833. .21932
/estimated_length=unknown
32173. .32272
/estimated_length=unknown
49576. .49675
/estimated_length=unknown
64517. .64616
/estimated_length=unknown
85276. .85375
/estimated_length=unknown
106616. .106715
/estimated_length=unknown
126405. .126504
/estimated_length=unknown
152877. .152976
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 202656;
Best Local Similarity 97.6%; Pred.No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCGGATGCCAGTCCCTCATCGCTGCGCCGCGCGC 41
|||||
Db 106967 AAGCCTCGGATGCCAGTCCCTCATCGCTGCGCCGCGCGC 106927
|||||

RESULT 47
AC141411/c
LOCUS AC141411 202882 bp DNA linear HTG 14-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-908J13, WORKING DRAFT
SEQUENCE AC141411 6 unordered pieces.
ACCESSION AC141411
VERSION AC141411.1 GI:28951157
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 202882)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 202882)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1643405
Center clone name: RP11-908J13

Summary Statistics
Consensus quality: 200623 bases at least Q40
Consensus quality: 200957 bases at least Q30
Consensus quality: 201268 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 202382; sum-of-contigs estimation
Quality coverage: 10.09 in Q20 bases; agarose-fp estimation
Quality coverage: 8.98 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 3071: contig of 3071 bp in length
* 3072: gap of unknown length
* 3172: contig of 12955 bp in length
* 16126: gap of unknown length
* 16127: contig of 22338 bp in length
* 16227: gap of unknown length
* 38565: contig of 35003 bp in length
* 73667: gap of unknown length
* 73668: contig of 64657 bp in length
* 138425: gap of unknown length
* 138525: contig of 64358 bp in length.
-----Location/Qualifiers
1. .202882
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

```

/chromosome="16"
/clone="RP11-908J13"
/clone_lib="RPC1 human BAC library 11"
3072..3171
/estimated_length=unknown
16127..16226
/estimated_length=unknown
38565..38664
/estimated_length=unknown
73668..73767
/estimated_length=unknown
138425..138524
/estimated_length=unknown

Query Match      100.0%; Score 41; DB 14; Length 202882;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCG 41
|||||
Db 38970 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCG 38930
|||||

FEATURES
      source
      1..204500
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /chromosome="16"
      /clone_lib="RPC1 human BAC library 11"
      1080..1179
      /estimated_length=unknown
      2334..2433
      /estimated_length=unknown
      4476..4575
      /estimated_length=unknown
      7755..7854
      /estimated_length=unknown
      14690..14789
      /estimated_length=unknown
      20824..20923
      /estimated_length=unknown
      25586..25685
      /estimated_length=unknown
      31076..31175
      /estimated_length=unknown
      41944..42043
      /estimated_length=unknown
      61501..61600
      /estimated_length=unknown
      101722..101821
      /estimated_length=unknown
      132226..132325
      /estimated_length=unknown

ORIGIN
Query Match      100.0%; Score 41; DB 14; Length 204500;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCG 41
|||||
Db 101600 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCG 101640
|||||

RESULT 49
AC141253/c
LOCUS AC141253
DEFINITION Homo sapiens chromosome 16 clone RP11-126903, WORKING DRAFT
ACCESSION AC141253
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 204500)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 204500)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 2749953
Center clone name: RPC1-11_1381A15
-----
Summary Statistics
Consensus quality: 192455 bases at least Q40
Consensus quality: 197383 bases at least Q30
Consensus quality: 199302 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Quality coverage: 7.7 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.66 in Q20 bases; agarose-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 1079: contig of 1079 bp in length
* 1080 1179: gap of unknown length

```

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 204638)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 204638)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 2707269
Center clone name: RPCI-11_126903

Summary Statistics
Consensus quality: 199061 bases at least Q40
Consensus quality: 200424 bases at least Q30
Consensus quality: 201383 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 203438; sum-of-contigs estimation
Quality coverage: 11.16 in Q20 bases; agarose-fp estimation
Quality coverage: 9.65 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1075: contig of 1075 bp in length
* 1076 1175: gap of unknown length
* 1176 2298: contig of 1123 bp in length
* 2298 2399: gap of unknown length
* 2399 4411: contig of 2013 bp in length
* 4411 4511: gap of unknown length
* 4511 6238: contig of 1727 bp in length
* 6238 6339: gap of unknown length
* 6339 10193: contig of 3855 bp in length
* 10193 10294: gap of unknown length
* 10294 17059: contig of 6766 bp in length
* 17059 17159: gap of unknown length
* 17160 24203: contig of 7044 bp in length
* 24203 24303: gap of unknown length
* 24303 24304: gap of 5556 bp in length
* 24304 29859: contig of 5556 bp in length
* 29859 29959: gap of unknown length
* 29959 35329: contig of 5370 bp in length
* 35329 35430: gap of unknown length
* 35430 46589: contig of 11160 bp in length
* 46589 46689: gap of unknown length
* 46689 59464: contig of 12775 bp in length
* 59464 59565: gap of unknown length
* 59565 93991: contig of 34427 bp in length
* 93991 94091: gap of unknown length
* 94091 204638: contig of 110547 bp in length.
FEATURES
source Location/Qualifiers
1..204638
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-126903"
/clone_lib="RPCI human BAC library 11"

gap 1076..1175
/estimated_length=unknown
gap 2299..2398
/estimated_length=unknown
gap 4412..4511
/estimated_length=unknown
gap 6239..6338
/estimated_length=unknown
gap 10194..10293
/estimated_length=unknown
gap 17060..17159
/estimated_length=unknown
gap 24204..24303
/estimated_length=unknown
gap 29860..29959
/estimated_length=unknown
gap 35330..35429
/estimated_length=unknown
gap 46590..46689
/estimated_length=unknown
gap 59465..59564
/estimated_length=unknown
gap 93992..94091
/estimated_length=unknown
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 204638;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCG 41
|||||
DB 59769 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCG 59729
|||||
RESULT 50
AC141607 215974 bp DNA linear HTG 18-MAR-2003
Homo sapiens chromosome 16 clone RP11-644A22, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
AC141607
AC141607.1 GI:29029192
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 215974)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 215974)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1541822
Center clone name: RPCI-11_644A22

Summary Statistics
Consensus quality: 210022 bases at least Q40
Consensus quality: 211176 bases at least Q30
Consensus quality: 212214 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 214874; sum-of-contigs estimation
Quality coverage: 7.64 in Q20 bases; agarose-fp estimation

Quality coverage: 6.26 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1006: contig of 1006 bp in length
 * 1007 1106: gap of unknown length
 * 1107 2415: contig of 1309 bp in length
 * 2416 2515: gap of unknown length
 * 2516 7493: contig of 4978 bp in length
 * 7494 7593: gap of unknown length
 * 7594 14882: contig of 7289 bp in length
 * 14883 14983: gap of unknown length
 * 14983 25966: contig of 10984 bp in length
 * 25967 26066: gap of unknown length
 * 26067 37590: contig of 11523 bp in length
 * 37590 37690: gap of unknown length
 * 37690 52557: contig of 14868 bp in length
 * 52558 52657: gap of unknown length
 * 52658 70475: contig of 17817 bp in length
 * 70475 70574: gap of unknown length
 * 70575 86827: contig of 16253 bp in length
 * 86828 123298: gap of unknown length
 * 86928 123298: contig of 36371 bp in length
 * 123299 123399: gap of unknown length
 * 123399 159741: contig of 36343 bp in length
 * 159741 159842: gap of unknown length
 * 159842 215974: contig of 56133 bp in length.

FEATURES

source

1. 215974
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-644A22"
 /clone_lib="RPC1 human BAC library 11"
 /clone_1106
 1007..1106
 /estimated_length=unknown
 2416..2515
 /estimated_length=unknown
 7494..7593
 /estimated_length=unknown
 14883..14982
 /estimated_length=unknown
 25967..26066
 /estimated_length=unknown
 37590..37689
 /estimated_length=unknown
 52558..52657
 /estimated_length=unknown
 70475..70574
 /estimated_length=unknown
 86828..86927
 /estimated_length=unknown
 123299..123398
 /estimated_length=unknown
 159741..159841
 /estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 215974;
 Best Local Similarity 97.6%; Pred. No. 0.012;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCG 41
 |||||||
 Db 86666 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCG 86706
 |||||||

RESULT 51

AC138969/c

LOCUS

DEFINITION

AC138969

VERSION

HTG.

SOURCE

ORGANISM

1 (bases 1 to 216759)

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Apr 7, 2003 this sequence version replaced gi:27805381.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center and Los

National Laboratory

www.shgc.stanford.edu

Quality: Phrap Quality >=40 100% of Sequence;
 Estimated Total Number of Errors is 0.
 NOTE: This insert is not the entire sequence of the clone (entire
 sequence is 241kb). It is clipped at the overlap with AC136624. The
 number of bases overlapped is 130609. Large tandem repeat 1 to
 75000. Unsure number of dinucleotide repeats from 18586-18838.
 Force join at 18810. Unsure number of dinucleotide repeats from
 62780-62985. Force join at 62870.

FEATURES

source

Location/Qualifiers

1. 216759

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="16"

/clone="RP11-958N24"

1. 75000

/note="Large tandem repeat 1 to 75000."

18586..18838

/note="Unsure number of dinucleotide repeats from
 18586-18838. Force join at 18810."

62780..62985

/note="Unsure number of dinucleotide repeats from
 62780-62985. Force join at 62870."

ORIGIN

Query Match 100.0%; Score 41; DB 8; Length 216759;
 Best Local Similarity 97.6%; Pred. No. 0.012;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCG 41
 |||||||
 Db 79414 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCG 79374
 |||||||

RESULT 52

AC126755

LOCUS

DEFINITION

AC126755

VERSION

HTG.

SOURCE

ORGANISM

1 (bases 1 to 223432)

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Apr 7, 2003 this sequence version replaced gi:27805381.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center and Los

National Laboratory

www.shgc.stanford.edu

Quality: Phrap Quality >=40 100% of Sequence;
 Estimated Total Number of Errors is 0.
 NOTE: This insert is not the entire sequence of the clone (entire
 sequence is 241kb). It is clipped at the overlap with AC136624. The
 number of bases overlapped is 130609. Large tandem repeat 1 to
 75000. Unsure number of dinucleotide repeats from 18586-18838.
 Force join at 18810. Unsure number of dinucleotide repeats from
 62780-62985. Force join at 62870.

```

VERSION      AC126755.3  GI:29570366
KEYWORDS     HTG.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homnidae; Homo.
REFERENCE    1 (bases 1 to 223432)
AUTHORS      DOE Joint Genome Institute, Stanford Human Genome Center and Los
             Alamos National Laboratory.
TITLE        Direct Submission
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 223432)
AUTHORS      DOE Joint Genome Institute.
TITLE        Direct Submission
JOURNAL      Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
             Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE    3 (bases 1 to 223432)
AUTHORS      DOE Joint Genome Institute.
TITLE        Direct Submission
JOURNAL      Submitted (14-SEP-2002) Production Sequencing Facility, DOE Joint
             Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE    4 (bases 1 to 223432)
AUTHORS      DOE Joint Genome Institute, Stanford Human Genome Center and Los
             Alamos National Laboratory.
TITLE        Direct Submission
JOURNAL      Submitted (07-APR-2003) DOE Joint Genome Institute, 2800 Mitchell
             Drive, Walnut Creek, CA 94598, USA
COMMENT      On Apr 7, 2003 this sequence version replaced gi:22857527.
             Draft Sequence Produced by DOE Joint Genome Institute
             www.jgi.doe.gov
             Finishing Completed at Stanford Human Genome Center and Los Alamos
             National Laboratory
             www.shgc.stanford.edu
             Quality: Phrap Quality >=40 99.9% of Sequence;
             Estimated Total Number of Errors is 1.1.
             NOTE: Large tandem repeat 31000 to 120000. Unsure number of
             dinucleotide repeats from 55000-55100. Force join at 55065. Unsure
             number of dinucleotide repeats from 94330-94487. Force join at
             94368.

FEATURES     Location/Qualifiers
             1..223432
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /chromosome="16"
             /clone="RP11-1212A22"
             31000..120000
             /note="NOTE: Large tandem repeat 31000 to 120000."
             55000..55100
             /note="Unsure number of dinucleotide repeats from
             55000-55100. Force join at 55065."
             94330..94487
             /note="Unsure number of dinucleotide repeats from
             94330-94487. Force join at 94368."

ORIGIN
Query Match      100.0%; Score 41; DB 8; Length 223432;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
    |||
Db 34333 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 34373
    |||

RESULT 53
LOCUS      HSA323057
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
            NRS-118R.
ACCESSION  AJ323057
VERSION    AJ323057.1  GI:15867436

```

```

KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homnidae; Homo.
REFERENCE    1 (bases 1 to 865)
AUTHORS      Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
             Podowski, R.M., Matuhkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
             Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I.,
             Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
TITLE        NotI flanking sequences: a tool for gene discovery and verification
             of the human genome
JOURNAL      Nucleic Acids Res. 30 (14), 3163-3170 (2002)
PUBMED      12136098
REFERENCE    2 (bases 1 to 865)
AUTHORS      Zabarovsky, E.R.
TITLE        Direct Submission
JOURNAL      Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
             Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
             Sweden
FEATURES     Location/Qualifiers
             1..865
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /clone="NRS-118R"

ORIGIN
Query Match      96.1%; Score 39.4; DB 8; Length 865;
Best Local Similarity 95.1%; Pred. No. 0.1;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
    |||
Db 235 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 195
    |||

RESULT 54
AC141236/c
LOCUS      AC141236
DEFINITION Homo sapiens chromosome 16 clone LA16c-350G9, WORKING DRAFT
             SEQUENCE, 5 unordered pieces.
ACCESSION  AC141236
VERSION    AC141236.1  GI:28913016
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homnidae; Homo.
REFERENCE    1 (bases 1 to 38848)
AUTHORS      DOE Joint Genome Institute.
TITLE        Sequencing of Human Chromosome 16
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 38848)
AUTHORS      DOE Joint Genome Institute.
TITLE        Direct Submission
JOURNAL      Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
             Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT      -----Genome Center
             Center: Joint Genome Institute
             Center Code: JGI
             Web site: http://www.jgi.doe.gov
             -----
             Project Information
             Center Project Name: 1220753
             Center clone name: LANL-16c_350G9
             -----
             Summary Statistics
             Consensus quality: 35738 bases at least Q40
             Consensus quality: 36543 bases at least Q30
             Consensus quality: 37150 bases at least Q20

```

```

Estimated insert size: 4000; agarose-fp estimation
Quality coverage: 14.51 in Q20 bases; agarose-fp estimation
Quality coverage: 15.1 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1051: contig of 1051 bp in length
* 1152: gap of unknown length
* 1152: contig of 1200 bp in length
* 2352: gap of unknown length
* 2452: contig of 7364 bp in length
* 9816: gap of unknown length
* 9916: contig of 6689 bp in length
* 16605: gap of unknown length
* 16705: 38848: contig of 22144 bp in length.
*
* Location/Qualifiers
*   1..38848
*     /organism="Homo sapiens"
*     /mol_type="genomic DNA"
*     /db_xref="taxon:9606"
*     /chromosome="16"
*     /clone="LA16c-350G9"
*     /clone_lib="Los Alamos human chromosome 16 cosmid
*     libraries; LA16NC01 and LA16NC02"
*     1052..1151
*       /estimated_length=unknown
*     2352..2451
*       /estimated_length=unknown
*     9816..9915
*       /estimated_length=unknown
*     16605..16704
*       /estimated_length=unknown
*
* ORIGIN
*
* Query Match          96.1%; Score 39.4; DB 14; Length 38848;
* Best Local Similarity 95.1%; Pred. No. 0.049;
* Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
*
* QY 1  AAGCCTCCGATGCCAGTCCTCATCGTCGGCCGCGCG 41
*      |||||
* Db 10119 AAGCCTCCGATGCCAGTCCTCATCGTCGGCCGCG 10079
*
* RESULT 55
* AC040158
* LOCUS          129473 bp      DNA      linear      HTG 03-SEP-2000
* DEFINITION     Homo sapiens chromosome 16 clone CTA-133B4, WORKING DRAFT SEQUENCE,
*                 14 unordered pieces.
* AC040158
* VERSION        AC040158.3 GI:9965546
* KEYWORDS       HTG: HTGS_PHASE1; HTGS_DRAFT.
* SOURCE         Homo sapiens (human)
* ORGANISM       Homo sapiens
*                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
*                 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
*                 Homnidae; Homo.
* REFERENCE      1 (bases 1 to 129473)
* AUTHORS        DOE Joint Genome Institute.
* TITLE          Sequencing of Human Chromosome 16
* JOURNAL         Unpublished
* REFERENCE      2 (bases 1 to 129473)
* AUTHORS        DOE Joint Genome Institute.
* TITLE          Direct Submission
* JOURNAL         Submitted (11-APR-2000) Production Sequencing Facility, DOE Joint
*                 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
* COMMENT        On Sep 3, 2000 this sequence version replaced gi:9090652.
* -----Genome Center

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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 0
Center clone name: CIT978SKA_133B4
-----
Summary Statistics
Consensus quality: 90046 bases at least Q40
Consensus quality: 99266 bases at least Q30
Consensus quality: 104098 bases at least Q20
Estimated insert size: 125000; agarose-fp estimation
Estimated insert size: 128173; sum-of-contigs estimation
Quality coverage: 4.51 in Q20 bases; agarose-fp estimation
Quality coverage: 4.4 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1718: contig of 1718 bp in length
* 1719: gap of unknown length
* 1819: contig of 2014 bp in length
* 3833: gap of unknown length
* 3933: contig of 1635 bp in length
* 5567: gap of unknown length
* 5668: contig of 1853 bp in length
* 7521: gap of unknown length
* 7621: contig of 1526 bp in length
* 9146: gap of unknown length
* 9247: contig of 1898 bp in length
* 11145: gap of unknown length
* 11245: contig of 1502 bp in length
* 12747: gap of unknown length
* 12847: contig of 1722 bp in length
* 14569: gap of unknown length
* 14669: contig of 4728 bp in length
* 19397: gap of unknown length
* 19496: contig of 6138 bp in length
* 25635: gap of unknown length
* 25735: contig of 11046 bp in length
* 36781: gap of unknown length
* 36880: contig of 13343 bp in length
* 50224: gap of unknown length
* 50324: contig of 20989 bp in length
* 71313: gap of unknown length
* 71413: 129473: contig of 58061 bp in length.
*
* Location/Qualifiers
*   1..129473
*     /organism="Homo sapiens"
*     /mol_type="genomic DNA"
*     /db_xref="taxon:9606"
*     /chromosome="16"
*     /clone="CTA-133B4"
*     /clone_lib="Caltech human BAC library A"
*     1719..1818
*       /estimated_length=unknown
*     3833..3933
*       /estimated_length=unknown
*     5568..5667
*       /estimated_length=unknown
*     7521..7620
*       /estimated_length=unknown
*     9147..9246
*       /estimated_length=unknown
*     11145..11244
*       /estimated_length=unknown
*     12747..12846
*       /estimated_length=unknown
*
* FEATURES
* source

```

gap
gap
gap
gap
gap
gap
gap

```

gap      14569..14668
/estimated_length=unknown
gap      19397..19496
/estimated_length=unknown
gap      25635..25734
/estimated_length=unknown
gap      36781..36880
/estimated_length=unknown
gap      50224..50323
/estimated_length=unknown
gap      71313..71412
/estimated_length=unknown

ORIGIN
Query Match      96.1%; Score 39.4; DB 14; Length 129473;
Best Local Similarity 95.1%; Pred. No. 0.039;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCGCG 41
Db 47443 AAGCCTCCGATGCCAGTCCCTCATCGTGGCTGTCGCG 47483

AC141602      144161 bp      DNA      linear      HTG 18-MAR-2003
Homo sapiens chromosome 16 clone RP11-1381B13, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
AC141602
AC141602.1 GI:29029187
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 144161)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 144161)
DOE Joint Genome Institute.
Direct Submission
Submitted (18-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

-----
Project Information
Center Project Name: 2749975
Center clone name: RPCI-11_1381B13
-----
Summary Statistics
Consensus quality: 140581 bases at least Q40
Consensus quality: 141190 bases at least Q30
Consensus quality: 141648 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 143061; sum-of-contigs estimation
Quality coverage: 7.62 in Q20 bases; agarose-fp estimation
Quality coverage: 9.38 in Q20 bases; sum-of-contigs estimation
Quality coverage: 9.38 in Q20 bases; agarose-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 1363: contig of 1363 bp in length
* 1364 1463: gap of unknown length
* 1464 4438: contig of 2975 bp in length

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* 4439 4538: gap of unknown length
* 4539 8092: contig of 3554 bp in length
* 8093 8192: gap of unknown length
* 8193 13626: contig of 5434 bp in length
* 13627 13726: gap of unknown length
* 13727 21117: contig of 7391 bp in length
* 21118 21217: gap of unknown length
* 21218 31407: contig of 10190 bp in length
* 31408 31507: gap of unknown length
* 31508 42598: contig of 11091 bp in length
* 42599 42698: gap of unknown length
* 42699 55092: contig of 12394 bp in length
* 55093 72553: contig of 17361 bp in length
* 72554 88814: contig of 16161 bp in length
* 88815 88915: gap of unknown length
* 88916 123281: contig of 34367 bp in length
* 123282 123381: gap of unknown length
* 123382 144161: contig of 20780 bp in length.

FEATURES
Location/Qualifiers
1..144161
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone_lib="RPCI human BAC library 11"
1364..1463
/estimated_length=unknown
4439..4538
/estimated_length=unknown
8093..8192
/estimated_length=unknown
13627..13726
/estimated_length=unknown
21118..21217
/estimated_length=unknown
31408..31507
/estimated_length=unknown
42599..42698
/estimated_length=unknown
55093..55192
/estimated_length=unknown
72554..72653
/estimated_length=unknown
88815..88914
/estimated_length=unknown
123282..123381
/estimated_length=unknown

ORIGIN
Query Match      96.1%; Score 39.4; DB 14; Length 144161;
Best Local Similarity 95.1%; Pred. No. 0.039;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCGCG 41
Db 123042 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCGCG 123082

RESULT 57
AC154112
LOCUS
DEFINITION
Pan troglodytes clone RP43-11J15, WORKING DRAFT SEQUENCE, 13
ordered pieces.
AC154112
AC154112.3 GI:68342116
HTG; HTGS_PHASE2; HTGS_DRAFT.
KEYWORDS
Pan troglodytes (chimpanzee)
SOURCE
Pan troglodytes
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```

REFERENCE
AUTHORS

Hominidae; Pan.
1 (bases 1 to 183396)
Eichler,E., Johnson,M., Antonellis,A., Avele,K., Bass,D.,
Benjamin,B., Bera,J., Blakesley,R.W., Bouffard,G.G., Brinkley,C.,
Brooks,S., Chu,G., Coleman,H., Engle,J., Fukenko,T., Gestole,M.,
Greene,A., Guan,X., Gupta,J., Haghghi,P., Han,J., Hansen,N.,
Ho,S.-L., Hu,P., Hunter,G., Hurie,B., Idol,J.R., Kwong,P.,
Laric,P., Larson,S., Lee-Lin,S.-Q., Legaspi,R., Madden,M.,
Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B.,
McDowell,J., Mojidi,H.A., Mullikin,J.C., Oestreicher,J.S., Park,M.,
Portnoy M.E., Prasad,A., Puri,O., Reddix-Dugue,N., Sante,A.,
Schandler,K., Schueler,M.G., Sison,C., Stantripop,S., Sante,A.,
Taye,A., Thomas,J.W., Thomas,P.J., Tsipouri,V., Ung,L., Vogt,J.L.,
Wetherby,K.D., Withers,T.R., Young,A. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 183396)
Green,E.D.
Direct Submission
Submitted (23-DEC-2004) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
3 (bases 1 to 183396)
Green,E.D.
Direct Submission
Submitted (30-JUN-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On Jun 30, 2005 this sequence version replaced gi:58219703.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: e2g
Center clone name: 011J15

COMMENT

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is generally based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies; the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 179496 bases at least Q40
Consensus quality: 180898 bases at least Q30
Consensus quality: 181644 bases at least Q20
Insert size: 174000; agarose-fp
Insert size: 182196; sum-of-contigs
Quality coverage: 12.44x in Q20 bases; agarose-fp
Quality coverage: 11.88x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and the accession number will be preserved.
* 1 2055: contig of 2055 bp in length
* 2056 2155: gap of unknown length
* 2156 27273: contig of 25118 bp in length
* 27274 27373: gap of unknown length

* 27374	43148: contig of 15775 bp in length
* 43149	43248: gap of unknown length
* 43249	45468: contig of 2220 bp in length
* 45469	45588: gap of unknown length
* 45569	62555: contig of 17087 bp in length
* 62556	62755: gap of unknown length
* 62756	85032: contig of 22277 bp in length
* 85033	85132: gap of unknown length
* 85133	99815: contig of 14683 bp in length
* 99816	99915: gap of unknown length
* 99916	122872: contig of 22957 bp in length
* 122873	122972: gap of unknown length
* 122973	134501: contig of 11529 bp in length
* 134502	134601: gap of unknown length
* 134602	140529: contig of 5928 bp in length
* 140530	140629: gap of unknown length
* 140630	160723: contig of 20094 bp in length
* 160724	160823: gap of unknown length
* 160824	173513: contig of 12690 bp in length
* 173514	173613: gap of unknown length
* 173614	183396: contig of 9783 bp in length.

FEATURES
Location/Qualifiers
1..183396
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-11J15"
/clone_lib="RP43"
/note="BAC resource: <http://bacpac.chori.org/>"
misc_feature
1..2055
/note="assembly_fragment"
clone_end:SP6
vector_side:left
2056..2155
/estimated_length=unknown
2156..27273
/note="assembly_fragment"
27274..27373
/estimated_length=unknown
27374..43148
/note="assembly_fragment"
43149..43248
/estimated_length=unknown
43249..45468
/note="assembly_fragment"
45469..45568
/estimated_length=unknown
45569..62555
/note="assembly_fragment"
62556..62755
/estimated_length=unknown
62756..85032
/note="assembly_fragment"
85033..85132
/estimated_length=unknown
85133..99815
/note="assembly_fragment"
99816..99915
/estimated_length=unknown
99916..122872
/note="assembly_fragment"
122873..122972
/estimated_length=unknown
122973..134501
/note="assembly_fragment"
134502..134601
/estimated_length=unknown
134602..140529
/note="assembly_fragment"
140530..140629
/estimated_length=unknown
140630..160723
/note="assembly_fragment"

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gap          160724..160823
/estimated length=unknown
misc_feature 160824..173513
/notes="assembly_fragment"
gap          173514..173613
/estimated length=unknown
misc_feature 173614..183396
/notes="assembly_fragment
clone_end:T7
vector_side:right"

ORIGIN
Query Match          96.1%; Score 39.4; DB 14; Length 183396;
Best Local Similarity 95.1%; Pred.No. 0.037;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCGC 41
|||||
Db 62806 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCGC 62846

RESULT 58
AC092137/c
LOCUS          184891 bp DNA linear PRI 07-APR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-344H15, complete sequence.
ACCESSION AC092137
VERSION AC092137.3 GI:28973806
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 184891)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 184891)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL DOE Joint Genome Institute.
REFERENCE 3 (bases 1 to 184891)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 184891)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 5 (bases 1 to 184891)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 6 (bases 1 to 184891)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (07-APR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 7 (bases 1 to 184891)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 15, 2003 this sequence version replaced gi:25229204.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1
NOTE: Unsure number of dinucleotide repeats from 93650-94165.
Forced join at 94008. The number of missing bases by PCR is 100.
Location/Qualifiers
1..184891
/organism="Homo sapiens"

FEATURES
source
1..184891
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-344H15"
/misc_feature 93650..94165
/notes="NOTE: Unsure number of dinucleotide repeats from 93650-94165.
Forced join at 94008. The number of missing bases by PCR is 100."
bases by PCR is 100."

ORIGIN
Query Match          96.1%; Score 39.4; DB 8; Length 184891;
Best Local Similarity 95.1%; Pred.No. 0.037;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCGC 41
|||||
Db 116614 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCGC 116574

RESULT 59
AC126763
LOCUS          187721 bp DNA linear PRI 18-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-1390J18, complete sequence.
ACCESSION AC126763
VERSION AC126763.4 GI:29029241
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 187721)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 187721)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 187721)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 187721)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 5 (bases 1 to 187721)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 18, 2003 this sequence version replaced gi:24270685.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
Location/Qualifiers
1..187721
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1390J18"
```


* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 83902: contig of 83902 bp in length
* 83903 84002: gap of unknown length
* 84003 94898: contig of 10896 bp in length
* 94899 94998: gap of unknown length
* 94999 120178: contig of 25180 bp in length
* 120179 120278: gap of unknown length
* 120279 142935: contig of 22657 bp in length
* 142936 143035: gap of unknown length
* 143036 196687: contig of 53652 bp in length.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 587090
Center clone name: RP11-470K5

Summary Statistics
Consensus quality: 194751 bases at least Q40
Consensus quality: 195030 bases at least Q30
Consensus quality: 195153 bases at least Q20
Estimated insert size: 197000; agarose-fp estimation
Estimated insert size: 195279; sum-of-contigs
estimation
Quality coverage: 0.99 in Q20 bases; agarose-fp
estimation
Quality coverage: 1 in Q20 bases; sum-of-contigs
estimation.
Location/Qualifiers
1. 196687
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosomes="16"
/clone="RP11-470K5"
83903..84002
/estimated_length=unknown
94899..94998
/estimated_length=unknown
120179..120278
/estimated_length=unknown
142936..143035
/estimated_length=unknown
ORIGIN
Query Match 96.1%; Score 39.4; DB 14; Length 196687;
Best Local Similarity 95.1%; Pred. No. 0.036; 1; Indels 0; Gaps 0;
Matches 39; Conservative 1; Mismatches 1;
QY 1 AAGCCTCCGGATCCAGTCCCTCATCGCTGCGCCGCGCG 41
|||||
Db 120055 AAGCCTCCGGATCCAGTCCCTCATCGCTGCGCTGCGCG 120095
AC141467 215222 bp DNA linear HTG 16-MAR-2003
Homo sapiens chromosome 16 clone RP11-927M3, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
AC141467
AC141467.1 GI:28975020
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 215222)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16

JOURNAL
REFERENCE 2 (bases 1 to 215222)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1650763
Center clone name: RPC1-11_927M3

Summary Statistics
Consensus quality: 207729 bases at least Q40
Consensus quality: 209189 bases at least Q30
Consensus quality: 210079 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 214122; sum-of-contigs estimation
Quality coverage: 6.85 in Q20 bases; agarose-fp estimation
Quality coverage: 5.63 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1037: contig of 1037 bp in length
* 1038 1137: gap of unknown length
* 1138 5338: contig of 4201 bp in length
* 5339 5439: gap of unknown length
* 5439 9722: contig of 4284 bp in length
* 9723 9822: gap of unknown length
* 9823 15226: contig of 5404 bp in length
* 15227 15326: gap of unknown length
* 15327 21907: contig of 6581 bp in length
* 21908 22007: gap of unknown length
* 22008 28900: contig of 6893 bp in length
* 28901 29000: gap of unknown length
* 29001 41504: contig of 12504 bp in length
* 41505 41604: gap of unknown length
* 41605 56820: contig of 15216 bp in length
* 56821 56920: gap of unknown length
* 56921 80192: contig of 23272 bp in length
* 80193 80292: gap of unknown length
* 80293 117096: contig of 36804 bp in length
* 117097 117196: gap of unknown length
* 117197 156379: contig of 39183 bp in length
* 156380 156479: gap of unknown length
* 156480 215222: contig of 58743 bp in length.
Location/Qualifiers
1. 215222
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosomes="16"
/clone="RP11-927M3"
/clone_lib="RPC1 human BAC library 11"
1038..1137
/estimated_length=unknown
5339..5438
/estimated_length=unknown
9723..9822
/estimated_length=unknown
15227..15326
/estimated_length=unknown
21908..22007
/estimated_length=unknown
28901..29000
FEATURES
source

gap /estimated length=unknown
41505. .41604
gap /estimated length=unknown
56821. .56920
gap /estimated length=unknown
80193. .80292
gap /estimated length=unknown
117097. .117196
gap /estimated length=unknown
156380. .156479
gap /estimated length=unknown

ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 215222;
Best Local Similarity 95.1%; Pred. No. 0.036;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCCG 41
Db 28672 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCGCG 28712

RESULT 63
AC144881/c
LOCUS
DEFINITION
AC144881 215960 bp DNA linear HTG 18-JUL-2003
Gorilla gorilla gorilla clone CH255-120J14, WORKING DRAFT SEQUENCE,
19 unordered pieces.

AC144881
HTG: HTGS_PHASE1; HTGS DRAFT.
Gorilla gorilla gorilla (lowland gorilla)
Gorilla gorilla gorilla
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Gorilla.

REFERENCE
AUTHORS
Eichler,E.E., Johnson,M.E., Antonellis,A., Ayele,K.,
Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., Chu,G.,
Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X., Gupta,J.,
Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurie,B.,
Idol,J.R., Karlins,E., Kwong,P., Laric,P., Lee-Lin,S.-Q.,
Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C.,
Maskari,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E.,
Prasad,A., Reddik-Dugue,N., Schandler,K., Schueler,M.G., Shah,K.,
Sison,C., Stantrippop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V.,
Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
NISC Comparative Sequencing Initiative

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (23-MAY-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
Green,E.D.
Direct Submission
Submitted (18-JUL-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Jul 18, 2003 this sequence version replaced gi:31044296.

COMMENT
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: niscxoo@nhgri.nih.gov
----- Project Information
Center project name: eni
Center clone name: 120J14
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 209508 bases at least Q40

Consensus quality: 210752 bases at least Q30
Consensus quality: 211509 bases at least Q20
Insert size: 220000; agarose-fp
Insert size: 214160; sum-of-contigs
Quality coverage: 11.70x in Q20 bases; agarose-fp
Quality coverage: 12.02x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 2293: contig of 2293 bp in length
2294 2393: gap of unknown length
2394 4498: contig of 2105 bp in length
4499 4598: gap of unknown length
4599 7155: contig of 2557 bp in length
7156 7255: gap of unknown length
7256 10105: contig of 2850 bp in length
10106 10205: gap of unknown length
10206 13671: contig of 3466 bp in length
13672 13771: gap of unknown length
13772 15857: contig of 2086 bp in length
15858 15957: gap of unknown length
15958 20009: contig of 4052 bp in length
20010 20109: gap of unknown length
20110 24472: contig of 4363 bp in length
24473 24572: gap of unknown length
24573 27197: contig of 2625 bp in length
27198 27297: gap of unknown length
27298 33250: contig of 5953 bp in length
33251 33350: gap of unknown length
33351 39952: contig of 6602 bp in length
39953 40052: gap of unknown length
40053 52004: contig of 11952 bp in length
52005 52104: gap of unknown length
52105 67492: contig of 15388 bp in length
67493 67592: gap of unknown length
67593 85255: contig of 17663 bp in length
85256 85355: gap of unknown length
85356 107738: contig of 22383 bp in length
107739 107838: gap of unknown length
107839 126829: contig of 18991 bp in length
126830 126929: gap of unknown length
126930 146098: contig of 19169 bp in length
146099 146198: gap of unknown length
146199 183617: contig of 37419 bp in length
183618 183717: gap of unknown length
183718 215960: contig of 32243 bp in length.

FEATURES

source
1. .215960
/organism="Gorilla gorilla gorilla"
/mol_type="genomic DNA"
/sub_species="gorilla"
/db_xref="taxon:9595"
/clones="CH255-120J14"
/clone_lib="CH255"
1. .2293
/note="assembly_fragment"
2294.2393
/estimated_length=unknown
2394.4498
/note="assembly_fragment"
4499.4598
/estimated_length=unknown
4599.7155
/note="assembly_fragment"
7156.7255
/estimated_length=unknown
7256.10105

misc_feature

gap

misc_feature

gap

misc_feature

gap

misc_feature

gap /note="assembly_fragment"
10106. 10205
/estimated_length=unknown
misc_feature 10206. .13671
/note="assembly_fragment"
gap 13672. .13771
/estimated_length=unknown
misc_feature 13772. .15857
/note="assembly_fragment"
gap 15858. .15957
/estimated_length=unknown
misc_feature 15958. .20009
/note="assembly_fragment"
gap 20010. .20109
/estimated_length=unknown
misc_feature 20110. .24472
/note="assembly_fragment"
gap 24473. .24572
/estimated_length=unknown
misc_feature 24573. .27197
/note="assembly_fragment"
gap 27198. .27297
/estimated_length=unknown
misc_feature 27298. .33250
/note="assembly_fragment"
gap 33251. .33350
/estimated_length=unknown
misc_feature 33351. .39952
/note="assembly_fragment"
gap 39953. .40052
/estimated_length=unknown
misc_feature 40053. .52004
/note="assembly_fragment"
gap 52005. .52104
/estimated_length=unknown
misc_feature 52105. .67492
/note="assembly_fragment"
gap 67493. .67592
/estimated_length=unknown
misc_feature 67593. .85255
/note="assembly_fragment"
gap 85256. .85355
/estimated_length=unknown
misc_feature 85356. .107738
/note="assembly_fragment"
gap 107739. .107838
/estimated_length=unknown
misc_feature 107839. .126829
/note="assembly_fragment"
gap 126830. .126925
/estimated_length=unknown
misc_feature 126930. .146098
/note="assembly_fragment
clone_end:sp6
vector_side:right"
gap 146099. .146198
/estimated_length=unknown
misc_feature 146199. .183617
/note="assembly_fragment"
gap 183618. .183717
/estimated_length=unknown
misc_feature 183718. .215960
/note="assembly_fragment
clone_end:T7
vector_side:right"

ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 215960;
Best Local Similarity 95.1%; Pred.No. 0.036;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 AAGCTTCGGATGCCAGTCCTCCTCGCTGCCGCGCGC 41
|||||

Db 41238 AAGCTTCGGATGCCAGTCCTCCTCGCTGCCGCGCGC 41198
RESULT 64
AC141303/c
LOCUS
DEFINITION AC141303 218593 bp DNA linear HTG 11-MAR-2003
Homo sapiens chromosome 16 clone RP11-795L17, WORKING DRAFT
SEQUENCE, 15 unordered pieces.
ACCESSION AC141303
VERSION AC141303.1 GI:28913083
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (Bases 1 to 218593)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (Bases 1 to 218593)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1600065
Center clone name: RPCI-11_795L17

Summary Statistics
Consensus quality: 206479 bases at least Q40
Consensus quality: 210696 bases at least Q30
Consensus quality: 212699 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Quality coverage: 6.63 in Q20 bases; agarose-fp estimation
Quality coverage: 5.37 in Q20 bases; sum-of-contrigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1100: contig of 1100 bp in length
* 1101 1200: gap of unknown length
* 1201 2911: contig of 1711 bp in length
* 2912 3011: gap of unknown length
* 3012 6661: contig of 3650 bp in length
* 6662 6761: gap of unknown length
* 6762 11364: contig of 4603 bp in length
* 11365 11464: gap of unknown length
* 11465 17383: contig of 5919 bp in length
* 17384 17483: gap of unknown length
* 17484 24477: contig of 6994 bp in length
* 24478 24577: gap of unknown length
* 24578 30168: contig of 5591 bp in length
* 30169 30268: gap of unknown length
* 30269 39963: contig of 9695 bp in length
* 39964 40063: gap of unknown length
* 40064 53361: contig of 13298 bp in length
* 53362 53461: gap of unknown length
* 53462 67963: contig of 14502 bp in length
* 67964 88063: gap of unknown length
* 88064 84693: contig of 16630 bp in length
* 84694 84793: gap of unknown length
* 84794 102881: contig of 18088 bp in length

* 102882 102981: gap of unknown length
* 102982 123663: contig of 20682 bp in length
* 123664 123763: gap of unknown length
* 123764 166750: contig of 42987 bp in length
* 166751 166850: gap of unknown length
* 166851 218593: contig of 51743 bp in length.

FEATURES

source

Location/Qualifiers
1. .218593
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-795L17"
/clone_lib="RPCI human BAC library 11"
1101. .1200
2912. .3011
/estimated_length=unknown
6662. .6761
/estimated_length=unknown
11365. .11464
/estimated_length=unknown
17384. .17483
/estimated_length=unknown
24478. .24577
/estimated_length=unknown
30169. .30268
/estimated_length=unknown
39964. .40063
/estimated_length=unknown
53362. .53461
/estimated_length=unknown
67964. .68063
/estimated_length=unknown
84694. .84793
/estimated_length=unknown
102882. .102981
/estimated_length=unknown
123664. .123763
/estimated_length=unknown
166751. .166850
/estimated_length=unknown

ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 218593;
Best Local Similarity 95.1%; Pred. No. 0.036;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGGCCGNCGCG 41
|||||
Db 7733 AAGCTCCGGATGCCAGTCCCTCATCGTCGGCTGGTCGCG 7693
|||||

RESULT 65

AC141401 192549 bp DNA linear HTG 14-MAR-2003
LOCUS Homo sapiens chromosome 16 clone RP11-1000N11, WORKING DRAFT
DEFINITION SEQUENCE, 14 unordered pieces.

ACCESSION AC141401
VERSION AC141401.1 GI:28951147
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 192549)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192549)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission

JOURNAL

COMMENT

Submitted (14-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information

Center Project Name: 1678827
Center clone name: RPCI-11_1000N11

Summary Statistics

Consensus quality: 186509 bases at least Q40
Consensus quality: 188167 bases at least Q30
Consensus quality: 189310 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 191249; sum-of-contigs estimation
Quality coverage: 4.93 in Q20 bases; agarose-fp estimation
Quality coverage: 4.54 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 2751: contig of 2751 bp in length
* 2752 2851: gap of unknown length
* 2852 5567: contig of 2716 bp in length
* 5568 5667: gap of unknown length
* 5668 9517: contig of 3850 bp in length
* 9518 9617: gap of unknown length
* 9618 14758: contig of 5141 bp in length
* 14759 14858: gap of unknown length
* 14859 21951: contig of 7093 bp in length
* 21952 22051: gap of unknown length
* 22052 34179: contig of 12128 bp in length
* 34180 34279: gap of unknown length
* 34280 43482: contig of 9203 bp in length
* 43483 43582: gap of unknown length
* 43583 53114: contig of 9532 bp in length
* 53115 53214: gap of unknown length
* 53215 66390: contig of 13176 bp in length
* 66391 66490: gap of unknown length
* 66491 83717: contig of 17227 bp in length
* 83718 83818: gap of unknown length
* 83818 109612: contig of 25794 bp in length
* 109612 109711: gap of unknown length
* 109712 140463: contig of 30752 bp in length
* 140464 140563: gap of unknown length
* 140564 164642: contig of 24079 bp in length
* 164643 164742: gap of unknown length
* 164743 192549: contig of 27807 bp in length.
Location/Qualifiers
1. 192549
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1000N11"
/clone_lib="RPCI human BAC library 11"
2752. .2851
/estimated_length=unknown
5568. .5667
/estimated_length=unknown
9518. .9617
/estimated_length=unknown
14759. .14858
/estimated_length=unknown
21952. .22051
/estimated_length=unknown
34180. .34279

FEATURES

source

gap

gap

gap

gap

gap

gap

```

/estimated_length=unknown
43483..43582
/estimated_length=unknown
53115..53214
/estimated_length=unknown
66391..66490
/estimated_length=unknown
83718..83817
/estimated_length=unknown
109612..109711
/estimated_length=unknown
140464..140563
/estimated_length=unknown
164643..164742
/estimated_length=unknown

ORIGIN
Query Match          92.2%; Score 37.8; DB 14; Length 192549;
Best Local Similarity 92.7%; Pred. No. 0.11;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 41
|||||
Db 109263 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCTCG 109303
|||||

RESULT 66
AC138872
LOCUS      131818 bp      DNA      linear      HTG 21-JAN-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-16405, WORKING DRAFT
ACCESSION AC138872
VERSION    AC138872.1 GI:27805284
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 131818)
AUTHORS   DOE Joint Genome Institute.
TITLE     Sequencing of Human Chromosome 16
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 131818)
AUTHORS   DOE Joint Genome Institute.
TITLE     Direct Submission
JOURNAL   Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT   -----Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -----
            Project Information
            Center Project Name: 469682
            Center clone name: RPC1-11_16405
            -----
            Summary Statistics
            Consensus quality: 127808 bases at least Q40
            Consensus quality: 128485 bases at least Q30
            Consensus quality: 129118 bases at least Q20
            Estimated insert size: 180000; agarose-fp estimation
            Estimated insert size: 130618; sum-of-contigs estimation
            Quality coverage: 9.99 in Q20 bases; agarose-fp estimation
            Quality coverage: 13.77 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 13 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.

```

```

* 1275: contig of 1275 bp in length
* 1276: gap of unknown length
* 1376: contig of 1208 bp in length
* 2584: gap of unknown length
* 2684: contig of 1310 bp in length
* 3994: gap of unknown length
* 4094: contig of 2051 bp in length
* 6144: gap of unknown length
* 6244: gap of unknown length
* 8080: contig of 1836 bp in length
* 8081: gap of unknown length
* 8181: contig of 2041 bp in length
* 10222: gap of unknown length
* 10322: contig of 3053 bp in length
* 13374: gap of unknown length
* 13375: gap of unknown length
* 13474: gap of unknown length
* 13475: contig of 4244 bp in length
* 17719: gap of unknown length
* 17818: contig of 5537 bp in length
* 23356: gap of unknown length
* 23456: contig of 15793 bp in length
* 32456: gap of unknown length
* 39249: contig of 17361 bp in length
* 39349: gap of unknown length
* 56710: gap of unknown length
* 56810: contig of 18249 bp in length
* 75059: gap of unknown length
* 75159: contig of 56660 bp in length.

FEATURES
            Location/Qualifiers
            1..131818
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /chromosome="16"
               /clone_lib="RPC1 human BAC library 11"
            1276..1375
               /estimated_length=unknown
            2584..2683
               /estimated_length=unknown
            3994..4093
               /estimated_length=unknown
            6145..6244
               /estimated_length=unknown
            8081..8180
               /estimated_length=unknown
            10222..10321
               /estimated_length=unknown
            13375..13474
               /estimated_length=unknown
            17719..17818
               /estimated_length=unknown
            23356..23455
               /estimated_length=unknown
            39249..39348
               /estimated_length=unknown
            56710..56809
               /estimated_length=unknown
            75059..75158
               /estimated_length=unknown

ORIGIN
Query Match          88.8%; Score 36.4; DB 14; Length 131818;
Best Local Similarity 94.7%; Pred. No. 0.31;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 38
|||||
Db 56520 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCTC 56557
|||||

RESULT 67
AC140805
LOCUS      51437 bp      DNA      linear      HTG 03-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone LA16c-374G11, WORKING DRAFT
SEQUENCE, 11 unordered pieces.

```

```

ACCESSION      AC140805
VERSION        AC140805.1 GI:28631186
KEYWORDS       HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE         Homo sapiens
ORGANISM       Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
               Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1 (bases 1 to 51437)
AUTHORS        DOE Joint Genome Institute.
TITLE          Sequencing of Human Chromosome 16
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 51437)
AUTHORS        DOE Joint Genome Institute.
TITLE          Direct Submission
JOURNAL        Submitted (03-MAR-2003) Production Sequencing Facility, DOE Joint
               Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT        -----Genome Center
               Center: Joint Genome Institute
               Center Code: JGI
               Web site: http://www.jgi.doe.gov
               -----
               Project Information
               Center Project Name: 1223059
               Center clone name: LANL-16c_374G11
               -----
               Summary Statistics
               Consensus quality: 44663 bases at least Q40
               Consensus quality: 46358 bases at least Q30
               Consensus quality: 47357 bases at least Q20
               Estimated insert size: 4000; agarose-fp estimation
               Quality coverage: 14.38 in Q20 bases; agarose-fp estimation
               Quality coverage: 11.4 in Q20 bases; sum-of-contigs estimation.
               * NOTE: This is a 'working draft' sequence. It currently
               * consists of 11 contigs. The true order of the pieces
               * is not known and their order in this sequence record is
               * arbitrary. Gaps between the contigs are represented as
               * runs of N, but the exact sizes of the gaps are unknown.
               * This record will be updated with the finished sequence
               * as soon as it is available and the accession number will
               * be preserved.
               *
               1 1000: contig of 1000 bp in length
               * 1101: gap of unknown length
               * 2330: contig of 1230 bp in length
               * 2430: gap of unknown length
               * 2431: contig of 1031 bp in length
               * 3462: gap of unknown length
               * 3561: gap of unknown length
               * 4769: gap of unknown length
               * 4869: contig of 1022 bp in length
               * 5991: gap of unknown length
               * 5991: gap of unknown length
               * 7171: contig of 1181 bp in length
               * 7172: gap of unknown length
               * 7272: gap of unknown length
               * 8794: contig of 1522 bp in length
               * 8894: gap of unknown length
               * 14431: contig of 5537 bp in length
               * 14531: gap of unknown length
               * 29913: contig of 15383 bp in length
               * 30013: gap of unknown length
               * 32595: contig of 2582 bp in length
               * 32596: gap of unknown length
               * 32696: contig of 18742 bp in length.
               Location/Qualifiers
               1. .51437
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /chromosome="16"
               /clone="LA16c-374G11"
               /clone_lib="Los Alamos human chromosome 16 cosmid
               libraries; LA16NC01 and LA16NC02"
               1001. .1100
gap

```

```

/estimated_length=unknown
2331. .2430
/estimated_length=unknown
3462. .3561
/estimated_length=unknown
4769. .4868
/estimated_length=unknown
5891. .5990
/estimated_length=unknown
7172. .7271
/estimated_length=unknown
8794. .8893
/estimated_length=unknown
14431. .14530
/estimated_length=unknown
29914. .30013
/estimated_length=unknown
32596. .32695
/estimated_length=unknown

ORIGIN
Query Match      88.3%; Score 36.2; DB 14; Length 51437;
Best Local Similarity 90.2%; Pred. No. 0.42;
Matches 37; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCGCGCGC 41
    |||||
Db 14351 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCGCGCGC 14391

RESULT 68
AC148537 162696 bp DNA linear HTG 26-MAY-2004
LOCUS Pan troglodytes clone CH251-160D4, WORKING DRAFT SEQUENCE, 8
DEFINITION AC148537
ACCESSION AC148537.3 GI:47679103
VERSION HTG; HTGS PHASE2; HTGS DRAFT.
KEYWORDS Pan troglodytes (chimpanzee).
SOURCE Pan troglodytes
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
          Primates; Catarrhini;
          Hominidae; Pan.
REFERENCE 1 (bases 1 to 162696)
AUTHORS Eichler,E., Johnson,M., Antonellis,A., Ayele,K., Benjamin,B.,
          Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G.,
          Coleman,B., Coleman,H., Daki,N., Engle,J., Guan,X., Gupta,J.,
          Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B.,
          Idol,J.R., Jones,C., Karlins,E., Kim,H., Kwong,P., Laric,P.,
          Larson,S., Lee-Lin,S.-Q., Legaspi,R., Madden,M., Maduro,Q.L.,
          Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J.,
          Mullikin,J.C., Paguirigan,C., Park,M., Portnoy,M.E., Prasad,A.,
          Puri,O., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K.,
          Sison,C., Stantropop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V.,
          Vogt,J.L., Wetherby,K.D., Young,A. and Green,E.D.
          NISC Comparative Sequencing Initiative
          Unpublished
          2 (bases 1 to 162696)
          Green,E.D.
          Direct Submission
          Submitted (18-MAR-2004) NIH Intramural Sequencing Center, 8717
          Grovemont Circle, Gaithersburg, MD 20877, USA
          3 (bases 1 to 162696)
          Green,E.D.
          Direct Submission
          Submitted (26-MAY-2004) NIH Intramural Sequencing Center, 8717
          Grovemont Circle, Gaithersburg, MD 20877, USA
          On May 26, 2004 this sequence version replaced gi:46849620.
          -----Genome Center
          Center: NIH Intramural Sequencing Center
          Center code: NISC
          Web site: http://www.nisc.nih.gov
          Contact: nisc_zoo@nhgri.nih.gov

```

----- Project Information
Center project name: ezi
Center Clone name: 160D04

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 160789 bases at least Q40
Consensus quality: 161396 bases at least Q30
Consensus quality: 161739 bases at least Q20
Insert size: 193000; agarose-fp
Insert coverage: 161996; sum-of-contigs
Quality coverage: 7.88x in Q20 bases; agarose-fp
Quality coverage: 9.39x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 355: contig of 355 bp in length
* 356 455: gap of unknown length
* 456 23039: contig of 22584 bp in length
* 23040 23139: gap of unknown length
* 23140 36152: contig of 13013 bp in length
* 36153 36252: gap of unknown length
* 36253 71082: contig of 34830 bp in length
* 71083 71182: gap of unknown length
* 71183 113878: contig of 42696 bp in length
* 113879 113979: gap of unknown length
* 113979 119879: contig of 5901 bp in length
* 119880 119979: gap of unknown length
* 119980 152776: contig of 32797 bp in length
* 152777 152876: gap of unknown length
* 152877 162696: contig of 9820 bp in length.

FEATURES
source

Location/Qualifiers
1. .162696
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="CH251-160D4"
/clone_lib="CH251"
/note="BAC resource: <http://bacpac.chori.org/>"
misc_feature
1. .355
/note="assembly_fragment
clone_end:SP6
vector_side:left"
gap
356. .455
/estimated_length=unknown
misc_feature
456. .23039
/note="assembly_fragment"
gap
23040. .23139
/estimated_length=unknown
misc_feature
23140. .36152
/note="assembly_fragment"
gap
36153. .36252

/estimated_length=unknown
36253. .71082
/note="assembly_fragment"
71083. .71182
/estimated_length=unknown
71183. .113878
/note="assembly_fragment"
113879. .113978
/estimated_length=unknown
113979. .119879
/note="assembly_fragment"
119880. .119979
/estimated_length=unknown
119980. .152776
/note="assembly_fragment"
152777. .152876
/estimated_length=unknown
152877. .162696
/note="assembly_fragment
vector_side:right"

ORIGIN

Query Match 88.3%; Score 36.2; DB 14; Length 162696;
Best Local Similarity 90.2%; Pred. No. 0.34;
Matches 37; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 AAGCTTCGGATGCCAGTCCCTCATCGCTGCCGCGCG 41
|||||
Db 35682 AAGCTTCGGATGCCAGTCCCTCATCGCTGCCGCGCG 35722
|||||

RESULT 69
AC141276/c

LOCUS AC141276 166278 bp DNA linear HTG 11-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-232G22, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
AC141276
AC141276.1 GI:28913056
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 166278)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166278)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 495619
Center clone name: RPCI-11_232G22

Summary Statistics
Consensus quality: 164621 bases at least Q40
Consensus quality: 164724 bases at least Q30
Consensus quality: 164817 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 165978; sum-of-contigs estimation
Quality coverage: 13.19 in Q20 bases; agarose-fp estimation
Quality coverage: 13.9 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1053: contig of 1053 bp in length
 * 1054 1153: gap of unknown length
 * 1154 17390: contig of 16237 bp in length
 * 17391 17490: gap of unknown length
 * 17491 36178: contig of 18688 bp in length
 * 36179 36278: gap of unknown length
 * 36279 166278: contig of 130000 bp in length.

FEATURES

source

1. 166278
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-232G22"
 /clone_lib="RPCI human BAC library 11"
 1054. 1153
 /estimated_length=unknown
 17391. 17490
 /estimated_length=unknown
 36179. 36278
 /estimated_length=unknown

ORIGIN

Query Match 88.3%; Score 36.2; DB 14; Length 166278;
 Best Local Similarity 90.2%; Pred. No. 0.34;
 Matches 37; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCTCATCGTGGCCGCGCG 41
 |||||
 Db 36623 AAGCCTCCGATGCCAGTCCTCATCGTGGCCGCGCG 36583

RESULT 70

AC141080 198295 bp DNA linear HTG 07-MAR-2003
 LOCUS Homo sapiens chromosome 16 clone RP11-902P10, WORKING DRAFT
 DEFINITION SEQUENCE, 4 unordered pieces.

ACCESSION AC141080.1 GI:28875940
 VERSION AC141080
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

1 (bases 1 to 198295)
 DOE Joint Genome Institute.
 Unpublished
 Sequencing of Human Chromosome 16
 2 (bases 1 to 198295)
 DOE Joint Genome Institute.

Direct Submission
 Submitted (07-MAR-2003) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT

-----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: <http://www.jgi.doe.gov>

 Project Information
 Center Project Name: 1641242

Center clone name: RPCI-11_902P10

Summary Statistics
 Consensus quality: 195612 bases at least Q40
 Consensus quality: 196104 bases at least Q30
 Consensus quality: 196475 bases at least Q20

Estimated insert size: 176000; agarose-fp estimation
 Estimated insert size: 197995; sum-of-contigs estimation
 Quality coverage: 9.57 in Q20 bases; agarose-fp estimation
 Quality coverage: 8.51 in Q20 bases; sum-of-contigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 2067: contig of 2067 bp in length
 * 2068 2167: gap of unknown length
 * 2168 16911: contig of 14744 bp in length
 * 16912 17011: gap of unknown length
 * 17012 36673: contig of 19862 bp in length
 * 36674 198295: gap of unknown length
 * 36774 198295: contig of 161522 bp in length.

FEATURES

source

1. 198295
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-902P10"
 /clone_lib="RPCI human BAC library 11"
 2068. 2167
 /estimated_length=unknown
 16912. 17011
 /estimated_length=unknown
 36674. 36773
 /estimated_length=unknown

ORIGIN

Query Match 86.3%; Score 35.4; DB 14; Length 198295;
 Best Local Similarity 94.6%; Pred. No. 0.57;
 Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCCGATGCCAGTCCTCATCGTGGCCGCGCG 40
 |||||
 Db 197694 CTTCCGATGCCAGTCCTCATCGTGGCCGCGCG 197730

RESULT 71

AC141270/c 202023 bp DNA linear HTG 11-MAR-2003
 LOCUS Homo sapiens chromosome 16 clone RP11-1403C5, WORKING DRAFT
 DEFINITION SEQUENCE, 16 unordered pieces.

ACCESSION AC141270.1 GI:28913050
 VERSION AC141270
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

1 (bases 1 to 202023)
 DOE Joint Genome Institute.
 Unpublished
 Sequencing of Human Chromosome 16
 2 (bases 1 to 202023)
 DOE Joint Genome Institute.

Direct Submission
 Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT

-----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: <http://www.jgi.doe.gov>

 Project Information
 Center Project Name: 2758439

```
Center clone name: RPCI-11_1403C5
-----
Summary Statistics
Consensus quality: 188196 bases at least Q40
Consensus quality: 193761 bases at least Q30
Consensus quality: 196373 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 200523; sum-of-contigs estimation
Quality coverage: 6.9 in Q20 bases; agarose-fp estimation
Quality coverage: 6.05 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1163: contig of 1163 bp in length
* 1164 1263: gap of unknown length
* 1264 2684: contig of 1420 bp in length
* 2684 2784: gap of unknown length
* 2784 3977: contig of 1194 bp in length
* 3977 4078: gap of unknown length
* 4078 6062: contig of 1984 bp in length
* 6062 6162: gap of unknown length
* 6162 8287: contig of 2126 bp in length
* 8287 8388: gap of unknown length
* 8388 11347: contig of 2960 bp in length
* 11347 14447: gap of unknown length
* 14447 14935: contig of 3498 bp in length
* 14935 15035: gap of unknown length
* 15035 18719: contig of 3684 bp in length
* 18719 23842: contig of 5023 bp in length
* 23842 23943: gap of unknown length
* 23943 28674: contig of 4732 bp in length
* 28674 28774: gap of unknown length
* 28774 37698: contig of 8924 bp in length
* 37698 37798: gap of unknown length
* 37798 49026: contig of 11228 bp in length
* 49026 49126: gap of unknown length
* 49126 69390: contig of 20264 bp in length
* 69390 69491: gap of unknown length
* 69491 98117: contig of 28627 bp in length
* 98117 98218: gap of unknown length
* 98218 123984: contig of 25767 bp in length
* 123984 124084: gap of unknown length
* 124084 124085: contig of 77939 bp in length.
* 124085 202023: contig of 77939 bp in length.
*
Location/Qualifiers
1. .202023
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosomes="16"
/clone="RP11-1403C5"
/clone_lib="RPCI human BAC library 11"
1164. .1263
/estimated_length=unknown
2684. .2783
/estimated_length=unknown
3978. .4077
/estimated_length=unknown
6062. .6161
/estimated_length=unknown
8288. .8387
/estimated_length=unknown
11348. .11447
/estimated_length=unknown
14936. .15035
/estimated_length=unknown
18720. .18819
/estimated_length=unknown
```

```
gap
23843. .23942
/estimated_length=unknown
28675. .28774
/estimated_length=unknown
37699. .37798
/estimated_length=unknown
49027. .49126
/estimated_length=unknown
69391. .69490
/estimated_length=unknown
98118. .98217
/estimated_length=unknown
123985. .124084
/estimated_length=unknown
ORIGIN
Query Match 84.4%; Score 34.6; DB 14; Length 202023;
Best Local Similarity 87.8%; Pred. No. 0.98;
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAGCCTCGGATGCCAGTCCCTCATCGCTGCCCGGCGCG 41
|||||
Db 124133 AAGCCTCGGATGAGCAGTCCCTCATCGCTGCCCGGAGCG 124093
|||||
RESULT 72
AC140888/c
AC140888/c
LOCUS
DEFINITION
Homo sapiens chromosome 16 clone RP11-1374G10, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
AC140888
AC140888
AC140888.1 GI:28849999
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 159468)
AUTHORS
DOE Joint Genome Institute.
TITLE
Sequencing of Human Chromosome 16
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 159468)
AUTHORS
DOE Joint Genome Institute.
TITLE
Direct Submission
JOURNAL
Unpublished
COMMENT
Submitted (05-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Project Name: 2747404
Center clone name: RPCI-11_1374G10
-----
Summary Statistics
Consensus quality: 154250 bases at least Q40
Consensus quality: 155068 bases at least Q30
Consensus quality: 155682 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 158368; sum-of-contigs estimation
Quality coverage: 7.76 in Q20 bases; agarose-fp estimation
Quality coverage: 8.62 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1068: contig of 1068 bp in length
```


AX281458
AX281458.1
GI:16608713

ADONIS
Bickel, R. S., Johnson, R. L., Antonevics, R. A., Ayerle, R. J., Benjamine, P.,
Blakesley, R. W., Boake, A., Bouffard, G. G., Brinkley, C., Brooks, S.,
Chu, G., Coleman, H., Engle, J., Gestole, M., Guan, X., Gupta, J.,
Gutierrez, P., Haghghi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P.,
Hunter, G., Hurle, B., Idol, J. R., Jones, C., Kwong, P., Leric, P.,

Larson, S., Lee-Lin, S.-Q., Legaspi, R., Madden, M., Maduro, Q.L.,
 Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
 Mullikin, J.C., Oestreicher, J.S., Park, M., Portnoy, M.E., Prasad, A.,
 Puri, O., Reddix-Dugue, N., Rosas, B., Schandler, K., Schueler, M.G.,
 Simon, C., Stantripp, S., Stephen, E., Taye, A., Thomas, J.W.,
 Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and
 Green, E.D.
 NISC Comparative Sequencing Initiative
 Unpublished
 2 (bases 1 to 187328)
 Green, E.D.
 Direct Submission
 Submitted (04-AUG-2004) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA
 3 (bases 1 to 187328)
 Green, E.D.
 Direct Submission
 Submitted (17-DEC-2004) NIH Intramural Sequencing Center, 5625
 Fishers Lane, Rockville, MD 20852, USA
 On Dec 17, 2004 this sequence version replaced gi:50950307.
 ----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: <http://www.nisc.nih.gov>
 Contact: nisc_zoo@nhgri.nih.gov
 ----- Project Information
 Center project name: hdd
 Center clone name: 022E04

The sequence data in this record represents an 'enhanced'
 version of a Phase 2 submission. Specifically, the indicated
 order and orientation of each sequence contig has been
 established using one or more of the following: read-pair
 data from individual subclones, overlaps with neighboring
 clones, alignment with available reference sequence (e.g.,
 human), and/or confirmation by PCR testing. In addition,
 the sequence assembly is generally based on at least 8X average
 coverage in Q20 bases and has been reviewed to rule out
 gross misassemblies, the low-quality ends of sequence
 contigs have been trimmed away, and each base is associated
 with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 182980 bases at least Q40
 Consensus quality: 184487 bases at least Q30
 Consensus quality: 185588 bases at least Q20
 Insert size: 205000; agarose-fp
 Insert size: 186228; sum-of-contigs
 Quality coverage: 8.35x in Q20 bases; agarose-fp
 Quality coverage: 9.19x in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 12 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

* 1 680: contig of 680 bp in length
 * 681 780: gap of unknown length
 * 781 13903: contig of 13123 bp in length
 * 13904 14003: gap of unknown length
 * 14004 23574: contig of 9571 bp in length
 * 23575 23674: gap of unknown length
 * 23675 26625: contig of 2951 bp in length
 * 26626 26725: gap of unknown length
 * 26726 33344: contig of 6619 bp in length
 * 33345 33444: gap of unknown length
 * 33445 39599: contig of 6155 bp in length

* 39600 39699: gap of unknown length
 * 39700 79220: contig of 39521 bp in length
 * 79221 79320: gap of unknown length
 * 79321 110884: contig of 31564 bp in length
 * 110885 110984: gap of unknown length
 * 110985 139631: contig of 28647 bp in length
 * 139632 139731: gap of unknown length
 * 139732 158383: contig of 18652 bp in length
 * 158384 158483: gap of unknown length
 * 158484 160485: contig of 2002 bp in length
 * 160486 160585: gap of unknown length
 * 160586 187328: contig of 26743 bp in length.
 Location/Qualifiers
 1..187328
 /organism="Papio anubis"
 /mol_type="genomic DNA"
 /db_xref="taxon:9555"
 /clone="RP41-22E4"
 /clone_lib="RP41"
 /note="BAC resource: <http://bacpac.chori.org/>"
 1..680
 /note="assembly_fragment
 clone_end:T7
 vector_side:left"
 681..780
 /estimated_length=unknown
 781..13903
 /note="assembly_fragment"
 13904..14003
 /estimated_length=unknown
 14004..23574
 /note="assembly_fragment"
 23575..23674
 /estimated_length=unknown
 23675..26625
 /note="assembly_fragment"
 26626..26725
 /estimated_length=unknown
 26726..33344
 /note="assembly_fragment"
 33345..33444
 /estimated_length=unknown
 33445..39599
 /note="assembly_fragment"
 39600..39699
 /estimated_length=unknown
 39700..79220
 /note="assembly_fragment"
 79221..79320
 /estimated_length=unknown
 79321..110884
 /note="assembly_fragment"
 110885..110984
 /estimated_length=unknown
 110985..139631
 /note="assembly_fragment"
 139632..139731
 /estimated_length=unknown
 139732..158383
 /note="assembly_fragment"
 158384..158483
 /estimated_length=unknown
 158484..160485
 /note="assembly_fragment"
 160486..160585
 /estimated_length=unknown
 160586..187328
 /note="assembly_fragment
 clone_end:SP6
 vector_side:right"
 ORIGIN
 Query Match 70.7%; Score 29; DB 14; Length 187328;

Best Local Similarity 83.8%; Pred. No. 46;
Matches 31; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGCGCCGCGN 37
|||||
Db 13858 AAGCTCCGGATGCCAGTCCCTCATCGTCGCGCGTC 13894
|||||

RESULT 76
AY596297 27/c
WPCOMMENT

Sequence split into 32 fragments LOCUS AY596297 Accession AY596297

Fragment Name	Begin	End
AY596297_00	1	110000
AY596297_01	100001	210000
AY596297_02	200001	310000
AY596297_03	300001	410000
AY596297_04	400001	510000
AY596297_05	500001	610000
AY596297_06	600001	710000
AY596297_07	700001	810000
AY596297_08	800001	910000
AY596297_09	900001	1010000
AY596297_10	1000001	1110000
AY596297_11	1100001	1210000
AY596297_12	1200001	1310000
AY596297_13	1300001	1410000
AY596297_14	1400001	1510000
AY596297_15	1500001	1610000
AY596297_16	1600001	1710000
AY596297_17	1700001	1810000
AY596297_18	1800001	1910000
AY596297_19	1900001	2010000
AY596297_20	2000001	2110000
AY596297_21	2100001	2210000
AY596297_22	2200001	2310000
AY596297_23	2300001	2410000
AY596297_24	2400001	2510000
AY596297_25	2500001	2610000
AY596297_26	2600001	2710000
AY596297_27	2700001	2810000
AY596297_28	2800001	2910000
AY596297_29	2900001	3010000
AY596297_30	3000001	3110000
AY596297_31	3100001	3131724

Continuation (28 of 32) of AY596297 from base 2700001 (AY596297 Haloarcula marismortui

Query Match 69.3%; Score 28.4; DB 1; Length 110000;
Best Local Similarity 81.6%; Pred. No. 77;
Matches 31; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGTCGCGCCGCGC 40
|||||
Db 41062 GCCTCCGAAGCGGTCTCTCATCGTCGCGCCGCGC 41025
|||||

RESULT 77
AC116286
LOCUS
DEFINITION Rattus norvegicus clone CH230-372F11, WORKING DRAFT SEQUENCE, 2
173370 bp DNA linear HTG 15-NOV-2002
unordered pieces.
AC116286
VERSION AC116286.7 GI:25013250
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Murinae; Rattus.
1 (bases 1 to 173370)
Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Ayoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

REFERENCE
AUTHORS

```

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GUDE
Center clone name: CH230-372F11
----- Summary Statistics
Assembly program: Phrap; version 0.980329
Consensus quality: 164395 bases at least Q40
Consensus quality: 16506 bases at least Q30
Consensus quality: 166400 bases at least Q20
Estimated insert size: 167474; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
  (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
  * consists of 2 contigs. The true order of the pieces
  * is not known and their order in this sequence record is
  * arbitrary. Gaps between the contigs are represented as
  * runs of N, but the exact sizes of the gaps are unknown.
  * This record will be updated with the finished sequence
  * as soon as it is available and the accession number will
  * be preserved.
* 1 172229: contig of 172229 bp in length
* 172230 172329: gap of unknown length
* 172330 173370: contig of 1041 bp in length.
FEATURES
    Location/Qualifiers
        1..173370
            /organism="Rattus norvegicus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10116"
            /clone="CH230-372F11"
        misc_feature
            1..2547
                /note="wgs end_extension
                clone_end:7"
        misc_feature
            3694..4596
                /note="clone boundary
                clone_end:77
                site:
                    end sequence:B2220031"
                    complement(164094..165012)
                    /note="clone_boundary
                    clone_end:Sp6
                    site:
                        end sequence:B2220033"
                        171121..172229
                        /note="wgs end_extension
                        clone_end:Sp6"
        gap
            172230..172329
                /estimated_length=unknown
ORIGIN
Query Match
Best Local Similarity 61.5%; Score 25.2; DB 14; Length 173370;
Matches 29; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 4 CCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCGC 41
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 149617 CTCAGATGCCAGTCCCTCATCTCTGGCAGGAGGG 149654
||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 78
AC126160
LOCUS AC126160 192405 bp DNA linear HTG 19-NOV-2002
DEFINITION Rattus norvegicus clone CH230-513K6, WORKING DRAFT SEQUENCE.
ACCESSION AC126160
VERSION AC126160.3 GI:25074406
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

Eukaryota: Metazoa; Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
1 (bases 1 to 192405)
Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Amin,A., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsebrooks,S., Aoyagi,M., Baca,E., Baden,H.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Barber,M., Barnstead,M., Benahmed,F.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Blyth,P., Brown,M.,
Biswal,K., Blair,J., Blankenburg,K., Burrell,K., Calderon,E.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Ceasar,H., Center,A.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Chen,Y., Chen,Z., Chu,J.,
Chacko,J., Chavez,D., Chen,G., Chen,Y., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Derramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gunaratne,P., Haaland,M., Hamil,C., Hamilton,C., Hamilton,K.,
Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,M.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhwari,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
Plopper,P., Poindexter,A., Popovic,D., Primus,E., Pu.L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorrelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Uemani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczek,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu.F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 192405)
Worley,K.C.
Direct Submission
Submitted (04-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 192405)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:22855903.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,

```

individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information

Center project name: KAGX
Center clone name: CH230-513K6

----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 172657 bases at least Q40
Consensus quality: 174253 bases at least Q30
Consensus quality: 175360 bases at least Q20
Estimated insert size: 178085; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 192405: contig of 192405 bp in length.

FEATURES

```

source      Location/Qualifiers
            1..192405
              /organism="Rattus norvegicus"
              /mol_type="genomic DNA"
              /db_xref="taxon:10116"
              /clone="CH230-513K6"
            misc_feature 1..2212
              /note="wgs contig"
            misc_feature 6017..7570
              /note="wgs contig"
            misc_feature complement(179873..180733)
              /note="clone boundary"
              clone_end:Sp6
              site:
                end_sequence:RXBVJ63TV"
            misc_feature 181620..183234
              /note="wgs end extension"
              clone_end:Sp6"
            misc_feature 191336..192405
              /note="wgs end extension"
              clone_end:Sp6"

```

ORIGIN

```

Query Match      61.5%; Score 25.2; DB 14; Length 192405;
Best Local Similarity 76.3%; Pred. No. 6.3e+02;
Matches 29; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 CCTCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
    |||||
Db 8518 CCTCAGATGCCAGTTCCTCATCTCTGGCAGGAGGG 8555
    |||||

```

RESULT 79
AY574424/c

LOCUS AY574424 371 bp DNA linear ENV 11-APR-2004
DEFINITION Uncultured bacterium isolate DGGE gel band 8-e-2 16S ribosomal RNA
gene, partial sequence.

ACCESSION AY574424

VERSION

AY574424.1 GI:46242060

KEYWORDS

ENV.
uncultured bacterium
SOURCE uncultured bacterium

ORGANISM

Bacteria; environmental samples.

REFERENCE

1 (bases 1 to 371)

AUTHORS

Holben,W.E., Feris,K.P., Kettunen,A. and Apajalahti,J.H.

TITLE

GC Fractionation Enhances Microbial Community Diversity Assessment

JOURNAL

Appl. Environ. Microbiol. 70 (4), 2263-2270 (2004)

PUBMED

15066821

AUTHORS

Holben,W.E., Feris,K.P., Kettunen,A. and Apajalahti,J.H.A.

TITLE

Direct Submission

JOURNAL

Submitted (17-MAR-2004) Microbial Ecology Program, The University

FEATURES

Location/Qualifiers

1..371

/organism="uncultured bacterium"

/mol_type="genomic DNA"

/isolates="DGGE gel band 8-e-2"

/isolation_source="chicken gastrointestinal tract"

/specific_host="chicken"

/db_xref="taxon:77133"

/environmental_sample

<1..>371

/product="16S ribosomal RNA"

ORIGIN

```

Query Match      61.0%; Score 25; DB 3; Length 371;
Best Local Similarity 73.2%; Pred. No. 2.3e+03;
Matches 30; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCTTCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
    |||||
Db 84 AAGCCCCGGGATTTCACCTCCCACTCGCGCGCGCGCTCG 44
    |||||

```

RESULT 80

AR621724/c

LOCUS

AR621724

DEFINITION

Sequence 3125 from patent US 6833447.

ACCESSION

AR621724

VERSION

AR621724.1

KEYWORDS

GI:59726206

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1424)

AUTHORS

Goldman,B.S., Hinkle,G.J., Slater,S.C. and Wiegand,R.C.

TITLE

Myxococcus xanthus genome sequences and uses thereof

JOURNAL

Patent: US 6833447-A 3125 21-DEC-2004;

JOURNAL

Monsanto Technology, LLC; St. Louis, MO

FEATURES

Location/Qualifiers

1..1424

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

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Query Match      60.0%; Score 24.6; DB 6; Length 1424;
Best Local Similarity 74.4%; Pred. No. 2.4e+03;
Matches 29; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
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Db 606 GCGCGCGGGGCCAGCCCTCGATGCTGCGCGGTAGCG 568
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RESULT 81

AR619747/c

LOCUS

AR619747

15268 bp DNA linear PAT 14-FEB-2005

1 Venter, J.C., Adams, M., Li, P.W. and Myers, E.W.
 TITLE Detection kits, such as nucleic acid arrays, for detecting the
 expression of 10,000 or more *Drosophila* genes and uses thereof
 JOURNAL Patent: WO 0171042-A 42775 27-SEP-2001;
 PE Corporation (NY) (US)

FEATURES
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 1. 5083
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 /mol_type="unassigned DNA"
 /db_xref="taxon:7242"

ORIGIN
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 Best Local Similarity 75.7%; Pred. No. 2.5e+03;
 Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GCTCTCGGATGCCAGTCCCTCATCGCTGGCGCCGCGNCG 39
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RESULT 84
 AE012414/c

LOCUS
 DEFINITION Xanthomonas campestris pv. campestris str. ATCC 33913, section 322
 of 460 of the complete genome.
 ACCESSION AE012414 AE008922
 VERSION AE012414.1 GI:21114210
 KEYWORDS
 SOURCE Xanthomonas campestris pv. campestris str. ATCC 33913
 ORGANISM Xanthomonas campestris pv. campestris str. ATCC 33913
 Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 Xanthomonadaceae; Xanthomonas.

REFERENCE
 AUTHORS
 1 (bases 1 to 12393)
 da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R.,
 Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida, N.F.,
 Jr., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.E.A.,
 Camarotte, G., Cannavan, F., Cardozo, J., Chamberg, F., Ciapina, L.P.,
 Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorry, H.,
 Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T.,
 Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A.,
 Katsuyama, A.M., Kishi, L.T., Leite, R.P. Jr., Lemos, E.G.M.,
 Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M.B.N.,
 Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M.,
 Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K.,
 Oliveira, M.C., Oliveira, V.R., Pereira, H.A. Jr., Rossi, A.,
 Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Takita, M.A.,
 Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M.,
 Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and Kitajima, J.P.
 Comparison of the genomes of two *Xanthomonas* pathogens with
 differing host specificities
 Nature 417 (6887), 459-463 (2002)

TITLE
 JOURNAL
 PUBMED
 12024217

REFERENCE
 AUTHORS
 2 (bases 1 to 12393)
 da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R.,
 Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida, N.F.,
 Jr., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.E.A.,
 Camarotte, G., Cannavan, F., Cardozo, J., Chamberg, F., Ciapina, L.P.,
 Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorry, H.,
 Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T.,
 Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A.,
 Katsuyama, A.M., Kishi, L.T., Leite, R.P. Jr., Lemos, E.G.M.,
 Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M.B.N.,
 Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M.,
 Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K.,
 Oliveira, M.C., Oliveira, V.R., Pereira, H.A. Jr., Rossi, A.,
 Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Takita, M.A.,
 Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M.,
 Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and Kitajima, J.P.
 Direct Submission
 Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade
 Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900.

FEATURES	source	Brazil	Location/Qualifiers	1. .12393
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				/strain="ATCC 33913"
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gene	CDS			/gene="XCC2999"
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gene	CDS			/note="XCC2999"
				/note="putative; ORF located using Glimmer/Genemark"
gene	CDS			/codon_start=1
				/transl_table=11
gene	CDS			/product="hypothetical protein"
				/protein_id="AAM42271.1"
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				/translation="MYVCDNPVCCASYGTHGTELTGLCSPSCMPHAHSDLPPTPGYLRA
gene	CDS			MALKAYREVANAAQMDLLDAAAP"
				470. .595
gene	CDS			/gene="XCC3000"
				470. .595
gene	CDS			/note="XCC3000"
				/note="putative; ORF located using Glimmer/Genemark"
gene	CDS			/codon_start=1
				/transl_table=11
gene	CDS			/product="hypothetical protein"
				/protein_id="AAM42272.1"
gene	CDS			/db_xref="GI:21114212"
				/translation="MAQLMRLGMLSSRTHSMHALATDAAMELLDYGSVAREISA"
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				/gene="XCC3001"
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gene	CDS			/note="XCC3001"
				/note="putative; ORF located using Glimmer/Genemark"
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				/transl_table=11
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				/protein_id="AAM42273.1"
gene	CDS			/db_xref="GI:21114213"
				/translation="MSQSNGWATAQAAPRFVDAPSQSQYVAPKKREQADVLRQVE
gene	CDS			AHLASGGAYEVITTPRPIGKSLAALRSTRVKG"
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gene	CDS			/note="orf37"
				/note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer/Genemark"
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				/transl_table=11
gene	CDS			/product="phage-related protein"
				/protein_id="AAM42274.1"
gene	CDS			/db_xref="GI:21114214"
				/translation="MLQRLERDYLKIRSGTSMRGVCVPACSKKLYTFEPKPVWIK
gene	CDS			CGREACKGHELVKDLDDYDFDDWSKFPMTQASPTASADAYLESSRGFALAPLRGLY
				TOESYDITKVEGTATFDALDKGQWNERLIDRPHFGKQAFAPGKSPYAGAWWCAP
gene	CDS			AAAEILMTVTEVEGIFDAIALLQHVCAVSAMCNAPDPESLRQLAKRAGNLPT
				LWGLNDPGARDYTHKHARRADALGNSRAALIQAOPVTGKIDWDLHLRAQAGDS
gene	CDS			OKQDAAATEARYOGDILLMARSATEKGLLMYDHNQASDFWLEYSRLYFEPDTRVFE
				KLLRDVEFEUSEIDPKLAKIRACSVNKIANYCEALYFORQVDESDEWYFRID
gene	CDS			FPHDANSYKGTFTGGHSSASEFKKRLISLAAGMFTGSGHQDLRIEETQAIKIVE
				AIDFVSGKHEARVLLGDIAVRDGEVVTANEEYDFSPKLRLLKSTQKSRLEITQDPE
gene	CDS			AFRMDLWMLQCFGTGHWAMTAFVGLFAEQIRAGKHSFPFLEATGAGAGKTTLL
				TFLKGLGRSDYEGDPKAKSGARFAMGOISMPVULLLEADSEPDKAHAKTEFWD
gene	CDS			ELKQFPGGGTLATRGVNGNDYEPFRGTIVISQNAVDASEALLTRIVKLHKFRP
				QVTTESIRPAADNLNALQVEELSHFLIKAVCEGAILLEFAERVVKFYEARLRKPDRLR
gene	CDS			ERVITKNHQAUMALLDCLRMWITIPPEIMIKATRDALLEMAFERQKAIASADHAQVFEW
				VEYLEATNGKPVNHSRDSATIAINQFAAKAAQFSQVVPDLKVLRLGLLADSRHH
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gene      5932. .6024
CDS       /gene="XCC3009"
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          /gene="XCC3009"
          /note="putative; ORF located using Glimmer/Genemark"

Query Match      59.0%; Score 24.2; DB 1; Length 12393;
Best Local Similarity 75.7%; Pred. No. 2.1e+03;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      5  CTCGGATCCAGTCCTCATCGCTGCGCCCGNCGCG 41
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Db      11465 CGCGGATGCCGTCGCTTGGCGTGGCCCTGTGCGG 11429

RESULT 85
AC020333      33483 bp      DNA      linear      HTG 03-JAN-2000
LOCUS      Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
DEFINITION      AC020333
ACCESSION      AC020333
VERSION      AC020333.1 GI:6664564
KEYWORDS      HTG; HTGS_PHASE2.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
      Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 33483)
AUTHORS      Adams,M. and Venter,J.C.
TITLE      Direct Submission
JOURNAL      Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
      Rockville, MD, USA
COMMENT      This sequence was identified as CDM:10212803 by the submitter.
      * NOTE: This is a 'working draft' sequence.
      * This sequence will be replaced
      * by the finished sequence as soon as it is available and
      * the accession number will be preserved.

FEATURES
      source
      1. .33483
      /organism="Drosophila melanogaster"
      /mol_type="genomic DNA"
      /db_xref="taxon:7227"

ORIGIN

Query Match      59.0%; Score 24.2; DB 14; Length 33483;
Best Local Similarity 75.7%; Pred. No. 1.7e+03;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      3  GCCTCGGATGCCAGTCCTCATCGCTGCGCCCGNCGC 39
      | | | | | | | | | | | | | | | | | | | | | |
Db      28360 GTCTCGGATGCCACACCCAGCGCTGGATGGGCG 28396

RESULT 86
BA000040_71
WPCOMMENT      Sequence split into 91 fragments LOCUS BA000040 Accession BA000040
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      BA000040_01      100001      210000
      BA000040_02      200001      310000
      BA000040_03      300001      410000
      BA000040_04      400001      510000
      BA000040_05      500001      610000
      BA000040_06      600001      710000
      BA000040_07      700001      810000
      BA000040_08      800001      910000
      BA000040_09      900001      1010000
      BA000040_10      1000001      1110000
      BA000040_11      1100001      1210000
      BA000040_12      1200001      1310000
      BA000040_13      1300001      1410000
      BA000040_14      1400001      1510000
      BA000040_15      1500001      1610000
      BA000040_16      1600001      1710000
      BA000040_17      1700001      1810000
      BA000040_18      1800001      1910000
      BA000040_19      1900001      2010000
      BA000040_20      2000001      2110000
      BA000040_21      2100001      2210000
      BA000040_22      2200001      2310000
      BA000040_23      2300001      2410000
      BA000040_24      2400001      2510000
      BA000040_25      2500001      2610000
      BA000040_26      2600001      2710000
      BA000040_27      2700001      2810000
      BA000040_28      2800001      2910000
      BA000040_29      2900001      3010000
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Continuation (72 of 91) of BA000040 from base 7100001 (BA000040 Bradyrhizobium japonicum)

Query Match	59.0%	Score 24.2;	DB 1;	Length 110000;
Best Local Similarity	75.7%;	Pred. No. 1.4e+03;		
Matches 28; Conservative	1;	Mismatches 8;	Indels 0;	Gaps 0;

Qy 4 CCTCCGGATGCAGTCCCTCATCGCTGGCCCCGNGCG 40
 | | | | | | | | | | | | | | | | | | | |
Db 62568 CTTCTGGTGCCAGTCACAGCAGCGACGCCCGGTGCG 62604
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RESULT 87
CP000050_13
WDCOMMENT

Sequence split into 52 fragments LOCUS CP000050 Accession CP000050

Fragment Name	Begin	End
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CP000050_02	200001	310000
CP000050_03	300001	410000
CP000050_04	400001	510000
CP000050_05	500001	610000
CP000050_06	600001	710000
CP000050_07	700001	810000
CP000050_08	800001	910000
CP000050_09	900001	1010000
CP000050_10	1000001	1110000
CP000050_11	1100001	1210000
CP000050_12	1200001	1310000
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Continuation (14 of 52) of CP000050 from base 1300001 (CP000050 Xanthomonas campestris p

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Query Match      59.0%; Score 24.2; DB 1; Length 110000;
Best Local Similarity 75.7%; Pred. No. 1.4e+03;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCTCATCGCTGGCCGCCGCG 41
Db 84070 CGCCGGATGGCGTCGCTGGCGCTGGCCCTCTCGG 84106

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RESULT 88	AC093438/c	LOCUS	AC093438	167344 bp	DNA	linear	INV 13-JUN-2002
DEFINITION			<i>Drosophila melanogaster</i>	3L BAC RP98-26C20		(Roswell Park Cancer Institute <i>Drosophila</i> BAC Library)	complete sequence.

LOCUS	AC093438	157344 bp	DNA	linear	INV 13-JUN-2002
DEFINITION	Drosophila melanogaster 3L BAC RP98-26C20 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence.				
ACCESSION	AC093438				
VERSION	AC093438.2	GI:21397245			
KEYWORDS	HTG.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1 (bases 1 to 157344)				

REFERENCE
AUTHORS

1 (bases 1 to 167344)
Purification, *Electrophoretic, Phosphoproteins*.

Muzny, D., Scherer, S., Adams, M.D., Holt, R.A., Evans, C.A.,
Gocayne, J.D., Tabor, P., Williamson, A., Homs, F.H.,
Dugan-Rocha, S., Sodergren, E.S., Hodgson, A.H., Chen, R.C.,
Ayle, M., Scott, G.S., Worley, K.W., Amaratides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Beeson, K.Y., Brown, M., Buhray, C.,
Buesam, A., Center, A., Chen, G., Chen, Z., Clerc-Blankenburg, K.,
Davisport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.E.,
Draper, H., Emery-Cohen, A., Ferreira, S., Garg, N.D.S., Houck, J.,
Hoscin, D., Howland, T.J., Hume, J., Ibegwan, C., Jallali, M., Kovar, C.,
Liu, W., Mattci, B., McIntosh, T.C., Morgan, M., May, M., Murphy, B.,
Nelson, K.A., Ndaasa, Y., Nguyen, N., Perez, L., Pittman, G.S., Puri, V.,
Schaefer, F., Shen, H., Strong, R., Tector, C., Wang, Q., Williams, S.M.,
Xiang, J., Zaveri, J.S., Zhou, J., Zorrilla, S., Smith, H.O.,
Wheeler, D., Weinstein, G., Gibbs, R. and Venter, J.C.

Direct Submission

TITLE

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Unpublished
2 (bases 1 to 167344)

Albrooks, S.L., Amaratunge, H.C., Ali-odunla, B., Ali-odman, F.R., Allen, C.,
Worley, K.C., Adams, C.,
Benton, J.J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J.,
Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhan, C.,
Burke, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Davy-Garroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
Foster, P., Franz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Correll, J.H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W.,
Loudesed, H., Lozada, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mathiney, E., McLeod, M.P., Meador, M.,
Mel, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Monabbat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojboom, I., Rolfe, M.,
Ruiz, S., Savery, G., Scher, S., Scott, G., Shen, H., Shoohtari, N.,
Sison, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H.,

Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, F., Teifrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Washington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Wu, C., Wu, Y., Wu, F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

Direct Submission

TITLE

JOURNAL

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AUTHORS

3 (bases 1 to 167344)

Worley, K.C., Adams, C., Radjo-Oduola, B., Ali-oesman, F.R., Allen, C., Alsbrooks, S.L., Amarutunge, H.C., Are, J.R., Banks, T., Barbara, J., Benton, J., Binaige, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chaves, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Delerich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, P., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kurehi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisleged, H., Lozada, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, M., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okuonu, G., Orghuanye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabar, P., Tamirisio, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Tetford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

Direct Submission

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4 (bases 1 to 167344)

Worley,K.C., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alesbrooks,S.L., Amaratunga,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowles,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bunay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chaves,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinth,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Rogues,M., Holloway,C.,
Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,

Db 155892 GTCTCCGATGCCACACCCAGCGCTGGAGTGGCG 155856

RESULT 89
AC091223/c
LOCUS

DEFINITION
Drosophila melanogaster 3L BAC RP98-4866 (Roswell Park Cancer
Institute Drosophila BAC Library) complete sequence.

AC091223
AC091223.2 GI:15412432

KEYWORDS
HTG.

SOURCE
Drosophila melanogaster (fruit fly)

ORGANISM
Drosophila melanogaster

REFERENCE
Sukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

AUTHORS
Muzny, D., Scherer, S., Adams, M.D., Holt, R.A., Evans, C.A.,
Gocayne, J.D., Tabor, P., Williamson, A., Homs, F.H.,
Dugan-Rocha, S.D., Sodergren, E.S., Hodgson, A.H., Chen, R.C.,
Ayele, M.A., Scott, G.S., Worley, K.W., Amaratunga, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Beeson, K.Y., Brown, M., Buhay, C.,
Busam, D.A., Center, A., Chen, G., Chen, Z., Clerc-Blankenburg, K.,
Davenport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.E.,
Draper, H., Emery-Cohen, A., Ferriera, S., Garg, N.D.S., Houck, J.,
Hostin, D., Howland, T.J., Hume, J., Ibegwam, C., Jalali, M., Kovar, C.,
Liu, W., Mattei, B., McIntosh, T.C., Morgan, M., Moy, M., Murphy, B.,
Nelson, K.A., Ndassa, Y., Nguyen, N., Perez, L., Pittman, G.S., Puri, V.,
Scheeler, F., Shen, H., Strong, R., Tector, C., Wang, Q., Williams, S.M.,
Xiang, J., Zaveri, J.S., Zhou, J., Zorrilla, S., Smith, H.O.,
Wheeler, D., Weinstock, G., Gibbs, R. and Venter, J.C.

Direct Submission
Unpublished

REFERENCE
2 (bases 1 to 170988)

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3 (bases 1 to 170988)

REFERENCE
Worley, K.C., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amarutunge, H.C., Are, J.R., Banks, T., Barbara, J.,
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Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyte, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
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Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
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Hollins, B., Honsi, F., Howard, S., Huber, J., Hulvyk, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jollivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulisege, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M.,
Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S.,
Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostrai, N.,
Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,

Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.,
Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S.,
Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

TITLE
JOURNAL

Submitted (01-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT
On Sep 1, 2001 this sequence version replaced gi:13549259.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least 2 exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.
Location/Qualifiers
1. 170988
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/chromosome="3L"
/clone="RP98-4866"

FEATURES
source

Query Match 59.0%; Score 24.2; DB 2; Length 170988;
Best Local Similarity 75.7%; Pred. No. 1.3e+03;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

ORIGIN
3 GCCTCCGATGCCAGTCCCTCATCTGCTGCGCCGCGC 39
DB 46778 GTCTCCGATGCCACACCCAGCGCTGGAGTGGCG 46742

RESULT 90
AC108990/c
LOCUS

DEFINITION
Rattus norvegicus clone CH230-239N24, *** SEQUENCING IN PROGRESS

AC108990 254095 bp DNA linear HTG 08-OCT-2002
***, 3 unordered pieces.

AC108990

VERSION
KEYWORDS
SOURCE
ORGANISM

AC108990.4 GI:23101240
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS

1. (bases 1 to 254095)
Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escoto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jacko, J., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karkathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensheva, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmood, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mahoney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokemele, O., Okwuonu, G., Olarnpungsoo, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.,
Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.

TITLE
JOURNAL
REFERENCE
AUTHORS

2 (bases 1 to 254095)
Worley, K. C.
Direct Submission
Submitted (03-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 254095)

REFERENCE
AUTHORS
TITLE
JOURNAL

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 18, 2002 this sequence version replaced gi:21737656.
The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GPNF
Center clone name: CH230-239N24
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 221155 bases at least Q40
Consensus quality: 223317 bases at least Q30
Consensus quality: 224925 bases at least Q20
Estimated insert size: 242501; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 234792: contig of 234792 bp in length
* 234793 234892: gap of unknown length
* 234893 252933: contig of 18041 bp in length
* 252934 253033: gap of unknown length
* 253034 254095: contig of 1062 bp in length.

FEATURES
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misc_feature

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gap

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/estimated_length=unknown

gap

252934..253033
/estimated_length=unknown

ORIGIN

Query Match 59.0%; Score 24.2; DB 14; Length 254095;
Best Local Similarity 75.7%; Pred. No. 1.2e+03;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 ACCCTCCGATGCCAGTCCCTCATCTGCGCCCGC 38

Db 209977 ACCCTCCGATGCCAGTCCCTCATCTGCGCCCGC 209941

RESULT 91

AE003541/c
LOCUS
DEFINITION
Drosophila melanogaster chromosome 3L, section 44 of 83 of the
complete sequence.
ACCESSION AE003541 AE002602 AE014296

[illegible]

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/old_locus_tag="CG10698"
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/db_xref="FLYBASE:FBgn0036278"
complement(join(28032..29422,30054..30205,31078..31283,
31348..31531,36114..37059,40098..40456))
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/old_locus_tag="CG10698"
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/db_xref="FLYBASE:FBgn0036278"
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/db_xref="GI:23093602"
/db_xref="FLYBASE:FBgn0036278"
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VPEHVDHAPQLSRGLLVYVAVNALFSLGNLLTWNIIKTRISRNSRHTWSAI
YSLMFLSLADVLVTWFCIIIGEAACVTVQWLANELTKLVKLFQMSLYLSTYVLVL
IGVDRWIAVYPMKSLNMAKRCHRLIGGTIILSLPQFFIFHARGPFVEEYFQC
VTHGFYTDQWQMTATFLVFTLLPCLIFGTMYSTPRTISSEKMFQSGKLANY5
TAKLPOTNRORLIHKAKMSLRISVIIIFLCWTVPYVNMIMFNLNPKRLGDD
LQDAIFFGMSNLNPLIYGAFHLCPCGKGSGGGNNNAYSINRGDSQRTPSMLT
AVTQVDGTGSSRQWRAFRQQSYRYSNSTAGPAAPFEQVGLLHVGPNGTPEGGS
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Query Match          59.0%; Score 24.2; DB 2; Length 265524;
Best Local Similarity 75.7%; Pred. No. 1.2e+03;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      3  GCTCCGGATGCAGTCCCTCATCGTGCCTCCGCGCG 39
      |||||
Db      166930  GTCTCCGGATGCCACACCCACACGCTGGAGTGGCG 166894
      |||||
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RESULT 92
BA000030_05
WPCOMMENT
Sequence split into 91 fragments LOCUS BA000030 Accession BA000030
Fragment Name      Begin      End
BA000030_00        1      110000
BA000030_01        100001  210000
BA000030_02        200001  310000
BA000030_03        300001  410000
BA000030_04        400001  510000
BA000030_05        500001  610000
BA000030_06        600001  710000
BA000030_07        700001  810000
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BA000030_08        800001  910000
BA000030_09        900001  1010000
BA000030_10       1000001  1110000
BA000030_11       1100001  1210000
BA000030_12       1200001  1310000
BA000030_13       1300001  1410000
BA000030_14       1400001  1510000
BA000030_15       1500001  1610000
BA000030_16       1600001  1710000
BA000030_17       1700001  1810000
BA000030_18       1800001  1910000
BA000030_19       1900001  2010000
BA000030_20       2000001  2110000
BA000030_21       2100001  2210000
BA000030_22       2200001  2310000
BA000030_23       2300001  2410000
BA000030_24       2400001  2510000
BA000030_25       2500001  2610000
BA000030_26       2600001  2710000
BA000030_27       2700001  2810000
BA000030_28       2800001  2910000
BA000030_29       2900001  3010000
BA000030_30       3000001  3110000
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BA000030_79       7900001  8010000
BA000030_80       8000001  8110000
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BA000030_81 8100001 8210000
BA000030_82 8200001 8310000
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BA000030_87 8700001 8810000
BA000030_88 8800001 8910000
BA000030_89 8900001 9010000
BA000030_90 9000001 9025608

Continuation (6 of 91) of BA000030 from base 500001 (BA000030 Streptomyces avermitilis)

Query Match

Best Local Similarity 58.5%; Score 24; DB 1; Length 110000;

Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCTCCGATGCCAGTCCCTCATCGTGGCCGCGCCG 40

Db 96716 ACCTCTCCGAGCCAGGCCACCTCGACGCCGCTGCG 96755

RESULT 93

AP008208_271

WPCOMMENT

Sequence split into 360 fragments LOCUS AP008208 Accession AP008208

Fragment Name	Begin	End
AP008208_000	1	110000
AP008208_001	100001	210000
AP008208_002	200001	310000
AP008208_003	300001	410000
AP008208_004	400001	510000
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AP008208_006	600001	710000
AP008208_007	700001	810000
AP008208_008	800001	910000
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AP008208_022	2200001	2310000
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AP008208_024	2400001	2510000
AP008208_025	2500001	2610000
AP008208_026	2600001	2710000
AP008208_027	2700001	2810000
AP008208_028	2800001	2910000
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AP008208_031	3100001	3210000
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Query Match 58.5%; Score 24; DB 15; Length 110000;
Best Local Similarity 72.5%; Pred. No. 1.6e+03;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCTCATCGCTGCGCCGCGC 40
    ||||| ||||| ||||| ||||| ||||| |||||
Db 91313 AAGCGCGCGCTGCCCGCCCTCCGTGCTGCCGGCCTC 91352

RESULT 94
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LOCUS AC011051 132830 bp DNA linear HTG 13-JUL-2000
DEFINITION Homo sapiens clone RP11-10C21, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC011051
VERSION AC011051.3 GI:9123812
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 132830)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collins,A.,
Cooke,P., DeArillano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marguis,N.,
McDwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Rilev,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
DIRECT SUBMISSION
Submitted (30-SEP-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6468837.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3043
Center clone name: 10_C_21
-----
* NOTE: This record contains 141 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 822: contig of 822 bp in length
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* 823	922: gap of 100 bp	* 33616	34394: contig of 779 bp in length
* 923	1738: contig of 816 bp in length	* 34395	34494: gap of 100 bp
* 1739	1838: gap of 100 bp	* 34495	35314: contig of 820 bp in length
* 1839	2649: contig of 811 bp in length	* 35315	35414: gap of 100 bp
* 2650	2749: gap of 100 bp	* 35415	36230: contig of 816 bp in length
* 2750	3556: contig of 807 bp in length	* 36231	36330: gap of 100 bp
* 3557	3656: gap of 100 bp	* 36331	37139: contig of 809 bp in length
* 3657	4451: contig of 795 bp in length	* 37140	37239: gap of 100 bp
* 4452	5390: contig of 839 bp in length	* 37240	38060: contig of 821 bp in length
* 4552	5390: contig of 839 bp in length	* 38061	38160: gap of 100 bp
* 5391	5490: gap of 100 bp	* 38161	38984: contig of 824 bp in length
* 5491	6306: contig of 816 bp in length	* 38985	39084: gap of 100 bp
* 6307	6406: gap of 100 bp	* 39085	39898: contig of 814 bp in length
* 6407	7228: contig of 822 bp in length	* 39899	39998: gap of 100 bp
* 7229	7328: gap of 100 bp	* 40789	40788: contig of 790 bp in length
* 7329	8134: contig of 806 bp in length	* 40889	40888: gap of 100 bp
* 8135	8234: gap of 100 bp	* 41762	41761: contig of 873 bp in length
* 8235	9055: contig of 821 bp in length	* 41862	41861: gap of 100 bp
* 9056	9155: gap of 100 bp	* 42671	42670: contig of 809 bp in length
* 9156	9958: contig of 803 bp in length	* 42771	42770: gap of 100 bp
* 9959	10058: gap of 100 bp	* 43581	43580: contig of 810 bp in length
* 10059	10889: contig of 831 bp in length	* 43581	43580: gap of 100 bp
* 10890	10989: gap of 100 bp	* 44487	44486: contig of 806 bp in length
* 10990	11795: contig of 806 bp in length	* 44587	44586: gap of 100 bp
* 11796	11895: gap of 100 bp	* 45392	45391: contig of 805 bp in length
* 11896	12701: contig of 806 bp in length	* 45492	45491: gap of 100 bp
* 12702	12801: gap of 100 bp	* 46315	46314: contig of 823 bp in length
* 12802	13603: contig of 802 bp in length	* 46415	46414: gap of 100 bp
* 13604	13703: gap of 100 bp	* 47229	47228: contig of 814 bp in length
* 13704	14477: contig of 774 bp in length	* 47329	47328: gap of 100 bp
* 14478	14577: gap of 100 bp	* 48170	48269: gap of 100 bp
* 14578	15363: contig of 786 bp in length	* 48270	49077: contig of 808 bp in length
* 15364	15463: gap of 100 bp	* 49078	49177: gap of 100 bp
* 15464	16267: contig of 804 bp in length	* 49178	49970: contig of 793 bp in length
* 16268	16367: gap of 100 bp	* 50071	50070: gap of 100 bp
* 16368	17190: contig of 823 bp in length	* 50899	50898: contig of 828 bp in length
* 17191	17290: gap of 100 bp	* 50999	51805: contig of 807 bp in length
* 17291	18109: contig of 819 bp in length	* 51806	51905: gap of 100 bp
* 18110	18209: gap of 100 bp	* 51906	52712: contig of 807 bp in length
* 18210	19036: contig of 827 bp in length	* 52713	52812: gap of 100 bp
* 19037	19136: gap of 100 bp	* 52813	53607: contig of 795 bp in length
* 19137	19900: contig of 764 bp in length	* 53608	53707: gap of 100 bp
* 19901	20000: gap of 100 bp	* 53708	54499: contig of 792 bp in length
* 20001	20833: contig of 833 bp in length	* 54500	54599: gap of 100 bp
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* 23563	24477: contig of 815 bp in length	* 57325	58138: contig of 814 bp in length
* 24478	24577: gap of 100 bp	* 58139	58238: gap of 100 bp
* 24578	25348: contig of 771 bp in length	* 58239	59049: contig of 811 bp in length
* 25349	25448: gap of 100 bp	* 59050	59149: gap of 100 bp
* 25449	26259: contig of 811 bp in length	* 59150	59375: contig of 826 bp in length
* 26260	26359: gap of 100 bp	* 60076	60075: gap of 100 bp
* 26360	27144: contig of 785 bp in length	* 60076	60904: contig of 829 bp in length
* 27145	27244: gap of 100 bp	* 61005	61004: gap of 100 bp
* 27245	28050: contig of 806 bp in length	* 61818	61817: contig of 813 bp in length
* 28051	28150: gap of 100 bp	* 61918	62726: contig of 809 bp in length
* 28151	28953: contig of 803 bp in length	* 62727	62826: gap of 100 bp
* 28954	29053: gap of 100 bp	* 63632	63631: contig of 805 bp in length
* 29054	29874: contig of 821 bp in length	* 63732	64529: contig of 798 bp in length
* 29875	29974: gap of 100 bp	* 64530	64629: gap of 100 bp
* 29975	30814: contig of 840 bp in length	* 64630	65438: contig of 809 bp in length
* 30815	30914: gap of 100 bp	* 65439	65538: gap of 100 bp
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* 31706	31805: gap of 100 bp		
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* 32712	33515: contig of 804 bp in length		
* 33516	33615: gap of 100 bp		

Query Match 58.5%; Score 24; DB 14; Length 132830;
Best Local Similarity 81.2%; Pred. No. 1.5e+03;

KEYWORDS
SOURCE
ORGANISM

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Bos taurus (cow)

REFERENCE
AUTHORS

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 236171)

REFERENCE
AUTHORS

Muzny, D., Maréchal, M., Metzger, M., Lee, S., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Altschuler, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biwalto, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabis, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gragegeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Haves, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hoques, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensueta, L., Lozsed, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartshayn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
2 (bases 1 to 236171)
Worley, K.C.
Submitted (30-APR-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
3 (bases 1 to 236171)
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

TITLE
JOURNAL
REFERENCE
AUTHORS

On Jun 29, 2005 this sequence version replaced gi:62988449.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas

(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: FFXF
Center clone name: CH240-82C7
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 22350 bases at least Q40
Consensus quality: 22478 bases at least Q30
Consensus quality: 226874 bases at least Q20
Estimated insert size: 225772; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1647: contig of 1647 bp in length
1648 1697: gap of 50 bp
1698 4756: contig of 3059 bp in length
4757 4806: gap of 50 bp
4807 27812: contig of 23006 bp in length
27813 27862: gap of 50 bp
27863 35577: contig of 7715 bp in length
35578 35627: gap of 50 bp
35628 77799: contig of 42172 bp in length
77800 77849: gap of 50 bp
77850 81497: contig of 3648 bp in length
81498 81547: gap of 50 bp
81548 83829: contig of 2282 bp in length
83830 83879: gap of 50 bp
83880 86633: contig of 2754 bp in length
86634 86683: gap of 50 bp
86684 91473: contig of 4790 bp in length
91474 91601: gap of 128 bp
91602 95198: contig of 3597 bp in length
95199 95248: gap of 50 bp
95249 105003: contig of 9755 bp in length
105004 105053: gap of 50 bp
105054 111222: contig of 6169 bp in length
111223 111272: gap of 50 bp
111273 112437: contig of 1165 bp in length
112438 115590: gap of 3153 bp
115591 122531: contig of 6941 bp in length
122532 122581: gap of 50 bp
122582 125026: contig of 2445 bp in length
125027 125115: gap of 89 bp
125116 128652: contig of 3537 bp in length
128653 128752: gap of unknown length
128753 130219: contig of 1467 bp in length
130220 130269: gap of 50 bp
130270 134001: contig of 3732 bp in length
134002 134051: gap of 50 bp
134052 142565: contig of 8514 bp in length

* 142566 142615: gap of 50 bp
* 142616 146534: contig of 3919 bp in length
* 146535 146584: gap of 50 bp
* 146585 159314: contig of 12730 bp in length
* 159315 159364: gap of 50 bp
* 159365 161847: contig of 2483 bp in length
* 161848 161947: gap of unknown length
* 161948 177733: contig of 15786 bp in length
* 177734 178000: gap of 267 bp
* 178001 188762: contig of 10762 bp in length
* 188763 188812: gap of 50 bp
* 188813 211713: contig of 22901 bp in length
* 211714 212063: gap of 350 bp
* 212064 227032: contig of 14569 bp in length
* 227033 227584: gap of 552 bp
* 227585 229483: contig of 1899 bp in length
* 229484 229583: gap of unknown length
* 229584 230628: contig of 1045 bp in length
* 230629 230728: gap of unknown length
* 230729 231738: contig of 1010 bp in length
* 231739 231838: gap of unknown length
* 231839 233118: contig of 1280 bp in length
* 233119 233218: gap of unknown length
* 233219 234568: contig of 1350 bp in length
* 234569 234668: gap of unknown length
* 234669 236171: contig of 1503 bp in length.

FEATURES
source

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="CH240-82C7"
1648. .1697
/estimated_length=50
4757. .4806
/estimated_length=50
27813. .27862
/estimated_length=50
35578. .35627
/estimated_length=50
77800. .77849
/estimated_length=50
81498. .81547
/estimated_length=50
83830. .83879
/estimated_length=50
86634. .86683
/estimated_length=50
91474. .91601

Query Match 58.5%; Score 24; DB 14; Length 236171;
Best Local Similarity 72.5%; Pred. No. 1.4e+03;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGCGCCGAGCC 40
|||||
Db 20751 AAGACTCCCTCCAGTCCATCATGGAGGCCCTGCCCC 20790
|||||

RESULT 98
AC012890/c
LOCUS AC012890 95614 bp DNA linear HTG 03-NOV-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
ACCESSION AC012890
VERSION AC012890.1 GI:6223432
KEYWORDS HTG; HTGS PHASE2.

SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 95614)
AUTHORS Adams, M. and Venter, J. C.

TITLE Direct Submission
JOURNAL Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10211172 by the submitter.
For further information on this sequence you may e-mail to
fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
source

Location/Qualifiers
1. .95614
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"

ORIGIN

Query Match 58.0%; Score 23.8; DB 14; Length 95614;
Best Local Similarity 77.1%; Pred. No. 1.9e+03;
Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 CTTCCGGATGCCAGTCCCTCATCGTCGCGCCGAGCC 38
|||||
Db 4714 CTTCCGGATTCAGATCCTCATAGCTGCGCCCTATC 4680
|||||

RESULT 99
AC005889

LOCUS AC005889 108924 bp DNA linear INV 30-OCT-1998
DEFINITION Drosophila melanogaster, chromosome 2L, region 30A3- 30A6, P1
clones DS06958 and DS03097, complete sequence.

ACCESSION AC005889 AC004726 AC005423
VERSION AC005889.1 GI:3810578
KEYWORDS HTG.

SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 108924)
AUTHORS

Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
Pfeiffer, B., Poon, L., Punch, E., Sequeira, A., Sethi, H., Snir, E.,
Svirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R.,
Zieran, L.L. and Rubin, G.M.

Sequencing of Drosophila chromosome 2L, region 30A3- 30A6
Unpublished (1998)

REFERENCE 2 (bases 1 to 108924)
AUTHORS

Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
Pfeiffer, B., Poon, L., Punch, E., Sequeira, A., Sethi, H., Snir, E.,
Svirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R.,
Zieran, L.L. and Rubin, G.M.

Direct Submission

TITLE Submitted (30-OCT-1998) Berkeley Drosophila Genome Project, MS
JOURNAL 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, US

COMMENT Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720

For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (<http://www.fruitfly.org/sequence/>) or send email
to bdgpf@fruitfly.berkeley.edu.

P1 library locations: 73-46, 33-25.

FEATURES
Source
Location/Qualifiers
1. 108924
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="v2; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2L"
/map="30A3- 30A6"
/clone="P1s DS06958 (D292) and DS03097 (D336)"
/clone_lib="P1 library, partial Sau3A in pNS582tet14Ad10"
/notes="DS03097 (D336) and DS06958 (D292) were completed
as a project. DS03097 extends from P1 end at bp 1 to P1
end at bp 48731. DS06958 extends from P1 end at bp 27620
to P1 end at bp 108,924."

ORIGIN

Query Match 58.0%; Score 23.8; DB 2; Length 108924;
Best Local Similarity 77.1%; Pred. No. 1.8e+03;
Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||||||| ||| ||||| ||||| ||||| |
Db 277 CCTCCGGATTGAGATCCTCATAGCTGGCCCTATC 311

RESULT 100
CP000076_54
WPCOMMENT

Sequence split into 71 fragments LOCUS CP000076 Accession CP000076

Fragment Name	Begin	End
CP000076_00	1	110000
CP000076_01	100001	210000
CP000076_02	200001	310000
CP000076_03	300001	410000
CP000076_04	400001	510000
CP000076_05	500001	610000
CP000076_06	600001	710000
CP000076_07	700001	810000
CP000076_08	800001	910000
CP000076_09	900001	1010000
CP000076_10	1000001	1110000
CP000076_11	1100001	1210000
CP000076_12	1200001	1310000
CP000076_13	1300001	1410000
CP000076_14	1400001	1510000
CP000076_15	1500001	1610000
CP000076_16	1600001	1710000
CP000076_17	1700001	1810000
CP000076_18	1800001	1910000
CP000076_19	1900001	2010000
CP000076_20	2000001	2110000
CP000076_21	2100001	2210000
CP000076_22	2200001	2310000
CP000076_23	2300001	2410000
CP000076_24	2400001	2510000
CP000076_25	2500001	2610000
CP000076_26	2600001	2710000
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CP000076_28	2800001	2910000
CP000076_29	2900001	3010000
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CP000076_41	4100001	4210000

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CP000076_62	6200001	6310000
CP000076_63	6300001	6410000
CP000076_64	6400001	6510000
CP000076_65	6500001	6610000
CP000076_66	6600001	6710000
CP000076_67	6700001	6810000
CP000076_68	6800001	6910000
CP000076_69	6900001	7010000
CP000076_70	7000001	7074893

Continuation (55 of 71) of CP000076 from base 5400001 (CP000076 Pseudomonas fluorescens)

Query Match 58.0%; Score 23.8; DB 1; Length 110000;
Best Local Similarity 77.1%; Pred. No. 1.8e+03;

Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||||||| ||| ||||| ||||| ||||| |
Db 66305 CCACCGGCTGCAAGTCCACACGCGCTTGACGCGCC 66339

Search completed: May 9, 2006, 22:56:49
Job time : 2213 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: May 9, 2006, 22:09:39 ; Search time 270 Seconds
(without alignments)
1012.046 Million cell updates/sec

Title: US-09-904-968A-1_N3336_COPY_3300_3340
Perfect score: 41
Sequence: 1 aagctcccgatgccagtc.....tcatcgctggccgncgcg 41

Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query %	Match Length	DB ID	Description	
1	41	100.0	53522	6	Aad30228 Human PKD	
2	41	100.0	53522	13	Adu03973 Human pol	
3	41	100.0	53522	14	Aeb35216 Human Gef	
4	41	100.0	53526	2	Aat94101 Human PKD	
5	41	100.0	53577	2	Aat18551 Human pol	
6	41	100.0	53577	2	Aat94108 Human PKD	
7	29.8	72.7	623	6	Abq16060 Oligonuc	
8	29.8	72.7	623	6	Abq16061 Oligonuc	
9	29.8	72.7	6423	6	Abq134569 Human met	
10	29.8	72.7	6423	6	Abq170310 Chemical	
11	29.8	72.7	6423	7	Ade99830 Complemen	
12	24.6	60.0	1424	14	Acl66662 M. xanthu	
13	24.6	60.0	15268	14	Acl64679 M. xanthu	
14	24.2	59.0	2202	4	Abl30357 Drosophil	
15	24.2	59.0	5083	4	Abl30356 Drosophil	
16	23	56.1	413	8	Abx51214 Bovine ES	
17	23	56.1	3750	12	Adq59193 MSI-H car	
18	22.6	55.1	768	13	Adt43870 Bacterial	
19	22.6	55.1	2213	13	Adr07671 Full leng	

20	22.6	55.1	22715	9	ADA02852	Ada02852 Human CBX
21	22.6	55.1	22715	10	ADB72590	Adb72590 Human CBX
22	22.6	55.1	22715	10	ADC85331	Adc85331 Mouse CBX
23	22.6	55.1	22715	12	ADM74447	Adm74447 Human car
24	22.4	54.6	622	10	ADK57630	Adk57630 Plant DNA
25	22.4	54.6	1269	11	ABD04866	Abd04866 Pseudomon
26	22.4	54.6	2940	10	ADF28721	Adf28721 Guanylate
27	22.4	54.6	3568	10	ADP28719	Adp28719 Human SAP
28	22.4	54.6	3568	13	ADS09784	Ads09784 Human the
29	22.4	54.6	3705	10	ADC51948	Adc51948 Human pos
30	22.4	54.6	3723	6	ABS67754	Abs67754 Human int
31	22.4	54.6	243390	13	ABD33366	Abd33366 Human can
32	22.4	54.6	243934	14	ADZ13446	Adz13446 Human can
33	22.2	54.1	8301	4	AAF90035	Aaf90035 Nucleotid
34	22.2	54.1	34071	4	AAF90033	Aaf90033 Nucleotid
35	22.2	54.1	42717	4	AAF90032	Aaf90032 Nucleotid
36	22	53.7	518	6	ABN98657	Abn98657 Arabidops
37	22	53.7	1281	14	ACL70733	Act70733 M. xanthu
38	22	53.7	1441	5	ABA20206	Ab20206 Human ner
39	22	53.7	2145	8	ACA43467	Ac43467 Prokaryot
40	22	53.7	2423	11	ADR42106	Adr42106 Human can
41	22	53.7	2423	11	ADR42064	Adr42064 Human can
42	22	53.7	2579	6	ABZ12243	Abz12243 Arabidops
43	22	53.7	4257	13	ADS45922	Ads45922 Bacterial
44	22	53.7	6052	4	AAK84334	Aak84334 Human imm
45	22	53.7	6430	14	ACL64206	Act64206 M. xanthu
46	22	53.7	75252	11	ACN44450	Act44450 Human gen
47	22	53.7	75252	11	ACN44450	Act44450 Human gen
48	22	53.7	90597	10	ADJ72363	Adj72363 Streptomy
49	22	53.7	90600	6	ABQ78872	Abq78872 S. roseos
50	21.8	53.2	289	10	ABX86165	Abx86165 Corn ear-
51	21.8	53.2	623	6	ABQ16058	Abq16058 Oligonuc
52	21.8	53.2	623	6	ABQ16059	Abq16059 Oligonuc
53	21.8	53.2	687	14	ACL72417	Act72417 M. xanthu
54	21.8	53.2	963	13	ADK56687	Adk56687 Plant ful
55	21.8	53.2	1057	14	ABE66674	Aeb66674 Rice geno
56	21.8	53.2	6423	6	ABL34568	Ab134568 Human met
57	21.8	53.2	6423	6	ABL70309	Ab170309 Chemical
58	21.8	53.2	6423	7	ADS99829	Ad99829 Bisleuphit
59	21.8	53.2	6492	4	ABL02587	Ab102587 Drosophil
60	21.8	53.2	9941	3	AAA81461	Aaa81461 N. mening
61	21.8	53.2	10528	14	ACL64482	Act64482 M. xanthu
62	21.8	53.2	16105	4	ABL02586	Ab102586 Drosophil
63	21.8	53.2	110000	3	AAA81490_03	Continuation (4 of
64	21.8	53.2	349980	3	AAF21607	Aaf21607 Neisseria
65	21.6	52.7	230	3	ABQ62923	Abq62923 Mycobacte
66	21.6	52.7	562	13	ADQ54664	Adq54664 Novel can
67	21.6	52.7	1689	14	ACL66884	Act66884 M. xanthu
68	21.6	52.7	18537	14	ACL64694	Act64694 M. xanthu
69	21.6	52.7	24883	13	ABD33069	Abd33069 Murine ca
70	21.6	52.7	349980	6	ABQ81846	Abq81846 Bifidobac
71	21.4	52.2	234	11	ABD06358	Abd06358 Pseudomon
72	21.4	52.2	292	6	ABQ99123	Abq99123 Human ORF
73	21.4	52.2	381	8	ABX51176	Abx51176 Bovine ES
74	21.4	52.2	381	8	ABX51132	Abx51132 Bovine ES
75	21.4	52.2	381	8	ABX50790	Abx50790 Bovine ES
76	21.4	52.2	395	8	ABX50908	Abx50908 Bovine ES
77	21.4	52.2	409	14	ACL68775	Act68775 M. xanthu
78	21.4	52.2	419	8	ABX50923	Abx50923 Bovine ES
79	21.4	52.2	444	11	ABD12724	Abd12724 Pseudomon
80	21.4	52.2	501	11	ABD12690	Abd12690 Pseudomon
81	21.4	52.2	526	12	ACH78213	Act78213 Human gen
82	21.4	52.2	572	4	ABA31177	Ab31177 Probe #96
83	21.4	52.2	572	4	AAK12507	Aak12507 Human bra
84	21.4	52.2	597	10	ADD68671	Add68671 Murine DN
85	21.4	52.2	630	2	AAK81396	Aak81396 Polynucle
86	21.4	52.2	654	11	ABD14505	Abd14505 Pseudomon
87	21.4	52.2	738	11	ABD14229	Abd14229 Pseudomon
88	21.4	52.2	816	11	ABD11508	Abd11508 Pseudomon
89	21.4	52.2	834	11	ABD11440	Abd11440 Pseudomon
90	21.4	52.2	909	11	ABD11189	Abd11189 Pseudomon
91	21.4	52.2	966	11	ABD14344	Abd14344 Pseudomon
92	21.4	52.2	1236	13	ADT47081	Adt47081 Bacterial

c 93	21.4	52.2	1305	9	ADA48031	AdA48031 Rice gene	166	21	51.2	1139	14	ADM69309	Adw69309 Deoxyhyph
c 94	21.4	52.2	1329	10	ADE07095	Ade07095 Novel cod	167	21	51.2	1139	14	ADW48041	Adw48041 Rat apopt
c 95	21.4	52.2	1329	14	ADU40252	Adu40252 Novel hum	168	21	51.2	1139	14	ADY78105	Ady78105 Rat eukar
c 96	21.4	52.2	1356	11	ADB06331	AdB06331 Pseudomon	169	21	51.2	1146	11	ABD14214	Abd14214 Pseudomon
c 97	21.4	52.2	1440	12	ADL94139	AdL94139 Human Rap	170	21	51.2	1236	3	AAC36186	Aac36186 Arabidops
c 98	21.4	52.2	1470	6	ABQ91417	Abq91417 M. capsul	171	21	51.2	1302	6	AAI70852	Aai70852 Wheat glu
c 99	21.4	52.2	1861	4	ABU19573	AbU19573 Drosophi	c 172	21	51.2	1302	8	ACA37686	AcA37686 Prokaryot
c 100	21.4	52.2	2000	11	ACL36154	ACL36154 Rice stre	c 173	21	51.2	1362	14	ACL71897	ACL71897 M. xanthu
c 101	21.4	52.2	2046	11	ABD06378	Abd06378 Pseudomon	c 174	21	51.2	1373	13	ADT15055	Adt15055 Plant CDN
c 102	21.4	52.2	2266	4	ABU02533	AbU02533 Drosophi	175	21	51.2	1737	14	ACL69099	ACL69099 M. xanthu
c 103	21.4	52.2	2751	13	ADS58538	AdS58538 Bacterial	176	21	51.2	1815	13	ADT44783	Adt44783 Bacterial
c 104	21.4	52.2	2886	13	ADT16481	Adt16481 Plant CDN	c 177	21	51.2	1845	11	ABDI4520	Abdi4520 Pseudomon
c 105	21.4	52.2	3274	14	ADM43466	Adw43466 Nemadicti	c 178	21	51.2	1887	13	ADS58861	AdS58861 Bacterial
c 106	21.4	52.2	3548	8	ABT19245	Abt19245 Aspergill	c 179	21	51.2	2185	10	ADB62402	AdB62402 Human CDN
c 107	21.4	52.2	3642	8	ABT21065	Abt21065 Aspergill	c 180	21	51.2	2256	13	ADW78707	Adw78707 Jiejie wh
c 108	21.4	52.2	3880	8	ABT18651	Abt18651 Aspergill	c 181	21	51.2	2421	14	ACL68693	ACL68693 M. xanthu
c 109	21.4	52.2	3880	8	ABT20467	Abt20467 Aspergill	c 182	21	51.2	3174	11	ADM03469	Adm03469 Human CDN
c 110	21.4	52.2	4236	14	ACL68904	ACL68904 M. xanthu	c 183	21	51.2	3672	8	ACA43496	AcA43496 Prokaryot
c 111	21.4	52.2	5879	8	ABT18057	Abt18057 Aspergill	c 184	21	51.2	3921	8	ACA40351	AcA40351 Prokaryot
c 112	21.4	52.2	5880	8	ABT19871	Abt19871 Aspergill	c 185	21	51.2	3921	14	ABE91813	ABE91813 DNA encod
c 113	21.4	52.2	6037	4	ABU02532	AbU02532 Drosophi	c 186	21	51.2	3975	8	ADA69835	Ada69835 Rice gene
c 114	21.4	52.2	6233	4	ABS33449	ABs33449 DNA encod	c 187	21	51.2	3975	11	ACL26811	ACL26811 Rice abio
c 115	21.4	52.2	6323	4	ABU19572	AbU19572 Drosophi	c 188	21	51.2	6798	4	AAH44043	Aah44043 Streptomy
c 116	21.4	52.2	6683	10	ADB53086	AdB53086 Primary r	c 189	21	51.2	6798	5	AAH78258	Aah78258 Nucleotid
c 117	21.4	52.2	6683	13	ADV41291	Adv41291 Rat cardi	c 190	21	51.2	6798	6	AAD31022	Aad31022 Streptomy
c 118	21.4	52.2	11854	14	ACL64574	ACL64574 M. xanthu	c 191	21	51.2	6798	13	ADP90610	Adp90610 Streptomy
c 119	21.4	52.2	18871	4	ABK42430	ABk42430 Genomic s	c 192	21	51.2	6798	13	ADR16784	Adr16784 Streptomy
c 120	21.4	52.2	18871	9	ADB60586	ADB60586 Connectiv	c 193	21	51.2	7628	14	ACL64412	ACL64412 M. xanthu
c 121	21.4	52.2	34662	14	ACL64798	ACL64798 M. xanthu	c 194	21	51.2	8077	6	AAD31028	Aad31028 Operon F
c 122	21.4	52.2	44567	14	ACL56117	Aad56117 Human BAT	c 195	21	51.2	8719	12	ADP90614	Adp90614 Streptomy
c 123	21.4	52.2	44567	9	ADA02479	Ada02479 Human BAT	c 196	21	51.2	8719	13	ADR16788	Adr16788 Streptomy
c 124	21.4	52.2	44567	10	ADB72218	ADB72218 Human BAT	c 197	21	51.2	8974	4	ABK42191	ABk42191 Genomic s
c 125	21.4	52.2	98546	11	ACN44790	ACn44790 Human gen	c 198	21	51.2	8974	9	ADB60347	AdB60347 Connectiv
c 126	21.2	51.7	477	13	ADE07634	AdE07634 Bacterial	c 199	21	51.2	10923	4	ABK42192	ABk42192 Connectiv
c 127	21.2	51.7	1029	10	ADE07634	AdE07634 Novel cod	c 200	21	51.2	10923	9	ADB60348	ADB60348 Connectiv
c 128	21.2	51.7	3288	5	AAS85789	Aas85789 DNA encod	c 201	21	51.2	10923	6	ABZ75344	ABz75344 Human R11
c 129	21.2	51.7	3288	5	AAS87346	Aas87346 DNA encod	c 202	21	51.2	23673	6	ABZ75344	ABz75344 Human R11
c 130	21.2	51.7	3288	5	AAS77395	Aas77395 DNA encod	c 203	21	51.2	39892	11	ACN44150_4	ACn44150_4
c 131	21.2	51.7	3288	5	AAS88746	Aas88746 DNA encod	c 204	21	51.2	41170	14	ACL64804	ACL64804 M. xanthu
c 132	21.2	51.7	3288	5	AAS86010	Aas86010 DNA encod	c 205	21	51.2	109519	5	AAS08693	Aas08693 Micromono
c 133	21.2	51.7	3575	10	ADE63964	AdE63964 Rat gene	c 206	21	51.2	110000	4	AAI99682_06	AAi99682_06
c 134	21.2	51.7	9154	10	ADE56030	Ade56030 Rat gene	c 207	21	51.2	110000	4	AAI99683_06	AAi99683_06
c 135	21.2	51.7	9154	10	ADE56034	Ade56034 Rat gene	c 208	21	51.2	143306	6	ABK49586	ABk49586 Human tra
c 136	21.2	51.7	110000	4	AAI99682_20	AAi99682_20	c 209	20.8	50.7	100	8	ADA72678	Ada72678 Rice gene
c 137	21.2	51.7	110000	4	AAI99683_20	AAi99683_20	c 210	20.8	50.7	270	10	ADF57793	AdF57793 Human pol
c 138	21	51.2	420	11	ABD14686	Abd14686 Pseudomon	c 211	20.8	50.7	352	4	AAK65757	Aak65757 Human imm
c 139	21	51.2	583	10	ADB57230	AdB57230 Toxicity-	c 212	20.8	50.7	352	4	AAK65758	Aak65758 Human imm
c 140	21	51.2	583	10	ADB51782	AdB51782 Primary r	c 213	20.8	50.7	368	4	AAK55348	Aak55348 Human imm
c 141	21	51.2	624	11	ABD14070	Abd14070 Pseudomon	c 214	20.8	50.7	372	8	ABZ54330	ABz54330 Aspergill
c 142	21	51.2	693	14	AEA43179	Aea43179 Perhydrol	c 215	20.8	50.7	451	9	ACH23802	Ach23802 Human adu
c 143	21	51.2	826	12	ADL16417	Adl16417 Human pro	c 216	20.8	50.7	462	4	ADL16510	AdL16510 Human ABC
c 144	21	51.2	893	4	ABA77068	AbA77068 Prolifera	c 217	20.8	50.7	462	5	AAS29559	Aas29559 Human end
c 145	21	51.2	929	3	AAF15097	Aaf15097 Trichoder	c 218	20.8	50.7	462	9	ADA27257	Ada27257 cDNA enco
c 146	21	51.2	929	13	ADU59138	AdU59138 Trichoder	c 219	20.8	50.7	462	10	ADAL12860	AdAl12860 Human ABC
c 147	21	51.2	929	14	ADZ97141	AdZ97141 Trichoder	c 220	20.8	50.7	478	12	ADN12937	Adn12937 Human pro
c 148	21	51.2	946	13	ADR21640	Adr21640 Human enz	c 221	20.8	50.7	496	13	ACF89534	ACf89534 Human S1R
c 149	21	51.2	972	9	ACD26650	ACd26650 Rat corpu	c 222	20.8	50.7	497	9	ACH27203	Ach27203 Human adu
c 150	21	51.2	972	9	ADA06988	Ada06988 Rat eukar	c 223	20.8	50.7	525	12	ACH69280	ACH69280 Human gen
c 151	21	51.2	972	10	ADI00806	Adi00806 Rat apopt	c 224	20.8	50.7	570	14	ACL69478	ACL69478 M. xanthu
c 152	21	51.2	972	12	ADM74631	Adm74631 3' end of	c 225	20.8	50.7	682	3	AAA62589	Aaa62589 Mycobacte
c 153	21	51.2	972	13	ADR70244	Adr70244 Rat apopt	c 226	20.8	50.7	682	9	ADA26951	Ada26951 DNA encod
c 154	21	51.2	972	14	ADW69319	Adw69319 Rat DNA s	c 227	20.8	50.7	717	8	ACA43744	AcA43744 Prokaryot
c 155	21	51.2	972	14	ADW48051	Adw48051 Rat apopt	c 228	20.8	50.7	800	8	ACF64391	ACf64391 Human MPO
c 156	21	51.2	972	14	ADY78115	Ady78115 Rat eukar	c 229	20.8	50.7	810	4	AAF60766	Aaf60766 Pseudomona
c 157	21	51.2	1024	14	ADM15641	Adm15641 Novel Euc	c 230	20.8	50.7	834	11	ACL29778	ACL29778 Rice abio
c 158	21	51.2	1053	4	AAH44045	Aah44045 Streptomy	c 231	20.8	50.7	891	12	ADIS7634	AdiS7634 Human bre
c 159	21	51.2	1065	5	AAH78255	Aah78255 Nucleotid	c 232	20.8	50.7	958	14	ACL63731	ACL63731 M. xanthu
c 160	21	51.2	1065	6	ABL41306	ABl41306 Streptomy	c 233	20.8	50.7	1134	6	ABU51021	ABu51021 Mouse Tab
c 161	21	51.2	1065	6	ABL41306	ABl41306 Streptomy	c 234	20.8	50.7	1134	9	ACD07907	ACd07907 DNA encod
c 162	21	51.2	1139	9	ACD26642	ACd26642 cDNA enco	c 235	20.8	50.7	1253	12	ADIS7635	AdiS7635 Human bre
c 163	21	51.2	1139	10	ADA06968	Ada06968 Rat eukar	c 236	20.8	50.7	1424	13	ADX31585	AdX31585 Plant ful
c 164	21	51.2	1139	12	ADM74635	Adm74635 Rat apopt	c 237	20.8	50.7	1661	6	ABU51010	ABu51010 Mouse Tab
c 165	21	51.2	1139	13	ADR70234	Adr70234 Rat corpu	c 238	20.8	50.7	1661	9	ACD07896	ACd07896 cDNA enco

C 239	20.8	50.7	1875	12	ADQ62872	Adq62872 Novel hum	312	20.6	50.2	3233	9	ADA74927	Ada74927 Human PRO
C 240	20.8	50.7	1887	8	ACA271178	Aca271178 Prokaryot	313	20.6	50.2	3233	9	ADA85005	Ada85005 Novel hum
C 241	20.8	50.7	2166	8	ACA43742	Aca43742 Prokaryot	314	20.6	50.2	3233	9	ADA84453	Ada84453 Novel hum
C 242	20.8	50.7	7000	8	ABZ74421	Abz74421 Secreted	315	20.6	50.2	3233	9	ADB29709	Adb29709 cDNA enco
C 243	20.8	50.7	7000	10	ADC20884	Adc20884 Human sec	316	20.6	50.2	3233	9	ADA80237	Ada80237 Human PRO
C 244	20.8	50.7	7000	10	ABZ67978	Abz67978 Human sec	317	20.6	50.2	3233	9	ADA85479	Ada85479 Human PRO
C 245	20.8	50.7	10813	6	ABQ88640	Abq88640 Human cof	318	20.6	50.2	3233	9	ADA46704	Ada46704 Human PRO
C 246	20.8	50.7	21635	11	ACN44628	Acn44628 Mouse gon	319	20.6	50.2	3233	9	ADB25000	Adb25000 Human PRO
C 247	20.8	50.7	27756	9	ADA02570	Ada02570 Human gat	320	20.6	50.2	3233	9	ADA93176	Ada93176 Human PRO
C 248	20.8	50.7	27756	10	ADB72308	Adb72308 Human gat	321	20.6	50.2	3233	9	ADB26526	Adb26526 cDNA enco
C 249	20.8	50.7	27756	10	ADZ595818	Adz595818 Human gat	322	20.6	50.2	3233	9	ADB30813	Adb30813 cDNA enco
C 250	20.8	50.7	113193	8	AAD54645	Aad54645 Streptomy	323	20.6	50.2	3233	9	ADA60741	Ada60741 Homo sapi
C 251	20.8	50.7	241748	14	ADZ13116	Adz13116 Murine ca	324	20.6	50.2	3233	9	ADB23888	Adb23888 Human PRO
C 252	20.6	50.2	93	2	AAQ63782	Aaq63782 Bovine tr	325	20.6	50.2	3233	9	ADA96217	Ada96217 Human PRO
C 253	20.6	50.2	514	7	AAJ78648	Aaj78648 Differenc	326	20.6	50.2	3233	9	ADA80789	Ada80789 Human PRO
C 254	20.6	50.2	683	3	AAQ63794	Aaq63794 Bovine tr	327	20.6	50.2	3233	9	ADA95665	Ada95665 Human PRO
C 255	20.6	50.2	659	3	AAQ08526	Aaq08526 DNA enco	328	20.6	50.2	3233	9	ADB25974	Adb25974 cDNA enco
C 256	20.6	50.2	699	4	AAF81479	Aaf81479 Bovine me	329	20.6	50.2	3233	9	ADB21459	Adb21459 Novel hum
C 257	20.6	50.2	701	2	AAQ63795	Aaq63795 Bovine tr	330	20.6	50.2	3233	9	ADA77238	Ada77238 Human PRO
C 258	20.6	50.2	702	3	AAA08525	Aaa08525 DNA enco	331	20.6	50.2	3233	9	ADB17978	Adb17978 cDNA enco
C 259	20.6	50.2	744	14	ACL69981	Ac169981 M. xanthu	332	20.6	50.2	3233	9	ADA86661	Ada86661 Novel hum
C 260	20.6	50.2	777	14	ACL66904	Ac166904 M. xanthu	333	20.6	50.2	3233	9	ADA87764	Ada87764 Novel hum
C 261	20.6	50.2	824	4	AAI94462	Aai94462 Human neu	334	20.6	50.2	3233	9	ADA46152	Ada46152 Novel hum
C 262	20.6	50.2	891	4	AAI94329	Aai94329 Human neu	335	20.6	50.2	3233	9	ADB28182	Adb28182 cDNA enco
C 263	20.6	50.2	930	10	ABZ66791	Abz66791 Orthosomy	336	20.6	50.2	3233	9	ADB28734	Adb28734 cDNA enco
C 264	20.6	50.2	1019	10	ADI60268	Adi60268 Secreted	337	20.6	50.2	3233	9	ADA76686	Ada76686 Human PRO
C 265	20.6	50.2	1026	13	ADU06864	Adu06864 Cell adhe	338	20.6	50.2	3233	9	ADA88316	Ada88316 Novel hum
C 266	20.6	50.2	1128	13	ADU06879	Adu06879 Cell adhe	339	20.6	50.2	3233	9	ADA97321	Ada97321 Human PRO
C 267	20.6	50.2	1206	14	AE991740	Aeb991740 DNA enco	340	20.6	50.2	3233	9	ADB27078	Adb27078 cDNA enco
C 268	20.6	50.2	1209	12	ADK13720	Adk13720 E. coli i	341	20.6	50.2	3233	9	ADB22011	Adb22011 Novel hum
C 269	20.6	50.2	1209	14	AE991857	Aeb991857 DNA enco	342	20.6	50.2	3233	9	ADA66702	Ada66702 Human PRO
C 270	20.6	50.2	1319	12	ADM08054	Adm08054 Human CAD	343	20.6	50.2	3233	9	ADB22563	Adb22563 Human PRO
C 271	20.6	50.2	1347	8	ABX56047	Abx56047 M. echino	344	20.6	50.2	3233	9	ADB23336	Adb23336 Human PRO
C 272	20.6	50.2	1398	5	AA888418	Aas88418 DNA enco	345	20.6	50.2	3233	9	ADA92058	Ada92058 Novel hum
C 273	20.6	50.2	1437	8	ACA27324	Aca27324 Prokaryot	346	20.6	50.2	3233	9	ADB15121	Adb15121 Human PRO
C 274	20.6	50.2	1565	5	AAS80911	Aas80911 DNA enco	347	20.6	50.2	3233	9	ADB38373	Adb38373 Novel hum
C 275	20.6	50.2	1610	10	ADI60463	Adi60463 Secreted	348	20.6	50.2	3233	9	ADB37821	Adb37821 Novel hum
C 276	20.6	50.2	1912	5	AAS88896	Aas88896 DNA enco	349	20.6	50.2	3233	10	ADB66293	Adb66293 Novel hum
C 277	20.6	50.2	2218	12	ADQ67316	Adq67316 Novel hum	350	20.6	50.2	3233	10	ADB89373	Adb89373 Human PRO
C 278	20.6	50.2	2280	13	ADU06882	Adu06882 Cell adhe	351	20.6	50.2	3233	10	ADB90105	Adb90105 Human PRO
C 279	20.6	50.2	3002	4	ABL21972	Ab121972 Drosophill	352	20.6	50.2	3233	10	ADB39206	Adb39206 Novel hum
C 280	20.6	50.2	3060	8	ADA69629	Ada69629 Rice gene	353	20.6	50.2	3233	10	ADB46829	Adb46829 Novel hum
C 281	20.6	50.2	3233	4	AAS21284	Aas21284 Human cDN	354	20.6	50.2	3233	10	ADB86436	Adb86436 Human PRO
C 282	20.6	50.2	3233	8	ACA03643	Aca03643 cDNA enco	355	20.6	50.2	3233	10	ADB77041	Adb77041 Novel hum
C 283	20.6	50.2	3233	8	ABX89181	Abx89181 DNA enco	356	20.6	50.2	3233	10	ADB34198	Adb34198 Human PRO
C 284	20.6	50.2	3233	8	ACDA1835	Acda1835 Human sec	357	20.6	50.2	3233	10	ADB35302	Adb35302 Human PRO
C 285	20.6	50.2	3233	8	ACA04084	Aca04084 Human cDN	358	20.6	50.2	3233	10	ADB33646	Adb33646 Human PRO
C 286	20.6	50.2	3233	9	ADA45600	Ada45600 Novel hum	359	20.6	50.2	3233	10	ADB34750	Adb34750 Human PRO
C 287	20.6	50.2	3233	9	ADA76031	Ada76031 Human PRO	360	20.6	50.2	3233	10	ADB35854	Adb35854 Human PRO
C 288	20.6	50.2	3233	9	ADA18681	Ada18681 Human PRO	361	20.6	50.2	3233	10	ADB46249	Adb46249 Novel hum
C 289	20.6	50.2	3233	9	ADA61304	Ada61304 Homo sapi	362	20.6	50.2	3233	10	ADC50122	Adc50122 Novel hum
C 290	20.6	50.2	3233	9	ADB19089	Adb19089 Novel hum	363	20.6	50.2	3233	10	ADC71669	Adc71669 Novel hum
C 291	20.6	50.2	3233	9	ADB27630	Adb27630 cDNA enco	364	20.6	50.2	3233	10	ADC59648	Adc59648 Novel hum
C 292	20.6	50.2	3233	9	ADA86109	Ada86109 Novel hum	365	20.6	50.2	3233	10	ADC52655	Adc52655 Novel hum
C 293	20.6	50.2	3233	9	ADB15673	Adb15673 Human PRO	366	20.6	50.2	3233	10	ADC57009	Adc57009 Novel hum
C 294	20.6	50.2	3233	9	ADA47459	Ada47459 Human PRO	367	20.6	50.2	3233	10	ADC60200	Adc60200 Novel hum
C 295	20.6	50.2	3233	9	ADA67254	Ada67254 Human PRO	368	20.6	50.2	3233	10	ADC50675	Adc50675 Novel hum
C 296	20.6	50.2	3233	9	ADB30261	Adb30261 cDNA enco	369	20.6	50.2	3233	10	ADC65202	Adc65202 Novel hum
C 297	20.6	50.2	3233	9	ADA85557	Ada85557 Novel hum	370	20.6	50.2	3233	10	ADC54300	Adc54300 Novel hum
C 298	20.6	50.2	3233	9	ADA96769	Ada96769 Human PRO	371	20.6	50.2	3233	10	ADC53261	Adc53261 Novel hum
C 299	20.6	50.2	3233	9	ADA79073	Ada79073 Human PRO	372	20.6	50.2	3233	10	ADC58784	Adc58784 Novel hum
C 300	20.6	50.2	3233	9	ADA87212	Ada87212 Novel hum	373	20.6	50.2	3233	10	ADC55662	Adc55662 Novel hum
C 301	20.6	50.2	3233	9	ADB16414	Adb16414 Human PRO	374	20.6	50.2	3233	10	ADC58232	Adc58232 Novel hum
C 302	20.6	50.2	3233	9	ADA91506	Ada91506 Novel hum	375	20.6	50.2	3233	10	ADD02906	Add02906 Novel hum
C 303	20.6	50.2	3233	9	ADB14569	Adb14569 Human PRO	376	20.6	50.2	3233	10	ADC89898	Adc89898 Novel hum
C 304	20.6	50.2	3233	9	ADB18530	Adb18530 Novel hum	377	20.6	50.2	3233	10	ADC69317	Adc69317 cDNA enco
C 305	20.6	50.2	3233	9	ADA93745	Ada93745 Human PRO	378	20.6	50.2	3233	10	ADC48206	Adc48206 Human PRO
C 306	20.6	50.2	3233	9	ADB19641	Adb19641 Novel hum	379	20.6	50.2	3233	10	ADD09735	Add09735 Human PRO
C 307	20.6	50.2	3233	9	ADB12953	Adb12953 Human PRO	380	20.6	50.2	3233	10	ADD04310	Add04310 Novel hum
C 308	20.6	50.2	3233	9	ACD98464	Acd98464 Novel hum	381	20.6	50.2	3233	10	ADC80266	Adc80266 Novel hum
C 309	20.6	50.2	3233	9	ADA74207	Ada74207 Human PRO	382	20.6	50.2	3233	10	ADD10773	Add10773 Human PRO
C 310	20.6	50.2	3233	9	ADB24440	Adb24440 Human PRO	383	20.6	50.2	3233	10	ADC47654	Adc47654 Human PRO
C 311	20.6	50.2	3233	9	ADA81964	Ada81964 Human PRO	384	20.6	50.2	3233	10	ADC79714	Adc79714 Novel hum

385	20.6	50.2	3233	10	ADD09183	Human PRO	Ad009183	Human PRO	458	20.6	50.2	3233	12	ADE91418	Novel hum
386	20.6	50.2	3233	10	ADD40896	Novel hum	Ad440896	Novel hum	459	20.6	50.2	3233	12	ADG01997	Human PRO
387	20.6	50.2	3233	10	ADD52035	CDNA enco	Ad52035	CDNA enco	460	20.6	50.2	3233	12	ADG21783	Novel hum
388	20.6	50.2	3233	10	ADD52775	CDNA enco	Ad52775	CDNA enco	461	20.6	50.2	3233	12	ADG19853	CDNA enco
389	20.6	50.2	3233	10	ADD53327	Novel hum	Ad53327	Novel hum	462	20.6	50.2	3233	12	ADG19853	CDNA enco
390	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	463	20.6	50.2	3233	12	ADG19853	CDNA enco
391	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	464	20.6	50.2	3233	12	ADG19853	CDNA enco
392	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	465	20.6	50.2	3233	12	ADG19853	CDNA enco
393	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	466	20.6	50.2	3233	12	ADG19853	CDNA enco
394	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	467	20.6	50.2	3233	12	ADG19853	CDNA enco
395	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	468	20.6	50.2	3233	12	ADG19853	CDNA enco
396	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	469	20.6	50.2	3233	12	ADG19853	CDNA enco
397	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	470	20.6	50.2	3233	12	ADG19853	CDNA enco
398	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	471	20.6	50.2	3233	12	ADG19853	CDNA enco
399	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	472	20.6	50.2	3233	12	ADG19853	CDNA enco
400	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	473	20.6	50.2	3233	12	ADG19853	CDNA enco
401	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	474	20.6	50.2	3233	12	ADG19853	CDNA enco
402	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	475	20.6	50.2	3233	12	ADG19853	CDNA enco
403	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	476	20.6	50.2	3233	12	ADG19853	CDNA enco
404	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	477	20.6	50.2	3233	12	ADG19853	CDNA enco
405	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	478	20.6	50.2	3233	12	ADG19853	CDNA enco
406	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	479	20.6	50.2	3233	12	ADG19853	CDNA enco
407	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	480	20.6	50.2	3233	12	ADG19853	CDNA enco
408	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	481	20.6	50.2	3233	12	ADG19853	CDNA enco
409	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	482	20.6	50.2	3233	12	ADG19853	CDNA enco
410	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	483	20.6	50.2	3233	12	ADG19853	CDNA enco
411	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	484	20.6	50.2	3233	12	ADG19853	CDNA enco
412	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	485	20.6	50.2	3233	12	ADG19853	CDNA enco
413	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	486	20.6	50.2	3233	12	ADG19853	CDNA enco
414	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	487	20.6	50.2	3233	12	ADG19853	CDNA enco
415	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	488	20.6	50.2	3233	12	ADG19853	CDNA enco
416	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	489	20.6	50.2	3233	12	ADG19853	CDNA enco
417	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	490	20.6	50.2	3233	12	ADG19853	CDNA enco
418	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	491	20.6	50.2	3233	12	ADG19853	CDNA enco
419	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	492	20.6	50.2	3233	12	ADG19853	CDNA enco
420	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	493	20.6	50.2	3233	12	ADG19853	CDNA enco
421	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	494	20.6	50.2	3233	12	ADG19853	CDNA enco
422	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	495	20.6	50.2	3233	12	ADG19853	CDNA enco
423	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	496	20.6	50.2	3233	12	ADG19853	CDNA enco
424	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	497	20.6	50.2	3233	12	ADG19853	CDNA enco
425	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	498	20.6	50.2	3233	12	ADG19853	CDNA enco
426	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	499	20.6	50.2	3233	12	ADG19853	CDNA enco
427	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco	500	20.6	50.2	3233	14	ADZ03052	Human sec
428	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
429	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
430	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
431	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
432	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
433	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
434	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
435	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
436	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
437	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
438	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
439	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
440	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
441	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
442	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
443	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
444	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
445	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
446	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
447	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
448	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
449	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
450	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
451	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
452	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
453	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
454	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
455	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
456	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							
457	20.6	50.2	3233	10	ADD53483	CDNA enco	Ad53483	CDNA enco							

ALIGNMENTS

RESULT 1

AAD30228
ID AAD30228 standard; DNA; 53522 BP.

XX
AAD30228;

XX
17-MAY-2002 (first entry)

DT
Human PKD1 gene.

DE
Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD;

XX
acquired cystic disease; transgenic animal; chromosome 16; ds.

XX
Homo sapiens.

OS
WO200206529-A2.

PN
24-JAN-2002.

XX
13-JUL-2001; 2001WO-US022035.

XX
13-JUL-2001; 2000US-0218261P.

PR
13-APR-2001; 2001US-0283691P.

XX
(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Germino GG, Watnick TJ, Phakdeekitcharoen B;
XX WPI; 2002-179805/23.
XX Novel primer for diagnosing polycystic kidney disease-associated
PT disorder, comprises regions having sequence that selectively hybridizes
PT to polycystic kidney disease gene sequence.
XX Claim 20; Page 127-156; 192pp; English.
XX The present invention relates to compositions and methods useful for the
CC identification and detection of polycystic kidney disease (PKD1) gene
CC mutations. The invention also relates to primers comprising a 5' region
CC having a sequence that selectively hybridizes to a PKD1 gene sequence and
CC optionally, to a PKD1 homologue sequence and an adjacent 3' region having
CC a sequence that selectively hybridizes to a PKD1 gene sequence and not to
CC a PKD1 homologue sequence. Primer pairs of the invention are useful for
CC detecting the presence or absence of a mutation in a PKD1 polynucleotide
CC in a sample, for identifying a subject at risk for a PKD1-associated
CC disorder such as autosomal dominant polycystic kidney disease (ADPKD) or
CC acquired cystic disease and for diagnosing a PKD1-associated disorder in
CC a subject. They are useful for selectively amplifying a region of a PKD1
CC gene. PKD1 DNA fragments are useful for detecting the presence of a mutant
CC PKD1 polynucleotide in a sample, as a probe for an amplification
CC reaction, in hybridisation or amplification assays of biological samples
CC to detect abnormalities of PKD1 expression and for engineering transgenic
CC animals. The present sequence is human PKD1 gene located on chromosome 16
XX
SQ Sequence 53522 BP; 8486 A; 17664 C; 15766 G; 11606 T; 0 U; 0 Other;
Query Match 100.0%; Score 41; DB 6; Length 53522;
Best Local Similarity 97.6%; Pred. No. 0.0003;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
DB 3300 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 3340
RESULT 2
ADU03973
ID ADU03973 standard; DNA; 53522 BP.
XX
AC ADU03973;
XX
DT 30-DEC-2004 (first entry)
XX
DE Human polycystic kidney disease 1 (PKD-1) gene.
XX
KW mutation detection; polycystic kidney disease; PKD; PKD-1; biomarker;
KW autosomal dominant polycystic kidney disease; ADPKD; gene; ds.
XX
OS Homo sapiens.
XX
PN CA2461106-A1.
XX
PD 11-OCT-2004.
XX
PF 08-APR-2004; 2004CA-02461106.
XX
PR 11-APR-2003; 2003US-00411915.
XX
PA (ATHE-) ATHENA DIAGNOSTICS INC.
XX
PI Jones JG, Hennigan AN, Flynn KE, Garces JA, Seltzer WK;
PI Palatucci CW, Wang J, Curran JA, Allen SK, Robichaud NJ;
PI WPI; 2004-776219/77.
XX
PT Novel nucleic acid comprising specific sequence capable of detecting
PT mutations in polycystic kidney disease-1 (PKD-1) or PKD-2 gene, useful
PT for detecting biomarkers of autosomal dominant polycystic kidney disease.

XX Disclosure; SEQ ID NO 1; 195pp; English.
XX
XX The invention relates to a novel isolated nucleic acid capable of
CC detecting mutations in polycystic kidney disease (PKD-1) or PKD-2 gene,
CC comprising a specific sequence. The invention further comprises: a
CC nucleic acid biomarker for autosomal dominant polycystic kidney disease
CC (ADPKD), comprising a PKD-1 or PKD-2 nucleic acid sequence having one or
CC more novel nucleotide alterations chosen from identified ADPKD associated
CC alterations, as given in the specification; a polypeptide biomarker for
CC ADPKD, comprising a PKD-1 or PKD-2 polypeptide sequence having one or
CC more novel amino acid alterations chosen from identified ADPKD associated
CC alterations, as given in the specification; a method for diagnosing ADPKD
CC in an individual; and a method for determining in an individual the
CC presence or absence of a mutant PKD gene. The PKD mutation detecting
CC isolated nucleic acid or the ADPKD nucleic acid biomarker is useful in
CC diagnosing ADPKD in an individual, or determining the presence or absence
CC of a mutant PKD gene in an individual. This polynucleotide sequence
CC represents a human polycystic kidney disease 1 (PKD-1) gene of the
CC invention. Note: This sequence was not shown in the specification, but
CC was retrieved from Genbank by the indexer.
XX
SQ Sequence 53522 BP; 8486 A; 17664 C; 15766 G; 11606 T; 0 U; 0 Other;
Query Match 100.0%; Score 41; DB 13; Length 53522;
Best Local Similarity 97.6%; Pred. No. 0.0003;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
DB 3300 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 3340
RESULT 3
AEB35216
ID AEB35216 standard; DNA; 53522 BP.
XX
AC AEB35216;
XX
DT 06-OCT-2005 (first entry)
XX
DE Human Gefitinib sensitivity-related gene, PKD1 SEQ ID 80.
XX
KW Cancer; cytostatic; non-small-cell lung cancer; epidermal growth factor;
KW therapy; gefitinib; ds; gene.
XX
OS Homo sapiens.
XX
PN WO2005070020-A2.
XX
PD 04-AUG-2005.
XX
PF 24-JAN-2005; 2005WO-US002325.
XX
PR 23-JAN-2004; 2004US-0538682P.
XX
PA (COLS) UNIV COLORADO.
XX
PI Bunn PA, Coldren CD, Franklin WA, Geraci MW, Helfrich BA;
PI Hirsch FR, Lapadat R, Sugita M, Witta SE;
XX
DR WPI; 2005-533944/54.
XX
PT Selecting cancer patient who is predicted to benefit from administration
PT of epidermal growth factor receptor inhibitor or its agonist, by
PT providing sample of tumor cells from the patient and detecting expression
PT of genes from panel of genes.
XX
PS Claim 28; SEQ ID NO 80; 379pp; English.
XX
CC The invention relates to selecting a cancer patient who is predicted to
CC benefit from therapeutic administration of an EGFR inhibitor or agonist,
CC or a drug having similar biological activity as EGFR inhibitor,

CC comprising providing a sample of tumor cells from a patient to be tested,
 CC and detecting in the sample the expression of genes chosen from a panel
 CC of genes (that have been correlated with sensitivity or resistance to the
 CC EGFR inhibitor) and selecting the patient as being predicted to benefit
 CC from therapeutic administration of the EGFR inhibitor, if the expression
 CC of the gene or genes in the patient's tumor cells is statistically more
 CC similar to the expression levels of the gene or genes that has been
 CC correlated with sensitivity to the EGFR inhibitor than to resistance to
 CC the EGFR inhibitor. Also included are identifying molecules that interact
 CC with the EGFR pathway to allow or enhance responsiveness to EGFR
 CC inhibitors, polynucleotides (for detecting the expression of genes that
 CC are indicative of sensitivity or resistance to gefitinib, or its agonist,
 CC or a drug having substantially similar biological activity as gefitinib,
 CC where the polynucleotides consist of at least two polynucleotides, where
 CC each polynucleotide is at least 5 nucleotides in length, and where each
 CC polynucleotide is complementary to an RNA transcript, or nucleotide
 CC derived from it, of a gene that is regulated differently in gefitinib-
 CC sensitive tumor cells as compared to gefitinib-resistant cells),
 CC antibodies (or their antigen binding fragments or peptides) for detecting
 CC the expression of genes that are indicative of sensitivity or resistance
 CC to gefitinib (or its agonist, or a drug having substantially similar
 CC biological activity as gefitinib, which antibody selectively binds to a
 CC protein encoded by a gene comprising, or expressing a transcript
 CC comprising, a nucleic acid sequence appearing as AEB35137-AEB35330,
 CC identifying a compound with the potential to enhance the efficacy of EGFR
 CC inhibitors and treating a patient suffering from cancer. The method is
 CC useful in selecting a cancer patient (especially non-small-cell lung
 CC cancer) who is predicted to benefit from therapeutic administration of an
 CC EGFR inhibitor or its agonist, or a drug having similar biological
 CC activity as EGFR inhibitor. The present sequence represents one of the
 CC 194 genes that have been correlated with sensitivity or resistance to the
 CC EGFR inhibitor.

SQ Sequence 53522 BP; 8486 A; 17665 C; 15766 G; 11605 T; 0 U; 0 Other;

Query Match 100.0%; Score 41; DB 14; Length 53522;
 Best Local Similarity 97.6%; Pred. No. 0.0003;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCGGATGCCAGTCCCTCATCGTGGCCGCGCG 41
 |||||
 DB 3300 AAGCCTCGGATGCCAGTCCCTCATCGTGGCCGCGCG 3340

RESULT 4

AAT94101
 ID AAT94101 standard; DNA; 53526 BP.

AC AAT94101;

XX 25-MAR-2003 (revised)

DT 01-JUN-1998 (first entry)

XX Human PKD1 gene.

XX Human; polycystic kidney disease 1; PKD1; treatment;
 KW autosomal dominant polycystic kidney disease; APKD; ss.

XX Homo sapiens.

XX WO9744457-A1.

XX 27-NOV-1997.

XX 22-MAY-1997; 97WO-US008799.

XX 24-MAY-1996; 96US-00655360.

PR 04-JUN-1996; 96US-00658136.

XX (GENZ) GENZYME CORP.

XX Klinger K, Burn T, Connors T, Dackowski W, Germino G, Qian F;

DR WPI; 1998-018511/02.

XX Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose
 PT human autosomal or adult onset polycystic kidney disease.

XX Claim 2; Page 90-118; 257pp; English.

CC The present sequence is the human polycystic kidney disease 1 (PKD1)
 CC gene. The PKD1 gene or polypeptide may be used to treat autosomal
 CC dominant polycystic kidney disease (APKD), and identify carriers of
 CC mutant PKD1 genes, i.e. subjects susceptible to APKD. Antibodies (Ab)
 CC that distinguish between normal and mutant PKD1 sequences can also be
 CC used in diagnostic tests. Anti-PKD1 Ab may also be used to perform
 CC subcellular and histochemical localisation studies, and to block the
 CC function of PKD1. Ab are also useful in rational drug design studies to
 CC identify and test inhibitors of PKD1. Sense and antisense sequences
 CC derived from the PKD1 gene may be used for detection and therapy. (Updated
 CC on 25-MAR-2003 to correct PR field.)

XX Sequence 53526 BP; 8486 A; 17665 C; 15768 G; 11607 T; 0 U; 0 Other;

Query Match 100.0%; Score 41; DB 2; Length 53526;

Best Local Similarity 97.6%; Pred. No. 0.0003;

Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCGGATGCCAGTCCCTCATCGTGGCCGCGCG 41
 |||||

DB 3300 AAGCCTCGGATGCCAGTCCCTCATCGTGGCCGCGCG 3340

RESULT 5

AAT18551

ID AAT18551 standard; DNA; 53577 BP.

XX AAT18551;

XX 06-MAY-1997 (first entry)

XX Human polycystic kidney disease normal PKD1 gene.

XX Adult onset polycystic kidney disease; APKD; autosomal dominant; mutant;
 KW transversion; transition; deletion; insertion; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT misc_feature 4379..5272
 FT /tag= a

FT /note= "specifically claimed region of intronless cDNA
 identified by exon trapping"

FT old_sequence replace(50652..50653, cg)

FT /tag= b

FT old_sequence /note= "changes Val codon to Leu codon"

FT replace(50796..50797, cg)

FT /tag= c

FT old_sequence /note= "replaces Val codon by Leu codon"

FT replace(51827..51828, cc)

FT /tag= d

FT /note= "insertion, results in frameshift"

XX WO9612033-A1.

XX 25-APR-1996.

XX 11-OCT-1995; 95WO-US013357.

XX 12-OCT-1994; 94US-00323443.

PR 31-JAN-1995; 95US-00381520.

XX (IGIG-) IG LAB INC.

PA (UYJO) UNIV JOHNS HOPKINS.

XX Klinger KW, Landes GM, Burn TC, Connors TD, Dackowski W;

PI Germino G, Qian F;
 XX WPI; 1996-222017/22.
 XX
 PT Isolated human polycystic kidney diseases gene and its mutants - useful
 PT for treatment of polycystic kidney disease and screening for carriers.
 XX
 XX
 PS Claim 1; Fig 1; 65pp; English.
 XX
 CC The present sequence is that of the normal human PKD1 gene from
 CC chromosome 16. Mutations in this gene (e.g. transitions, transversions,
 CC deletions and/or insertions) are associated with adult-onset polycystic
 CC kidney disease (APKD). The PKD1 locus is GC-rich (62.4%). Comparison of
 CC this sequence with a previously reported partial cDNA sequence revealed
 CC differences at three locations (see features table). The most significant
 CC difference is the presence of two additional cytosine residues on the
 CC plus-strand at position 4566 of the previously reported sequence. The
 CC insertion results in a frame-shift in the predicted protein coding
 CC sequence, leading to replacement of 92 C-terminal amino acids with a
 CC novel 12 amino acid C-terminus. The PKD1 gene contains 23 Alu repeats.
 CC There is a region consisting of 17 tandem copies of a perfect 27 bp
 CC repeat and two large CT-rich regions
 XX
 SQ Sequence 53577 BP; 8495 A; 17681 C; 15785 G; 11616 T; 0 U; 0 Other;
 Query Match 100.0%; Score 41; DB 2; Length 53577;
 Best Local Similarity 97.6%; Pred. No. 0.0003;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGCCTCCGGATCCAGTCCCTCATCGCTGGCCGCGGCGG 41
 DB 3300 AAGCCTCCGGATCCAGTCCCTCATCGCTGGCCGCGGCGG 3340
 RESULT 6
 ID AAT94108 standard; DNA; 53577 BP.
 AC AAT94108;
 XX
 XX 25-MAR-2003 (revised)
 DT 01-JUN-1998 (first entry)
 XX
 DE Human PKD1 locus between chromosomal markers ATP6C and D16S84.
 XX
 KW Human; polycystic kidney disease 1; PKD1; treatment;
 KW autosomal dominant polycystic kidney disease; APKD; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9744457-A1.
 XX
 XX 27-NOV-1997.
 XX
 XX 22-MAY-1997; 97WO-US008799.
 XX
 XX 24-MAY-1996; 96US-00655360.
 XX 04-JUN-1996; 96US-00658136.
 XX
 XX (GENZ) GENZYME CORP.
 XX
 XX Klinger K, Burn T, Connors T, Dackowski W, Germino G, Qian F;
 XX WPI; 1998-018511/02.
 DR
 XX Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose
 PT human autosomal or adult onset polycystic kidney disease.
 PT
 XX Example 5; Page 60-89; 257pp; English.
 XX
 CC The present sequence is the human polycystic kidney disease 1 (PKD1)
 CC locus between chromosomal markers ATP6C and D16S84. The PKD1 gene
 CC or polypeptide may be used to treat autosomal dominant polycystic kidney

CC disease (APKD), and identify carriers of mutant PKD1 genes, i.e. subjects
 CC susceptible to APKD. Antibodies (Ab) that distinguish between normal and
 CC mutant PKD1 sequences can also be used in diagnostic tests. Anti-PKD1 Ab
 CC may also be used to perform subcellular and histochemical localization
 CC studies, and to block the function of PKD1. Ab are also useful in
 CC rational drug design studies to identify and test inhibitors of PKD1.
 CC Sense and antisense sequences derived from the PKD1 gene may be used for
 CC detection and therapy. (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 53577 BP; 8495 A; 17684 C; 15782 G; 11616 T; 0 U; 0 Other;
 Query Match 100.0%; Score 41; DB 2; Length 53577;
 Best Local Similarity 97.6%; Pred. No. 0.0003;
 Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGCCTCCGGATCCAGTCCCTCATCGCTGGCCGCGGCGG 41
 DB 3300 AAGCCTCCGGATCCAGTCCCTCATCGCTGGCCGCGGCGG 3340
 RESULT 7
 ID ABQ16060/c
 XX ABQ16060 standard; DNA; 623 BP.
 AC ABQ16060;
 XX
 XX 12-JUL-2002 (first entry)
 DT
 XX
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 2651.
 XX
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200218632-A2.
 XX
 XX 07-MAR-2002.
 XX
 XX 01-SEP-2001; 2001WO-EP010074.
 XX
 XX 01-SEP-2000; 2000DE-01043826.
 XX 05-SEP-2000; 2000DE-01044543.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K, Guetig D;
 XX WPI; 2002-371829/40.
 DR
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.
 XX
 XX Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for


```
XX 01-JUL-2002 (first entry)
XX Chemically treated cell signalling DNA sequence complementary to#100.
XX Cell signalling; cytosine methylation; cell signalling disease; cancer;
XX tumour; cytostatic; ds.
XX Unidentified.
XX WO200202807-A2.
XX 10-JAN-2002.
XX 29-JUN-2001; 2001WO-EP007471.
XX 30-JUN-2000; 2000DB-01032529.
XX 01-SEP-2000; 2000DE-01043826.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-154758/20.
XX Nucleic acid, useful for diagnosis and therapy of diseases associated
XX with cell signaling e.g. cancer, comprises chemically modified genomic
XX sequences of genes associated with cell signaling.
XX Claim 1; SEQ ID NO 200; 24pp + Sequence Listing; English.
XX The invention relates to a nucleic acid comprising a sequence of at least
XX 18 bases of a segment of chemically pretreated DNA of genes associated
XX with cell signalling. The activity of the modified sequences of the
XX invention may be described as cytostatic. The object of the invention is
XX to provide the chemically modified DNA of genes associated with cell
XX signalling, as well as oligonucleotides and/or RNA-oligomers for
XX detecting cytosine methylations, as well as a method which is
XX particularly suitable for the diagnosis and/or therapy of genetic and
XX epigenetic parameters of genes associated with cell signalling. The
XX chemically modified DNA provided by the invention is useful for diagnosis
XX and therapy of diseases such as solid tumours and cancer. The sequences
XX given in records ABL70111-ABL70626 represent chemically pre-treated
XX genomic DNA's of genes associated with cell signalling. Note: The
XX sequence data for this patent is not represented in the printed
XX specification, but is based on sequence information supplied by the
XX European Patent Office
XX Sequence 6423 BP; 1625 A; 292 C; 1756 G; 2750 T; 0 U; 0 Other;
Query Match 72.7%; Score 29.8; DB 6; Length 6423;
Best Local Similarity 80.5%; Pred. No. 1.6;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 1 AAGCTTCGGATGCCAGTCCCTCATCGTCGGCCGCGCG 41
DB 1563 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGG 1523
RESULT 11
ADS99830/C
ID ADS99830 standard; DNA; 6423 BP.
XX ADS99830;
XX 02-DEC-2004 (first entry)
XX Complement of bisulphite treated metastasis-associated human gene #61.
XX Human; ds; gene; Bisulphite; metastasis; cancer; cytostatic;
XX DNA methylation; matrix-assisted laser desorption/ionisation; MALDI;
XX electrospray; mass spectrometry; CpG dinucleotide; solid tumour.
XX
```

```
OS Homo sapiens.
XX US2003148327-A1.
XX 07-AUG-2003.
XX 21-JAN-2003; 2003US-00240485.
XX 06-APR-2000; 2000DE-01019058.
XX 07-APR-2000; 2000DE-01019173.
XX 30-JUN-2000; 2000DE-01032529.
XX 01-SEP-2000; 2000DE-01043826.
XX 06-APR-2000; 2001WO-EP003970.
XX (OLEK/) OLEK A.
XX (PIEP/) PIEPENROCK C.
XX (BERL/) BERLIN K.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-010922/01.
XX New nucleic acid derived from chemically treated metastasis genes, useful
XX for diagnosis of cancers by analysis of cytosine methylation, also for
XX treatment.
XX Claim 1; SEQ ID NO 122; 9pp; English.
XX The invention relates to a nucleic acid comprising at least 18 bases from
XX a segment of the chemically pretreated DNA of genes associated with
XX metastasis, i.e. any of ADS99709-ADS99906 human genomic sequences or any
XX of the 19 sequences appearing as ADS99911-ADS99929. SEQ ID 2,4,6 etc are
XX the complements of SEQ ID 1,3,5, etc. Also included are an oligomer
XX (particularly an oligonucleotide or peptide nucleic acid) comprising at
XX least one base sequence of at least 9 bases which hybridises to (or is
XX identical with) the sequences referred to above, producing an array of
XX the oligomers on a carrier, obtaining genetic and/or epigenetic
XX parameters for diagnosis and/or therapy of diseases (or predisposition to
XX them) by analysis of cytosine methylation and a kit comprising a
XX bisulphite (disulphite or hydrogen sulphite) and the oligomers. In the
XX method of above 5-unmethylated cytosines in a genomic DNA sample are
XX converted chemically to uracil, or another base with hybridisation
XX properties different from those of cytosine, then fragments of the
XX treated DNA amplified (particularly by polymerase chain reaction) using
XX the oligomers and a polymerase (preferably heat stable) to produce
XX labelled amplicons. These are tested for hybridisation to an array of
XX oligomers and any hybridisation detected. The amplicons are labelled with
XX fluorescent or radioactive markers, or with a detachable mass marker to
XX allow their detection by mass spectrometry, specifically using the matrix
XX -assisted laser desorption/ionisation (MALDI) or electrospray techniques.
XX To improve detection in the mass spectrometer, fragments formed in the
XX instrument have only a single net charge (positive or negative). The
XX genomic DNA is from e.g. a cell line, biopsy sample, blood, or paraffin-
XX embedded tissue sample. Oligonucleotides or peptide-nucleic acids that
XX are complementary to (or identical with) parts of the nucleic acids listed
XX above may be used as primers for amplification of the nucleic acids or
XX their complements, and for determining cytosine methylation status and/or
XX single nucleotide polymorphisms in metastasis-related genes. They can be
XX used for analysis of diseases associated with methylation of CpG
XX dinucleotides and to determine (epi)genetic parameters for diagnosis
XX and/or therapy of disease (or predisposition). The genomic DNA sequences
XX are useful for diagnosis and therapy of solid tumours and cancer. The
XX present sequence is the complementary sequence to a bisulphite treated
XX human gene associated with metastasis. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030148327.
XX Sequence 6423 BP; 1625 A; 292 C; 1756 G; 2750 T; 0 U; 0 Other;
Query Match 72.7%; Score 29.8; DB 7; Length 6423;
Best Local Similarity 80.5%; Pred. No. 1.6;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
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```
QY      1  AAGCTTCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
      ||||||| ||| ||| ||||||||| ||||| : |||
      1563 AAACCTCGAATACCAATCCCTCATCGCTAAACCCGATCGCG 1523

RESULT 12
ID  ACL66662/c
AC  ACL66662 standard; DNA; 1424 BP.
XX
XX
DT  02-JUN-2005 (first entry)
XX
DE  M. xanthus gene sequence, seq id 3125.
XX
XX  Transgenic plant; DNA replication; gene regulation; gene expression;
KW  gene; ds.
XX
OS  Myxococcus xanthus.
XX
XX  US6833447-B1.
XX
XX  21-DEC-2004.
XX
XX  10-JUL-2001; 2001US-00902540.
XX
XX  10-JUL-2000; 2000US-0217883P.
XX
XX  (MONS ) MONSANTO TECHNOLOGY LLC.
XX
XX  Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX  WPI; 2005-028716/03.
XX
XX  New substantially purified Myxococcus xanthus nucleic acid molecule
PT  encoding a nitrite reductase, useful for determining gene expression,
PT  identifying mutations in a gene of interest, and for constructing
PT  mutations in a gene of interest.
XX
XX  Example 1; SEQ ID NO 1142; 25pp; English.
XX
XX  The invention relates to a substantially purified nucleic acid molecule
CC  encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC  recombinant DNA construct for expression of a nitrite reductase gene in a
CC  plant cell, and a plant cell comprising the recombinant DNA construct.
CC  The nucleic acid is useful for determining gene expression, identifying
CC  mutations in a gene of interest, and for constructing mutations in a gene
CC  of interest. Sequences given in records for SEQ IDs 1-1849 represent a
CC  set of 1849 contig and singleton sequences comprising coding sequences,
CC  DNA replication elements, promoters and other regulatory elements from
CC  the genome of the bacterium Myxococcus xanthus. Note: The sequence data
CC  for this patent did not form part of the printed specification, but was
XX  obtained in electronic format directly from USPTO
XX
XX  Sequence 15268 BP; 2318 A; 5524 C; 5125 G; 2301 T; 0 U; 0 Other;
PS
XX
XX  Query Match 60.0%; Score 24.6; DB 14; Length 15268;
XX  Best Local Similarity 74.4%; Pred. No. 95;
XX  Matches 29; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
XX
QY      3  GCCTCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
      ||||||| ||| ||| ||||||||| ||||| : |||
      14450 GGCGCGGGGGCGAGCCCTCGATGCTGCGCGGTAGCG 14412

Db
      14450 GGCGCGGGGGCGAGCCCTCGATGCTGCGCGGTAGCG 14412

RESULT 14
ID  ABL30357
XX
XX  ABL30357 standard; DNA; 2202 BP.
XX
XX  ABL30357;
XX
XX  26-MAR-2002 (first entry)
XX
XX  Drosophila melanogaster genomic polynucleotide SEQ ID NO 42544.
XX
XX  Drosophila; developmental biology; cell signalling; insecticide;
KW  pharmaceutical; gene; ds.
XX
XX  Drosophila melanogaster.
XX
XX  WO200171042-A2.
XX
XX  27-SEP-2001.
XX
XX  23-MAR-2001; 2001WO-US009231.
XX
XX  23-MAR-2000; 2000US-0191637P.
XX

QY      1  AAGCTTCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
      ||||||| ||| ||| ||||||||| ||||| : |||
      1563 AAACCTCGAATACCAATCCCTCATCGCTAAACCCGATCGCG 1523

RESULT 13
ID  ACL64679/c
AC  ACL64679 standard; DNA; 15268 BP.
XX
XX
XX  ACL64679;
XX
DT  02-JUN-2005 (first entry)
XX
XX
XX  Query Match 60.0%; Score 24.6; DB 14; Length 1424;
XX  Best Local Similarity 74.4%; Pred. No. 85;
XX  Matches 29; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
XX
QY      3  GCCTCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
      ||||||| ||| ||| ||||||||| ||||| : |||
      606 GGCGCGGGGGCGAGCCCTCGATGCTGCGCGGTAGCG 568

Db
      606 GGCGCGGGGGCGAGCCCTCGATGCTGCGCGGTAGCG 568

RESULT 13
ID  ACL64679/c
AC  ACL64679 standard; DNA; 15268 BP.
XX
XX
XX  ACL64679;
XX
DT  02-JUN-2005 (first entry)
XX
XX
```

PR 11-JUL-2000; 2000US-00614150.
XX (PEXE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX Claim 1; SEQ ID NO 42544; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2202 BP; 565 A; 605 C; 587 G; 445 T; 0 U; 0 Other;

Query Match 59.0%; Score 24.2; DB 4; Length 2202;
Best Local Similarity 75.7%; Pred. No. 1.2e+02;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCG 39
DB 80 GTCTCGGATGCCACACCCACAGCGCTGGAGTGGCG 116

RESULT 15
ABL30356
ID ABL30356 standard; DNA; 5083 BP.
XX
AC ABL30356;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42541.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEXE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 42541; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5083 BP; 1506 A; 1104 C; 1120 G; 1353 T; 0 U; 0 Other;

Query Match 59.0%; Score 24.2; DB 4; Length 5083;
Best Local Similarity 75.7%; Pred. No. 1.2e+02;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCG 39
DB 1080 GTCTCGGATGCCACACCCACAGCGCTGGAGTGGCG 1116

RESULT 16
ABX51214/C
ID ABX51214 standard; cDNA; 413 BP.
XX
AC ABX51214;
XX
DT 25-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #1143.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
OS Bos Taurus.
XX
PN US2002137160-A1.
XX
PD 26-SEP-2002.
XX
PF 26-OCT-2001; 2001US-00983965.
XX
PR 17-DEC-1998; 98US-0113678P.
PR 15-DEC-1999; 99US-00465231.
XX
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX
DR WPI; 2003-102386/09.
XX
PT Purified nucleic acid molecules, useful for genome mapping, gene
PT identification and analysis, cattle breeding or preparation of constructs
PT for cattle gene expression and genetically improved cattle.
XX
PS Claim 2; SEQ ID NO 1143; 38pp; English.
XX
CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 5912 nucleotide sequences,
CC appearing as ABX50072-ABX55983, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 5912 nucleic acid sequences or its complement or fragment) with a

CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The IMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the 5912
CC bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present
CC sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137160
XX
SQ Sequence 413 BP; 88 A; 125 C; 124 G; 76 T; 0 U; 0 Other;

Query Match 56.1%; Score 23; DB 8; Length 413;
Best Local Similarity 71.8%; Pred. No. 2.8e+02;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 ACCCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGNCGC 40
DB 267 AACACGCGGAGACCACTCCCATCGCAGCGCCCTGAAGC 229

RESULT 17
ADQ59193/c
ID ADQ59193 standard; DNA; 3750 BP.
XX
AC ADQ59193;
XX
DT 09-SEP-2004 (first entry)
XX
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:30.
XX
KW coding mononucleotide repeat; cMNR; gene; antibody; MSI-H tumour;
KW MSI-H carcinoma; high microsatellite instability tumour;
KW high microsatellite instability carcinoma; cytostatic; ds.
XX
OS Homo sapiens.
XX
PN KR2004008012-A.
XX
PD 28-JAN-2004.
XX
PF 15-JUL-2002; 2002KR-00041304.
XX
PR 15-JUL-2002; 2002KR-00041304.
XX
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
XX
PI Kim HG, Kim NG, Lee JS, Rhee HS;
XX
DR WPI; 2004-386326/36.
XX

XX Genes containing coding mononucleotide repeats are useful in developing
PT an antibody against MSI-H (hugh (sic high) microsatellite instability)
PT tumor.
XX
PS Claim 3; SEQ ID NO 30; 578pp; Korean.
XX
CC The present invention describes genes containing coding mononucleotide
CC repeats (cMNRs). The genes are useful for the development of an antibody
CC against MSI-H (hugh microsatellite instability) tumour. Also described:
CC (1) cDNA genes containing cMNRs with 10 or more nucleotide sequences, and
CC selected from the cDNA genes having the nucleotide sequences of SEQ ID
CC NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,
CC 37, 39, 41 and 43; (2) cDNA genes, which are frameshift mutated by
CC deletion or insertion of one or more base in the cMNRs; (3) genomic DNA

CC genes containing cMNRs with 10 or more nucleotide sequences, and selected
CC from the genomic DNA genes having the nucleotide sequences of SEQ ID
CC NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36,
CC 38, 40, 42 and 44; and (4) genomic DNA genes, which are frameshift
CC mutated by deletion or insertion of one or more base in the cMNRs. The
CC genes have cytostatic activity. The present sequence represents an MSI-H
CC carcinoma genomic DNA sequence from the present invention.
XX

SQ Sequence 3750 BP; 725 A; 1035 C; 1191 G; 799 T; 0 U; 0 Other;
Query Match 56.1%; Score 23; DB 12; Length 3750;
Best Local Similarity 71.8%; Pred. No. 3.1e+02;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGNCGC 41
DB 1817 GGCCTTCGCGCGCCCTCCCGCGCGCGCGCGCGCG 1779

RESULT 18
ADT43870/c
ID ADT43870 standard; cDNA; 768 BP.
XX
AC ADT43870;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #18621.

XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.

OS Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 42308; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX
 SQ Sequence 768 BP; 118 A; 284 C; 272 G; 94 T; 0 U; 0 Other;

Query Match 55.1%; Score 22.6; DB 13; Length 768;

Best Local Similarity 73.0%; Pred. No. 3.9e+02;

Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGCTGGCCGCGCG 39

Db 96 GCCTCCGATGCCAGTCCCTCATCGCTGGCCGCGCG 60

RESULT 19

ADRO7671/C

ID ADRO7671 standard; cDNA; 2213 BP.

AC ADRO7671;

XX

XX

DT 04-NOV-2004 (first entry)

XX

XX Full length human cDNA useful for treating neurological disease Seq 1177.

DE gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;

XX osteoporosis; neurological disease; Alzheimer's disease;

KW Parkinson's disease; dementia; short memory; cancer;

KW sense or motor function; emotional reaction; fear response; panic;

KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cyrostatic;

KW tranquiliser.

XX

OS Homo sapiens.

XX

XX EP1447413-A2.

PN

XX 18-AUG-2004.

PD

XX 12-FEB-2004; 2004EP-00003145.

XX

XX 14-FEB-2003; 2003JP-00102207.

PR

XX 09-MAY-2003; 2003JP-00131452.

XX

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

PA

XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;

PI Wakamatsu A, Ishii S, Nagai K, Irie R;

XX

DR WPI; 2004-583285/57.

DR

XX P-PSDB; ADRO9627.

XX

XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases.

PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX

XX Claim 1; SEQ ID NO 1177; 2686pp; English.

XX

XX This invention relates to novel, isolated full length human cDNA

XX molecules and the encoded proteins thereof. Specifically, it refers to

XX cDNA clones obtained by an oligo-capping method, where none of these

XX clones are identical to any known human mRNA. The present invention

XX describes an immunoassay to identify agonists and antagonists, as well as

XX antibodies, antisense molecules and siRNAs that can all be used to bind

CC to and modulate expression of the cDNA molecules. As such, these
 CC molecules are useful for diagnostic markers or therapeutic targets for
 CC the various diseases or morbid states. In particular, they are useful in
 CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
 CC disease, Parkinson's disease, dementia, short memory and various cancers,
 CC as well as for maintaining equilibrium of sense or motor function, and
 CC for treating emotional reaction, fear response and panic. Accordingly,
 CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
 CC cyrostatic and tranquilliser activities. This polynucleotide is a full
 CC length human cDNA sequence of the invention. NOTE: This sequence is not
 CC given in the sequence listing of the specification but can be obtained on
 CC CD-ROM from the European Patent Office, Vienna Sub-office.

XX
 SQ Sequence 2213 BP; 515 A; 629 C; 670 G; 399 T; 0 U; 0 Other;

Query Match 55.1%; Score 22.6; DB 13; Length 2213;

Best Local Similarity 73.0%; Pred. No. 4.1e+02;

Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41

Db 1688 CGCGGTTCCCTGGCTCTGGTGGCGCGCGCG 1652

RESULT 20

ADA02852

ID ADA02852 standard; DNA; 22715 BP.

XX

AC ADA02852;

XX

DT 06-NOV-2003 (first entry)

XX

XX Human CBX8 carcinoma associated gene, SEQ ID NO:1370.

XX

XX Human; carcinoma associated; oncogene; carcinoma; cancer; breast;

KW prostate; lymphoma; leukaemia; cyrostatic; gene therapy; drug screening;

KW gene; db.

XX

OS Homo sapiens.

XX

PN WO2003057146-A2.

XX

XX 17-JUL-2003.

XX

XX 26-DEC-2002; 2002WO-US041414.

XX

XX 26-DEC-2001; 2001US-00035832.

XX

XX (SAGR-) SAGRES DISCOVERY.

PA

XX Morris DW;

PI

XX WPI; 2003-587068/55.

DR

XX New recombinant nucleic acid encoding carcinoma associated protein,

PT useful for preparing compositions for treating carcinomas.

XX

XX Claim 1; SEQ ID NO 1370; 245pp; English.

XX

XX The invention relates to recombinant carcinoma associated (CA) nucleic

CC acid sequences from mouse and human (ADA01482-ADA03094), and to

CC recombinant carcinoma associated proteins (CAP) encoded by them. The

CC invention also encompasses expression vectors and host cells comprising a

CC CA nucleic acid, a polypeptide (especially an antibody) that specifically

CC binds to the protein, and a biochip comprising CA nucleic acid or

CC fragments thereof. The sequences of the invention were identified using

CC oncogenic retroviruses, which insert into the genome of the host organism

CC at random. Many of these do not carry transduced host oncogenes or

CC pathogenic trans-acting viral genes, meaning that cancer incidence is a

CC direct consequence of the effects of proviral integration into host

CC protooncogenes. The CA nucleic acid sequences can be used to diagnose

CC carcinoma (especially breast cancer, prostate cancer, lymphoma or

CC leukaemia) or a propensity to carcinoma by determination of the sequence

CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed human CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 22715 BP; 4607 A; 6738 C; 6685 G; 4685 T; 0 U; 0 Other;
Query Match 55.1%; Score 22.6; DB 9; Length 22715;
Best Local Similarity 73.0%; Pred. No. 4.5e+02;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGN 37
|||||
Db 15385 AAGCCTCCGGATGCCAGTCCCTCATCGTGTCTTGAG 15421
|||||

RESULT 21
ADB72590
ID ADB72590 standard; DNA; 22715 BP.
XX AC
XX ADB72590;
XX DT 04-DEC-2003 (first entry)
XX DE Human CBX8 gene.
XX KW human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
XX KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.
XX OS Homo sapiens.
XX PN WO2003008583-A2.
XX PD 30-JAN-2003.
XX PF 26-DEC-2001; 2001WO-US051291.
XX PR 02-MAR-2001; 2001US-00798586.
XX PR 23-OCT-2001; 2001US-00004113.
XX PR 08-NOV-2001; 2001US-00052482.
XX PR 30-NOV-2001; 2001US-00997722.
XX PR 20-DEC-2001; 2001US-00034650.
XX PA (SAGR-) SAGRES DISCOVERY.
XX PI Morris DW, Engelhard EK;
XX WPI; 2003-239337/23.
XX PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
XX PT cancers, neoplasm, adenocarcinoma, or sarcomas.
XX PS Claim 1; SEQ ID NO 418; 2304pp; English.
XX CC The invention relates to a novel recombinant nucleic acid comprising a
XX CC nucleotide sequence selected from any of the 660 sequences fully defined
XX CC in the specification. A polynucleotide of the invention has cytostatic
XX CC activity, and may have a use in gene therapy, or in a vaccine. The
XX CC recombinant nucleic acids and polypeptides are useful for treating
XX CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
XX CC sarcomas. The present sequence represents a human gene of the invention.

XX SQ Sequence 22715 BP; 4607 A; 6738 C; 6685 G; 4685 T; 0 U; 0 Other;
Query Match 55.1%; Score 22.6; DB 10; Length 22715;
Best Local Similarity 73.0%; Pred. No. 4.5e+02;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGN 37

Db 15385 AAGCCTCCGGATGCCAGTCCCTCATCGTGTCTTGAG 15421
|||||

RESULT 22
ADC85331
ID ADC85331 standard; DNA; 22715 BP.
XX AC
XX ADC85331;
XX DT 01-JAN-2004 (first entry)
XX DE Mouse Cbx8 coding sequence.
XX KW Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;
XX KW secreted; transmembrane; intracellular; ds.
XX OS Mus sp.
XX PN WO2003045230-A2.
XX PD 05-JUN-2003.
XX PF 02-DEC-2002; 2002WO-US038582.
XX PR 30-NOV-2001; 2001US-00997722.
XX PA (SAGR-) SAGRES DISCOVERY.
XX PI Morris DW, Engelhard EK;
XX WPI; 2003-513603/48.
XX PT New recombinant nucleic acid comprising a nucleotide sequence of any of
XX PT the carcinoma-associated (CA) genes, useful for screening for drug
XX PT candidates for diagnosing or treating carcinomas.
XX PS Claim 1; SEQ ID NO 117; 983pp; English.
XX CC The invention relates to a recombinant nucleic acid comprising a
XX CC nucleotide sequence selected from any of the fully defined carcinoma-
XX CC associated (CA) genes from the 50 tables given in the specification. The
XX CC CA proteins are secreted, transmembrane or intracellular proteins. The
XX CC recombinant nucleic acids are useful for screening for drug candidates
XX CC for diagnosing or treating carcinomas. Sequences given in ADC85215-
XX CC ADC85514 represent CA genes of the invention.

XX SQ Sequence 22715 BP; 4607 A; 6738 C; 6685 G; 4685 T; 0 U; 0 Other;
Query Match 55.1%; Score 22.6; DB 10; Length 22715;
Best Local Similarity 73.0%; Pred. No. 4.5e+02;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGN 37
|||||
Db 15385 AAGCCTCCGGATGCCAGTCCCTCATCGTGTCTTGAG 15421
|||||

RESULT 23
ADM74447
ID ADM74447 standard; DNA; 22715 BP.
XX AC
XX ADM74447;
XX DT 01-JUL-2004 (first entry)
XX DE Human carcinoma associated (CA) nucleic acid #58.
XX KW Human; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;
XX KW carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
XX KW cytostatic.
XX OS Homo sapiens.

XX PN US2004072154-A1.
XX PD 15-APR-2004.
XX PF 30-NOV-2001; 2001US-00997722.
XX PR 22-DEC-2000; 2000US-00747377.
XX PR 02-MAR-2001; 2001US-00798586.
XX (MORR/) MORRIS D W.
XX PA (ENGE/) ENGELHARD E K.
XX PI Morris DW, Engelhard EK;
XX WPI; 2004-328562/30.
XX New carcinoma associated gene or protein, useful for preparing a
XX composition for diagnosing or treating carcinoma e.g., leukemia or
XX lymphoma.
XX PS Claim 1; SEQ ID NO 118; 29pp; English.
XX The invention relates to new recombinant nucleic acids. The invention
XX also relates to a host cell comprising a recombinant nucleic acid or
XX expression vector, an expression vector comprising a recombinant nucleic
XX acid, a recombinant protein, a method of screening for drug candidates, a
XX method of screening for a bioactive agent capable of binding to a
XX carcinoma associated protein (CAP) encoded by a nucleotide sequence, a
XX method of screening for a bioactive agent capable of modulating the
XX activity of a CAP, a method of evaluating the effect of a candidate
XX carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting
XX the activity of a CAP, a method of treating carcinomas, a method of
XX neutralising the effect of a CAP and a method of diagnosing carcinoma or
XX propensity to carcinoma. A method of evaluating the effect of a candidate
XX carcinoma drug comprises administering the drug to a patient, removing a
XX cell sample from the patient and determining alterations in the
XX expression or activation of a gene comprising the nucleotide sequence. A
XX method of diagnosing carcinoma comprises determining the expression of
XX one or more genes comprising the nucleic acid sequence in a first tissue
XX type of a first individual and comparing the expression of the gene from
XX a second normal tissue type from the first individual or a second
XX unaffected individual, where a difference in the expression indicates
XX that the first individual has carcinoma. A method of inhibiting the
XX activity of a CAP comprises binding an inhibitor to the CAP. Treating
XX carcinomas comprises administering to a patient an inhibitor of CAP.
XX Neutralising the effect of a CAP comprises contacting an agent specific
XX for the CAP. The polypeptide specifically binds to the protein encoded by
XX the nucleic acid. It comprises an antibody that specifically binds to the
XX protein encoded by the nucleic acid. The nucleic acids are useful for
XX preparing a composition for diagnosing or treating carcinoma e.g.,
XX leukaemia or lymphoma. This sequence represents a human carcinoma
XX associated (CA) nucleic acid of the invention. Note: The sequence data
XX for this patent did not form part of the printed specification but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html.
XX SQ Sequence 22715 BP; 4607 A; 6738 C; 6685 G; 4685 T; 0 U; 0 Other;
Query Match 55.1%; Score 22.6; DB 12; Length 22715;
Best Local Similarity 73.0%; Pred. No. 4.5e+02;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
DY 15385 AAGCCTCCCGTGCCAGTCCCTCATCGCTGGCCCGG 37
||||| ||||| ||||| ||||| ||||| ||||| :
1 AAGCCTCCCGTGCCAGTCCCTCATCGCTGGCCCGG 37
DB 15385 AAGCCTCCCGTGCCAGTCCCTCATCGCTGGCTGTCTTGAG 15421
RESULT 24
ADK57630/c
ID ADK57630 standard; DNA; 622 BP.
XX
XX ADK57630;

XX DT 06-MAY-2004 (first entry)
XX DE Plant DNA sequence which confers altered metabolic characteristic #5013.
XX KW altered metabolic characteristic; plant; acid metabolism;
XX KW alcohol metabolism; fatty acid metabolism;
XX KW branched fatty acid metabolism; alkaloid metabolism;
XX KW amino acid metabolism; ester metabolism; glyceride metabolism;
XX KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;
XX KW terpene metabolism; isoprenoid metabolism; alkene metabolism;
XX KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
XX KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX Unidentified.
XX OS
XX XX
XX PN WO2003020936-A1.
XX XX 13-MAR-2003.
XX XX 30-AUG-2002; 2002WO-US027884.
XX XX 31-AUG-2001; 2001US-0316471P.
XX PA (DOWC) DOW CHEM CO.
XX PA (DOWC) DOW AGROSCIENCES LLC.
XX PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
XX PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX WPI; 2003-313091/30.
XX Novel genes that confer altered metabolic characteristics in Nicotiana
XX benthamiana plants, useful for altering the levels of metabolites e.g.
XX acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX Claim 1; SEQ ID NO 5013; 2576pp; English.
XX The invention comprises DNA sequences which confer an altered metabolic
XX characteristic when they are expressed in a plant. The DNA sequences of
XX the invention are useful for producing plants with an altered metabolic
XX characteristic, such as: altered acid metabolism, alcohol metabolism,
XX fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
XX base metabolism, altered amino acid metabolism, altered ester metabolism,
XX altered glyceride metabolism, altered phenolic metabolism, altered
XX carbohydrate metabolism, altered sterol, oxygenated terpene, or
XX isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
XX metabolism, ketone or quinone metabolism. The DNA sequences of the
XX invention may be used to provide disease resistance in a plant and gene
XX shuffling or sexual PCR procedures. The present nucleic acid represents a
XX DNA sequence of the invention.
XX SQ Sequence 622 BP; 151 A; 156 C; 172 G; 143 T; 0 U; 0 Other;
Query Match 54.6%; Score 22.4; DB 10; Length 622;
Best Local Similarity 70.0%; Pred. No. 4.5e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
DY 2 AGCCTCCCGATGCCAGTCCCTCATCGCTGGCCCGGCG 41
||||| ||||| ||||| ||||| ||||| ||||| :
136 AGCCTCCCGATGCCAAGCCAGATTGGTGGTGGCGCG 87
RESULT 25
ABD04866/c
ID ABD04866 standard; DNA; 1269 BP.
XX
XX ABD04866;
XX
XX 29-JUL-2004 (first entry)
XX
XX Pseudomonas aeruginosa polynucleotide #3470.
XX

XX 02-DEC-2002; 2002WO-US038526.
XX
XX 03-DEC-2001; 2001US-00005499.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Ghosh M, Tang YT, Wang JR, Wang Z, Zhao QA, Xu C, Mulero JJ;
XX Boyle BJ;
XX WPI; 2003-513756/48.
XX P-PSDB; ADF28720.
XX
XX New polynucleotides and polypeptides, useful for useful for treating
XX neurological conditions, e.g. spinal cord injury, cranial or cerebral
XX trauma, stroke, Alzheimer's disease, anxiety, autism, Parkinson's
XX disease, or paralysis.
XX
XX Claim 1; SEQ ID NO 629; 396pp; English.
XX
XX The invention relates to a novel isolated polynucleotide comprising any
XX of the 87 sequences fully defined in the specification or its mature
XX protein-coding portion. The polynucleotide of the invention demonstrates
XX neuroprotective, neurotropic, cerebroprotective and antiparkinsonian
XX activities whilst the polynucleotides, polypeptides and compounds may be
XX useful for treating neurological conditions including spinal cord injury,
XX cranial or cerebral trauma, stroke, Alzheimer's disease, anxiety, autism,
XX Parkinson's disease, tardive dyskinesia, paralysis, seizures or memory
XX disorders. The current sequence is that of the cDNA of the invention.
XX
XX Sequence 3568 BP; 624 A; 1278 C; 1128 G; 538 T; 0 U; 0 Other;
SQ
Query Match 54.6%; Score 22.4; DB 10; Length 3568;
Best Local Similarity 70.0%; Pred. No. 4.9e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGC 40
Db 1538 AAGACGACGACTGCCTGCCCTCTCTGCTACCCCTGCCG 1577
RESULT 28
ADS09784
ID ADS09784 standard; DNA; 3568 BP.
XX
XX ADS09784;
XX
XX 16-DEC-2004 (first entry)
XX
XX Human therapeutic DNA - SEQ ID 21.
XX
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
XX
XX Homo sapiens.
XX
XX WO2004080148-A2.
XX
XX 23-SEP-2004.
XX
XX 30-SRP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI; 2004-668857/65.
XX P-PSDB; ADS10468.
XX

PT New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX aplastic anemia or cancer for promoting wound healing.
XX
XX Claim 1; SEQ ID NO 21; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX be useful in preparing a composition for diagnosing or treating
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX disorders, such as aplastic anaemia or cancer, as well as for promoting
XX wound healing. The molecules may also be utilised during gene therapy
XX procedures. The current sequence is that of a human therapeutic DNA of
XX the invention. The current sequence is not shown explicitly within the
XX specification but can be accessed from the WIPO web-site.
XX
XX Sequence 3568 BP; 624 A; 1278 C; 1128 G; 538 T; 0 U; 0 Other;
SQ
Query Match 54.6%; Score 22.4; DB 13; Length 3568;
Best Local Similarity 70.0%; Pred. No. 4.9e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGC 40
Db 1538 AAGACGACGACTGCCTGCCCTCTCTGCTACCCCTGCCG 1577
RESULT 29
ADC51948
ID ADC51948 standard; DNA; 3705 BP.
XX
XX ADC51948;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human postsynaptic density protein encoding DNA SEQ ID NO:6.
XX
XX ds; gene; human; N-methyl-D-aspartic acid; NMDA;
XX receptor signal transfer; neuroprotective; neurotropic; antiparkinsonian;
XX gene therapy; neurodegenerative disease; Alzheimer's disease;
XX Parkinson's disease; postsynaptic density.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 120..3059
XX /*tag= a
XX /product= "postsynaptic density protein"
XX
XX WO2003044196-A1.
XX
XX 30-MAY-2003.
XX
XX 20-NOV-2002; 2002WO-JP012102.
XX
XX 20-NOV-2001; 2001JP-00354678.
XX 22-FEB-2002; 2002JP-00046786.
XX 07-AUG-2002; 2002JP-00229863.
XX
XX (DAUC) DAIICHI PHARM CO LTD.
XX (KAZU-) KAZUSA DNA RES INST FOUND.
XX
XX Ohara O, Nagase T, Ohishi M, Yokota H, Arai Y;
XX
XX WPI; 2003-468772/44.
XX P-PSDB; ADC51945.
XX
XX Agent for controlling N-methyl-D-aspartic acid receptor signal transfer
XX for treatment of Alzheimer's and Parkinson's disease.
XX
XX Claim 28; Page 126-129; 140pp; Japanese.
XX

CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with the expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a human CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 243390 BP; 65851 A; 48827 C; 53197 G; 74003 T; 0 U; 1512 Other;
Query Match 54.6%; Score 22.4; DB 13; Length 243390;
Best Local Similarity 70.0%; Pred. No. 5.8e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGCGCCGCGNC 40
DB 88961 ATGCCACCTGATGCTGTCTCCCTCCCTGCTGCTGGAGGC 88922

RESULT 32
ADZ13446/c
ID ADZ13446 standard; DNA; 243934 BP.

XX AC ADZ13446;

XX DT 16-JUN-2005 (first entry)

XX DE Human cancer-associated genomic DNA #82.

XX KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
XX KW cytostatic; gene; ds.

XX OS Homo sapiens.

XX PN WO2005031001-A2.

XX PD 07-APR-2005.

XX PF 23-SEP-2004; 2004WO-US031617.

XX PR 23-SEP-2003; 2003US-00669920.

XX PA (CHIR) CHIRON CORP.

XX PI Morris DW, Malandro MS;

XX DR WPI; 2005-273395/28.

XX PT Nucleic acid array useful for detecting cancer associated nucleic acid,
XX PT comprises two or more nucleic acid probes.

XX PS Disclosure; SEQ ID NO 966; 198pp; English.

XX CC The invention relates to a nucleic acid array for detecting a cancer
XX CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
XX CC The invention also relates to a peptide array comprising two or more
XX CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
XX CC that binds to a polypeptide, an isolated antibody or its fragment which
XX CC binds to a polypeptide, which is prepared by immunizing a host animal
XX CC with a composition comprising the polypeptide or its antigen binding
XX CC fragment and collecting cells from the host expressing antibodies against
XX CC the antigen or its antigen binding fragment, a composition comprising the
XX CC antibody and a carrier, a method of screening for anticancer activity, a
XX CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
XX CC method of treating cancer and a method of inhibiting expression of a CA
XX CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
XX CC nucleic acids. The antibody is useful for detecting the presence or
XX CC absence of cancer cells in an individual which involves contacting cells

CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents human cancer-associated genomic DNA of
CC the invention.

XX SQ Sequence 243934 BP; 66213 A; 49129 C; 53448 G; 74301 T; 0 U; 843 Other;

Query Match 54.6%; Score 22.4; DB 14; Length 243934;
Best Local Similarity 70.0%; Pred. No. 5.8e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGCGCCGCGNC 40
DB 89172 ATGCCACCTGATGCTGTCTCCCTCCCTGCTGCTGGAGGC 89133

RESULT 33
AAF90035
ID AAF90035 standard; DNA; 8301 BP.

XX AC AAF90035;

XX DT 06-AUG-2001 (first entry)

XX DE Nucleotide sequence of a type I polyketide synthase.

XX KW Metabolic pathway operon; polyketide; polyketide antibiotic;
XX KW type I polyketide synthase; ss.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT CDS 1..8301

XX FT /*tag= a

XX FT /product= "type I polyketide synthase"

XX PN WO20010497-A2.

XX PD 07-JUN-2001.

XX PF 27-NOV-2000; 2000WO-FR003311.

XX PR 29-NOV-1999; 99FR-00015032.

XX PR 07-JUN-2000; 2000US-0209800P.

XX PA (AVET) AVENTIS PHARMA SA.

XX PI Jeannin P, Pernodet J, Guerin M, Simonet P, Courtois S;

XX PI Cappellano C, Francou F, Raynal A, Ball M, Sezonov G, Taphile K;

XX PI Frostegard A;

XX DR WPI; 2001-374849/39.

XX DR P-PSDB; AAB83972.

XX PT Collection of nucleic acids from environmental samples, useful for

XX PT identifying e.g. genes encoding polyketide synthases and derived

XX PS Claim 35; Page 302-305; 356pp; French.

XX CC The specification describes a method for the preparation of a collection
XX CC of nucleic acids from organisms in a soil sample. The method comprises
XX CC milling a dried sample to produce microparticles; suspending these in
XX CC liquid buffer; extraction of nucleic acids from the microparticles;
XX CC passing nucleic acid-containing solution through a molecular sieve;
XX CC passing nucleic acid-enriched fractions through an anion exchange
XX CC chromatography material; and recovering fractions containing purified
XX CC nucleic acids. The nucleic acids are sources for sequences that encode

XX 01-AUG-2002 (first entry)
XX Arabidopsis thaliana expressed polynucleotide SEQ ID NO 425.
XX
XX Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
XX disease; crop; thale cress; tolerance factor; insect; pathogen;
XX nutrition; db.
XX
XX Arabidopsis thaliana.
XX
XX US2002023281-A1.
XX
XX 21-FEB-2002.
XX
XX 26-JAN-2001; 2001US-00770445.
XX
XX 27-JAN-2000; 2000US-0178472P.
XX
XX (GORL/) GORLACH J.
XX (ANY/) AN Y.
XX (HAMI/) HAMILTON C M.
XX (PRIC/) PRICE J L.
XX (RAIN/) RAINES T M.
XX (YUYI/) YU Y.
XX (RAME/) RAMEAKA J G.
XX (PAGE/) PAGE A.
XX (MATH/) MATHW A V.
XX (LEDF/) LEDFORD B L.
XX (WOES/) WOESSNER J P.
XX (HAAS/) HAAS W D.
XX (GARC/) GARCIA C A.
XX (KRIC/) KRICKER M.
XX (SLAT/) SLATER T.
XX (DAVI/) DAVIS K R.
XX (ALLE/) ALLEN K.
XX (HOFF/) HOFFMAN N.
XX (HURB/) HURBAN P.
XX
XX Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
XX WPI; 2002-403163/43.
XX
XX New Arabidopsis thaliana nucleic acid for identifying homologous genes,
XX producing compositions that modulate the expression or function of its
XX encoded protein, and mapping functional regions of protein.
XX
XX Claim 1; SEQ ID NO 425; 49pp + Sequence Listing; English.
XX
XX The invention relates to an Arabidopsis thaliana nucleic acid (I)
XX comprising a sequence capable of hybridising under stringent conditions
XX to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
XX given in the specification or its fragment. A polypeptide (II) encoded by
XX (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
XX genetically modified cell (IV) comprising an exogenous nucleic acid, is
XX useful for screening a candidate agent for its biological effect. (I) is
XX useful in identifying homologous or related genes, in producing
XX compositions that modulate the expression or function of its encoded
XX protein, mapping functional regions of the protein and in studying
XX associated physiological pathways. (I) is also useful for the genetic
XX manipulation of cells, particularly plant cells. (I) is also useful in
XX screening assays of various plant strains to determine the strains that
XX are best capable of withstanding a particular disease or environmental
XX stress. (II) and (III) are useful for screening of biologically active
XX agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
XX pathways. The screened agents are useful in improved methods of treating
XX crops to prevent or treat disease. (II) are also useful in screening
XX programs to identify agents that mimic or enhance the action of tolerance
XX factors. Such agents are useful in improved methods of treating crops to
XX enhance their tolerance to environmental stress. (I) is also useful for

CC enhancing or inhibiting production of a biosynthetic product in a plant.
CC (III) is useful for identifying other mediators that may induce
CC expression of proteins of interest, for establishing the extent to which
CC any specific insect and/or pathogen is responsible for damage to a
CC particular plant, for identifying other mediators that enhance or induce
CC tolerance to environmental stress, for identifying factors involved in
CC biosynthetic pathways of nutritional, commercial, or medicinal value and
CC for identifying productions of nutritional, commercial or medicinal
CC value. (IV) is useful in the study of genetic function and regulation,
CC for alteration of the cellular metabolism and for screening compounds
CC that may affect the biological function of the gene or gene products.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=99909770445
XX
XX Sequence 918 BP; 264 A; 226 C; 151 G; 270 T; 0 U; 7 Other;
SQ

Query Match 53.7%; Score 22; DB 6; Length 918;
Best Local Similarity 71.1%; Pred. No. 6.3e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCCTCATCTGCTGCGCCGCGCG 39
DB 508 AGCTCCGAGTCATGCTCTCGATCGCTGCTGCTACG 471

RESULT 37
ACL70733
ID ACL70733 standard; DNA; 1281 BP.
XX
XX ACL70733;
XX
XX 02-JUN-2005 (first entry)
XX
XX M. xanthus gene sequence, seq id 7196.
XX
XX Transgenic plant; DNA replication; gene regulation; gene expression;
XX gene; ds.
XX
XX Myxococcus xanthus.
XX
XX US6833447-B1.
XX
XX 21-DEC-2004.
XX
XX 10-JUL-2001; 2001US-00902540.
XX
XX 10-JUL-2000; 2000US-0217883P.
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX
XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX
XX WPI; 2005-028716/03.
XX
XX New substantially purified Myxococcus xanthus nucleic acid molecule
XX encoding a nitrite reductase, useful for determining gene expression,
XX identifying mutations in a gene of interest, and for constructing
XX mutations in a gene of interest.
XX
XX Example 2; SEQ ID NO 7196; 25pp; English.
XX
XX The invention relates to a substantially purified nucleic acid molecule
XX encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
XX recombinant DNA construct for expression of a nitrite reductase gene in a
XX plant cell, and a plant cell comprising the recombinant DNA construct.
XX The nucleic acid is useful for determining gene expression, identifying
XX mutations in a gene of interest, and for constructing mutations in a gene
XX of interest. Sequences given in records for SEQ IDs 1850-9691 represent a
XX set of about 7842 genes or partial genes from the genome of the bacterium
XX Myxococcus xanthus. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from USPTO

XX	Sequence	1281 BP; 200 A; 447 C; 443 G; 191 T; 0 U; 0 Other;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
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XX
SQ Sequence 1281 BP; 200 A; 447 C; 443 G; 191 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 14; Length 1281;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 24; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 12 TCACGATCCCTCATGCTGCCCGGNCGGC 41
Db 742 TACAGTACCTCAAGCCGCCCGGCGCG 771

RESULT 38
ABA20206
ID ABA20206 standard; DNA; 1441 BP.
XX
AC ABA20206;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 12537.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
OS Homo sapiens.
XX
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001334.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 04-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.

```
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249266P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system cancers
PT and metastases.
XX
XX Disclosure; SEQ ID NO 12537; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABAI1004-ABA21534) and proteins
CC (ABBI4678-ABBI8001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC cardiovascular disorders such as myocardial ischaemias; (c)
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1441 BP; 289 A; 432 C; 426 G; 294 T; 0 U; 0 Other;
SQ
Query Match 53.7%; Score 22; DB 5; Length 1441;
Best Local Similarity 71.1%; Pred. No. 6.4e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 1 AAGCCTCGGATGCCAGTCCCTCATCGCTGGCCGCGNC 38
Db | ||| ||| ||| ||| ||| ||| ||| ||| :|
676 ACCTCTCTGGATCCAGTCTCTATGTCCTGCGCTGCCAGTC 713
RESULT 39
ACA43467/c
ID ACA43467 standard; DNA; 2145 BP.
```

```
XX ACA43467;
XX 19-JUN-2003 (first entry)
XX Prokaryotic essential gene #25124.
XX
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX drug design; gene.
XX Pseudomonas putida.
XX WO200277183-A2.
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX P-PSDB; ABU39597.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 31337; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation. (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2145 BP; 370 A; 689 C; 710 G; 376 T; 0 U; 0 Other;
SQ
Query Match 53.7%; Score 22; DB 8; Length 2145;
```

```
Best Local Similarity 71.1%; Pred. No. 6.5e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGNCG 39
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 985 AGGCATCGGAGGCGAGCGCTCAGCGCGCGCGCGCG 948

RESULT 40
ADR42106/c
ID ADR42106 standard; cDNA; 2423 BP.
AC ADR42106;
XX
XX
DT 07-OCT-2004 (first entry)
XX
DE Human cancer inhibiting protein PP8857-encoding cDNA, SEQ ID NO:21.
XX
KW Human; PP8857; cancer inhibiting protein; recombinant preparation;
KW gene therapy; cancer; tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1863..2378
FT /*tag= a
FT /product= "Human cancer inhibiting protein PP8857"
XX
XX
PN CN1368511-A.
XX
PD 11-SEP-2002.
XX
PF 08-FEB-2001; 2001CN-00105312.
XX
PR 08-FEB-2001; 2001CN-00105312.
XX
PA (SHAN-) SHANGHAI INST ONCOLOGY.
XX
PI Gu J;
XX
XX
DR WPI; 2003-248949/25.
DR P-PSDB; ADR42065.
XX
PT New human protein with cancer inhibiting function for treating diseases,
PT such as, cancer.
XX
PS Example 3; SEQ ID NO 19; 40pp; Chinese.
XX
CC The invention relates to 12 novel human proteins with cancer inhibiting
CC functions, and to the polynucleotides encoding them. The invention also
CC relates to the recombinant preparation of the proteins, antagonists of
CC the proteins, and the use of the proteins, polynucleotides and
CC antagonists in therapeutic applications for treating diseases such as
CC cancers. The present sequence represents a specifically claimed cDNA
CC encoding a human cancer inhibiting protein of the invention. Note: The
CC present sequence is identical to SEQ ID NO:19 (ADR42064) referred to in
CC example 3.
XX
SQ Sequence 2423 BP; 473 A; 859 C; 729 G; 362 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 11; Length 2423;
Best Local Similarity 71.1%; Pred. No. 6.6e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGNCG 39
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 AGCCCCGGATGCCGCGCGCGAGCGCTGGGGGGCG 172

RESULT 41
ADR42064/c
ID ADR42064 standard; cDNA; 2423 BP.
XX
```

```
AC ADR42064;
XX
XX
DT 07-OCT-2004 (first entry)
XX
DE Human cancer inhibiting protein PP8857-encoding cDNA, SEQ ID NO:19.
XX
KW Human; PP8857; cancer inhibiting protein; recombinant preparation;
KW gene therapy; cancer; tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1863..2378
FT /*tag= a
FT /product= "Human cancer inhibiting protein PP8857"
XX
XX
PN CN1368511-A.
XX
PD 11-SEP-2002.
XX
PF 08-FEB-2001; 2001CN-00105312.
XX
PR 08-FEB-2001; 2001CN-00105312.
XX
PA (SHAN-) SHANGHAI INST ONCOLOGY.
XX
PI Gu J;
XX
XX
DR WPI; 2003-248949/25.
DR P-PSDB; ADR42065.
XX
PT New human protein with cancer inhibiting function for treating diseases,
PT such as, cancer.
XX
PS Example 3; SEQ ID NO 19; 40pp; Chinese.
XX
CC The invention relates to 12 novel human proteins with cancer inhibiting
CC functions, and to the polynucleotides encoding them. The invention also
CC relates to the recombinant preparation of the proteins, antagonists of
CC the proteins, and the use of the proteins, polynucleotides and
CC antagonists in therapeutic applications for treating diseases such as
CC cancers. The present sequence represents a cDNA encoding a human cancer
CC inhibiting protein of the invention. Note: The present sequence is
CC identical to SEQ ID NO:21 (ADR42106), which is claimed in Claim 5.
XX
SQ Sequence 2423 BP; 473 A; 859 C; 729 G; 362 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 11; Length 2423;
Best Local Similarity 71.1%; Pred. No. 6.6e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGNCG 39
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 AGCCCCGGATGCCGCGCGCGAGCGCTGGGGGGCG 172

RESULT 42
ABZ12243
ID ABZ12243 standard; DNA; 2979 BP.
XX
XX
AC ABZ12243;
XX
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 48.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
XX
PD 28-FEB-2002.
```


PR 24-FEB-2000; 2000US-0184664P.	PR 02-OCT-2000; 2000US-0237039P.
PR 02-MAR-2000; 2000US-0186350P.	PR 02-OCT-2000; 2000US-0237040P.
PR 16-MAR-2000; 2000US-0189874P.	PR 13-OCT-2000; 2000US-0239935P.
PR 17-MAR-2000; 2000US-0190076P.	PR 13-OCT-2000; 2000US-0239937P.
PR 18-APR-2000; 2000US-0198123P.	PR 20-OCT-2000; 2000US-0240960P.
PR 19-MAY-2000; 2000US-0205515P.	PR 20-OCT-2000; 2000US-0241221P.
PR 07-JUN-2000; 2000US-0209467P.	PR 20-OCT-2000; 2000US-0241785P.
PR 28-JUN-2000; 2000US-0214886P.	PR 20-OCT-2000; 2000US-0241786P.
PR 30-JUN-2000; 2000US-0215135P.	PR 20-OCT-2000; 2000US-0241787P.
PR 07-JUL-2000; 2000US-0216647P.	PR 20-OCT-2000; 2000US-0241808P.
PR 07-JUL-2000; 2000US-0216880P.	PR 20-OCT-2000; 2000US-0241809P.
PR 11-JUL-2000; 2000US-0217487P.	PR 20-OCT-2000; 2000US-0241826P.
PR 11-JUL-2000; 2000US-0217496P.	PR 01-NOV-2000; 2000US-0244617P.
PR 14-JUL-2000; 2000US-0218290P.	PR 08-NOV-2000; 2000US-0246474P.
PR 26-JUL-2000; 2000US-0220963P.	PR 08-NOV-2000; 2000US-0246475P.
PR 26-JUL-2000; 2000US-0220964P.	PR 08-NOV-2000; 2000US-0246476P.
PR 14-AUG-2000; 2000US-0224518P.	PR 08-NOV-2000; 2000US-0246477P.
PR 14-AUG-2000; 2000US-0224519P.	PR 08-NOV-2000; 2000US-0246478P.
PR 14-AUG-2000; 2000US-0225213P.	PR 08-NOV-2000; 2000US-0246523P.
PR 14-AUG-2000; 2000US-0225214P.	PR 08-NOV-2000; 2000US-0246523P.
PR 14-AUG-2000; 2000US-0225266P.	PR 08-NOV-2000; 2000US-0246524P.
PR 14-AUG-2000; 2000US-0225267P.	PR 08-NOV-2000; 2000US-0246525P.
PR 14-AUG-2000; 2000US-0225268P.	PR 08-NOV-2000; 2000US-0246526P.
PR 14-AUG-2000; 2000US-0225270P.	PR 08-NOV-2000; 2000US-0246527P.
PR 14-AUG-2000; 2000US-0225447P.	PR 08-NOV-2000; 2000US-0246528P.
PR 14-AUG-2000; 2000US-0225757P.	PR 08-NOV-2000; 2000US-0246532P.
PR 14-AUG-2000; 2000US-0225758P.	PR 08-NOV-2000; 2000US-0246609P.
PR 14-AUG-2000; 2000US-0225759P.	PR 08-NOV-2000; 2000US-0246610P.
PR 18-AUG-2000; 2000US-0226279P.	PR 08-NOV-2000; 2000US-0246611P.
PR 22-AUG-2000; 2000US-0226681P.	PR 08-NOV-2000; 2000US-0246613P.
PR 22-AUG-2000; 2000US-0226686P.	PR 17-NOV-2000; 2000US-0249207P.
PR 22-AUG-2000; 2000US-0227182P.	PR 17-NOV-2000; 2000US-0249208P.
PR 23-AUG-2000; 2000US-0227009P.	PR 17-NOV-2000; 2000US-0249209P.
PR 30-AUG-2000; 2000US-0228924P.	PR 17-NOV-2000; 2000US-0249210P.
PR 01-SEP-2000; 2000US-0228287P.	PR 17-NOV-2000; 2000US-0249211P.
PR 01-SEP-2000; 2000US-0229343P.	PR 17-NOV-2000; 2000US-0249212P.
PR 01-SEP-2000; 2000US-0229344P.	PR 17-NOV-2000; 2000US-0249213P.
PR 01-SEP-2000; 2000US-0229345P.	PR 17-NOV-2000; 2000US-0249214P.
PR 05-SEP-2000; 2000US-0229509P.	PR 17-NOV-2000; 2000US-0249215P.
PR 05-SEP-2000; 2000US-0229513P.	PR 17-NOV-2000; 2000US-0249216P.
PR 06-SEP-2000; 2000US-0230437P.	PR 17-NOV-2000; 2000US-0249217P.
PR 06-SEP-2000; 2000US-0230438P.	PR 17-NOV-2000; 2000US-0249218P.
PR 08-SEP-2000; 2000US-0231242P.	PR 17-NOV-2000; 2000US-0249244P.
PR 08-SEP-2000; 2000US-0231243P.	PR 17-NOV-2000; 2000US-0249245P.
PR 08-SEP-2000; 2000US-0231244P.	PR 17-NOV-2000; 2000US-0249264P.
PR 08-SEP-2000; 2000US-0231413P.	PR 17-NOV-2000; 2000US-0249265P.
PR 08-SEP-2000; 2000US-0231414P.	PR 17-NOV-2000; 2000US-0249297P.
PR 08-SEP-2000; 2000US-0232080P.	PR 17-NOV-2000; 2000US-0249299P.
PR 08-SEP-2000; 2000US-0232081P.	PR 01-DEC-2000; 2000US-0250160P.
PR 12-SEP-2000; 2000US-0231968P.	PR 01-DEC-2000; 2000US-0250391P.
PR 14-SEP-2000; 2000US-0232397P.	PR 05-DEC-2000; 2000US-0251030P.
PR 14-SEP-2000; 2000US-0232398P.	PR 05-DEC-2000; 2000US-0251988P.
PR 14-SEP-2000; 2000US-0232399P.	PR 05-DEC-2000; 2000US-0256719P.
PR 14-SEP-2000; 2000US-0232400P.	PR 06-DEC-2000; 2000US-0251479P.
PR 14-SEP-2000; 2000US-0232401P.	PR 08-DEC-2000; 2000US-0251856P.
PR 14-SEP-2000; 2000US-0232403P.	PR 08-DEC-2000; 2000US-0251868P.
PR 14-SEP-2000; 2000US-0233064P.	PR 08-DEC-2000; 2000US-0251869P.
PR 14-SEP-2000; 2000US-0233065P.	PR 08-DEC-2000; 2000US-0251989P.
PR 21-SEP-2000; 2000US-0234223P.	PR 08-DEC-2000; 2000US-0251990P.
PR 21-SEP-2000; 2000US-0234274P.	PR 11-DEC-2000; 2000US-0254097P.
PR 25-SEP-2000; 2000US-0234997P.	PR 05-JAN-2001; 2001US-0259678P.
PR 25-SEP-2000; 2000US-0234998P.	XX
PR 26-SEP-2000; 2000US-0235484P.	XX
PR 27-SEP-2000; 2000US-0235834P.	PA (HUMA-) HUMAN GENOME SCI INC.
PR 27-SEP-2000; 2000US-0235836P.	XX
PR 29-SEP-2000; 2000US-0236327P.	PI Rosen CA, Barash SC, Ruben SM;
PR 29-SEP-2000; 2000US-0236367P.	XX WPI; 2001-483426/52.
PR 29-SEP-2000; 2000US-0236368P.	DR
PR 29-SEP-2000; 2000US-0236369P.	XX
PR 29-SEP-2000; 2000US-0236370P.	PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PR 02-OCT-2000; 2000US-0236802P.	PT useful for preventing, diagnosing and/or treating cancers and metastasis.
PR 02-OCT-2000; 2000US-0237037P.	XX
PR 02-OCT-2000; 2000US-0237038P.	PS Disclosure; SEQ ID NO 39146; 3071pp + Sequence Listing; English.
	XX

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 6052 BP; 1066 A; 2155 C; 1805 G; 1026 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 4; Length 6052;
Best Local Similarity 71.1%; Pred. No. 6.8e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCGGATGCCAGTCCCTCATCGCTGCGCCCGGCG 39
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 AGCCCCGGATGCCGGCCCGGAGCGCTGGGGGGCG 181

RESULT 45
ACL64206/c
ID ACL64206 standard; DNA; 6430 BP.
XX
AC ACL64206;
XX
XX
DT 02-JUN-2005 (first entry)
XX
DE M. xanthus DNA fragment, seq id 669.
XX
XX Transgenic plant; DNA replication; gene regulation; gene expression; ds.
KW Myxococcus xanthus.
XX
OS
XX
PN US6833447-B1.
XX
PD 21-DEC-2004.
XX
XX 10-JUL-2001; 2001US-00902540.
XX
PR 10-JUL-2000; 2000US-0217883P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX
XX WPI; 2005-028716/03.

XX New substantially purified Myxococcus xanthus nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.
XX
XX Example 1; SEQ ID NO 669; 25pp; English.
XX
XX The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 1-1849 represent a
CC set of 1849 contig and singleton sequences comprising coding sequences,
CC DNA replication elements, promoters and other regulatory elements from

CC the genome of the bacterium Myxococcus xanthus. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO
XX
SQ Sequence 6430 BP; 982 A; 2222 C; 2190 G; 1035 T; 0 U; 1 Other;
Query Match 53.7%; Score 22; DB 14; Length 6430;
Best Local Similarity 80.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 12 TGCCAGTCCCTCATCGCTGCGCCCGGCGG 41
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2916 TACAGTACCTCAACGCCGCGCCGGCGCG 2887

RESULT 46
ADZ13665 4/c
Continuation (5 of 5) of ADZ13665 from base 400001 (Human cancer-associated genomic DNA
WP sequence split into 5 fragments LOCUS ADZ13665 Accession ADZ13665
WP Fragment Name Begin End
WP ADZ13665_0 1 110000
WP ADZ13665_1 100001 210000
WP ADZ13665_2 200001 310000
WP ADZ13665_3 300001 410000
WP ADZ13665_4 400001 443039

Query Match 53.7%; Score 22; DB 14; Length 43039;
Best Local Similarity 71.1%; Pred. No. 7.5e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGCTGCGCCGCGCGC 40
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 18237 GCCTCCTCAAGCGGGTCCCTGATCCTGACCCCGGAGC 18200

RESULT 47
ACN44450/c
ID ACN44450 standard; DNA; 75252 BP.
XX
AC ACN44450;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genomic sequence hCG27772.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
XX (SAGR-) SAGRES DISCOVERY.
PA
PI Morris DW;
XX
XX WPI; 2003-328604/31.

PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX
XX Claim 1; SEQ ID NO 904; Opp; English.
XX
XX The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for

CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX

SQ Sequence 75252 BP; 16571 A; 19384 C; 19541 G; 19756 T; 0 U; 0 Other;
Query Match 53.7%; Score 22; DB 11; Length 75252;
Best Local Similarity 71.1%; Pred. No. 7.6e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGCTGCGCGGCGC 40
DB 50417 GGCCCTGGATGCCACACCTCATCTCTGCCCGGTTAC 50380

RESULT 48
ADJ72363
ID ADJ72363 standard; DNA; 90597 BP.
XX
AC ADJ72363;
XX
DT 06-MAY-2004 (first entry)
XX
DE Streptomyces roseosporus daptomycin biosynthetic gene cluster DNA.
XX
KW ds; gene; antibacterial; gene therapy;
KW daptomycin biosynthesis gene cluster;
KW daptomycin non-ribosomal peptide synthetase; DptBC;
KW gram-positive bacterial infection.
XX
OS Streptomyces roseosporus.
XX
PN WO2003014297-A2.
XX
PD 20-FEB-2003.
XX
PF 31-JUL-2002; 2002WO-US024310.
XX
PR 06-AUG-2001; 2001US-0310385P.
PR 17-OCT-2001; 2001WO-US032354.
PR 10-MAY-2002; 2002US-0379866P.
XX
PA (CUBI-) CUBIST PHARM INC.
XX
PI Miao VPW, Brian P, Baltz RH, Coeffet-Legal MF;
XX
DR WPI; 2003-268192/36.
XX
PT New isolated nucleic acid molecule encoding a daptomycin non-ribosomal
PT peptide synthetase, useful for treatment of a gram-positive bacterial
PT infection of skeletal muscle, skin, bloodstream, kidneys, heart, lung and
PT bone.
XX
PS Disclosure; SEQ ID NO 1; 292pp; English.
XX
CC The invention relates to new isolated nucleic acid (NA) molecules from
CC the Streptomyces roseosporus daptomycin biosynthesis gene cluster,
CC especially a daptomycin non-ribosomal peptide synthetase (NRPS) or its
CC subunit, where the (NA) molecule encodes DptBC, and is not pRHB159. The
CC methods and compositions of the present invention are useful for
CC treatment of a gram-positive bacterial infection of any organ or tissue
CC in the body, including skeletal muscle, skin, bloodstream, kidneys,
CC heart, lung and bone. This sequence represents the daptomycin
CC biosynthesis gene cluster sequence.
XX
SQ Sequence 90597 BP; 12671 A; 32312 C; 31569 G; 14045 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 10; Length 90597;
Best Local Similarity 71.1%; Pred. No. 7.7e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCGCGGCGC 41
DB 14303 CCTCCGATGGTGTGCCACCGCGGTGCGCGGCCCG 14340

RESULT 49
ABQ78872
ID ABQ78872 standard; DNA; 90600 BP.
XX
AC ABQ78872;
XX
DT 23-OCT-2002 (first entry)
XX
DE S. roseosporus daptomycin biosynthetic gene cluster 90kb region.
XX
KW Daptomycin biosynthetic gene cluster; thioesterase; antibacterial;
KW fungicide; virucide; antiparasitic; immunomodulator; antilipemic;
KW cytostatic; gene therapy; antimitotic; immunomodulatory; siderophore;
KW anti-cholesterolemic; agrochemical; gene; ds.
XX
OS Streptomyces roseosporus.
XX
PN WO200259322-A2.
XX
PD 01-AUG-2002.
XX
PF 17-OCT-2001; 2001WO-US032354.
XX
PR 17-OCT-2000; 2000US-0240879P.
PR 28-FEB-2001; 2001US-0272207P.
PR 06-AUG-2001; 2001US-0310385P.
XX
PA (MIAO/) MIAO V P W.
PA (BRIA/) BRIAN P.
PA (BALT/) BALTZ R H.
PA (SILV/) SILVA C J.
XX
PI Miao VPW, Brian P, Baltz RH, Silva CJ;
XX
DR WPI; 2002-599794/64.
XX
PT Isolated nucleic acid molecule from a bacterial daptomycin biosynthetic
PT gene cluster encoding a thioesterase or thioesterase domain, useful for
PT generating novel linear and cyclic peptides, and products in a cell.
XX
PS Claim 7; Page 142-165; 227pp; English.
XX
CC The invention relates to a novel isolated nucleic acid molecule
CC comprising a sequence that encodes a thioesterase or thioesterase domain,
CC derived from a bacterial daptomycin biosynthetic gene cluster. The
CC proteins of the invention have antibacterial, fungicide, virucide,
CC antiparasitic, immunomodulator, antilipemic, and cytostatic activity. The
CC polynucleotides may have a use in gene therapy. The compositions and
CC methods of the present invention are useful for generating novel linear
CC and cyclic peptides and improving yield of a product in a cell expressing
CC an daptomycin non-ribosomal peptide synthetase (NRPS) to be used as new
CC compounds or in producing new compounds, such as antibiotics.
CC antifungals, antivirals, antiparasitics, antimitotics, antitumour agents,
CC immunomodulatory agents, anti-cholesterolemic agents, siderophores,
CC agrochemicals and cytostatics. The sequence represents the 90kb region of
CC the S. roseosporus daptomycin biosynthetic gene cluster
XX
SQ Sequence 90600 BP; 12671 A; 32312 C; 31571 G; 14046 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 6; Length 90600;
Best Local Similarity 71.1%; Pred. No. 7.7e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCGCGGCGC 41

KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
OS Unidentified.
XX US2004034888-A1.
XX 19-FEB-2004.
XX 28-APR-2003; 2003US-00425114.
PF 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 36530; 15pp; English.
PS
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 963 BP; 251 A; 214 C; 251 G; 247 T; 0 U; 0 Other;
Query Match 53.2%; Score 21.8; DB 13; Length 963;
Best Local Similarity 68.3%; Pred. No. 7.4e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 41
DB 566 ACGCCTCTGGATGATTGCCCTCACCTCTGGACCTGATGGG 526
RESULT 55
ID AEB66674/c
XX AEB66674 standard; DNA; 1057 BP.
XX
AC AEB66674;
XX
DT 22-SEP-2005 (first entry)

XX Rice genome derived DNA sequence, SEQ ID 1819.
DE
XX transcription; gene regulation; transgenic plant; RNA interference;
KW transformation; antibody; ds.
XX
OS Oryza sp.
XX JP2005185101-A.
XX 14-JUL-2005.
XX 11-DEC-2002; 2002JP-00383870.
XX 30-MAY-2002; 2002JP-00203269.
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
XX Kikuchi H, Hayashizaki Y, Ootomo Y, Matsuura K, Murakami K;
PI Kishimoto N, Sato K, Nagata T, Kawakami N, Yazaki J, Ishikawa M;
PI Doi K, Kawai J;
XX WPI; 2005-566181/58.
XX
XX Novel DNA encoding transcription factor, derived from rice plant, useful
PT for obtaining transcriptional-regulatory regions in plant and for
PT producing modified plant.
XX
XX Claim 1; SEQ ID NO 1819; 2928pp; Japanese.
PS
XX The invention relates to a novel DNA sequence encoding a transcription
CC factor derived from a plant. The invention further comprises antisense
CC RNA sequences, ribozyme activity RNA, RNAi sequences, a vector,
CC transformed plant cells, antibodies and proteins, all related to the
CC novel plant DNA sequences of the invention. The novel DNA is preferably
CC derived from a rice-genome database. The invention further provides a
CC method for determining the transcription regulatory regions of the rice
CC genome. The novel DNA is useful for controlling the expression of a gene
CC in a plant and for producing a modified plant with desired and different
CC characteristics. The plant DNA and method enables the acquisition of many
CC transcriptional-regulatory regions. This polynucleotide represents a DNA
CC sequence taken from a rice genome clone library for use in the invention.
CC Note: This sequence is not shown in the specification. It has been
CC retrieved from a sequence listing in electronic format from the Japanese
CC Patent Office. The invention claims DNA sequences of SEQ ID Nos 1 to
CC 28469 and encoded protein sequences of SEQ ID Nos 28470 to 56791.
CC However, the sequence listing only provided the DNA sequences of SEQ ID
CC Nos 1 to 3032.
XX
SQ Sequence 1057 BP; 233 A; 279 C; 284 G; 261 T; 0 U; 0 Other;
Query Match 53.2%; Score 21.8; DB 14; Length 1057;
Best Local Similarity 68.3%; Pred. No. 7.4e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 41
DB 452 AAGCCTCGTATTGGAGTCCCTCATCACGACCGGTGCGC 412
RESULT 56
ID ABL34568
XX ABL34568 standard; DNA; 6423 BP.
XX
AC ABL34568;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human metastasis associated gene SEQ ID NO: 121.
XX

PT Isolated nucleotide sequences of *Neisseria meningitidis* which can be used
PT in the diagnosis and treatment of *N. meningitidis* infection and other
PT *Neisserial* infections, for example, *N. gonorrhoea*.
XX

PS Claim 7; Page 326-329; 1760pp; English.

XX The present invention describes methods of obtaining immunogenic proteins
CC from *Neisseria* genomic sequences. AAA81453 to AAA82414 represent
CC specifically claimed *Neisseria meningitidis* genomic DNA sequences;
CC AAA81260 to AAA81303 and AA825620 to AA825663 represent *Neisseria* DNA
CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
CC *Neisseria meningitidis* DNA sequences; and AAA81322 to AAA81452 represent
CC *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to *Neisserial* bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against *Meningococcus B*; against all serotypes; and/or against all
CC pathogenic *Neisseriae*. Identification of sequences from the bacterium
CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious *Meningococcus B*
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions
XX

SQ Sequence 9941 BP; 2330 A; 2662 C; 2649 G; 2300 T; 0 U; 0 Other;

Query Match 53.2%; Score 21.8; DB 3; Length 9941;
Best Local Similarity 68.3%; Pred. No. 8.2e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGCG 41

Db 1752 AAGCCGCCCTGCGAGTACGGTATGCGCGCGCGATGCG 1792

RESULT 61

ACL64482/C

ID ACL64482 standard; DNA; 10528 BP.

XX AC

XX AC

DT 02-JUN-2005 (first entry)

XX M. xanthus DNA fragment, seq id 945.

DE Transgenic plant; DNA replication; gene regulation; gene expression; ds.

XX Myxococcus xanthus.

XX US6833447-B1.

XX 21-DEC-2004.

XX 10-JUL-2001; 2001US-00902540.

XX 10-JUL-2000; 2000US-0217883P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;

XX WPI; 2005-028716/03.

XX New substantially purified *Myxococcus xanthus* nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT

PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.

XX Example 1; SEQ ID NO 945; 25pp; English.

XX The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 1-1849 represent a
CC set of 1849 contig and singleton sequences comprising coding sequences,
CC DNA replication elements, promoters and other regulatory elements from
CC the genome of the bacterium *Myxococcus xanthus*. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO
XX

SQ Sequence 10528 BP; 1463 A; 3512 C; 3806 G; 1747 T; 0 U; 0 Other;

Query Match 53.2%; Score 21.8; DB 14; Length 10528;
Best Local Similarity 68.3%; Pred. No. 8.2e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGCG 41

Db 8588 ACGCCTCCGGCGCCAGGCCCTTCATCGAGCCCGCGCGTG 8548

RESULT 62

ABL02586

ID ABL02586 standard; cDNA; 16105 BP.

XX AC

XX ABL02586;

DT 26-MAR-2002 (first entry)

XX *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 2240.

XX *Drosophila*; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.

XX *Drosophila melanogaster*.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEXE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX P-PSDB; ABB58483.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from *Drosophila* and for elucidating cell signaling and cell-cell
PT interactions.

XX Claim 1; SEQ ID NO 2240; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC


```
DR WPI; 2000-013262/01.
XX
PT Isolation of polynucleotides from mycobacterial genomes, useful for
PS detection of Mycobacteria and for combating tuberculosis.
XX
PS Claim 23; Page 90; 161pp; English.
XX
CC The present invention describes a method for isolating a polynucleotide
CC of interest that is present or is expressed in a genome of a first
CC mycobacterium strain and that is absent or altered in a genome of a
CC second mycobacterium strain, which is different from the first strain
CC using a bacterial artificial chromosome (BAC) vector. Recombinant BAC
CC vectors, which are preferably immobilised, can be used to detect
CC mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological
CC samples. The polynucleotides identified are useful as probes or primers
CC for detecting a given mycobacterium of interest. By aligning the
CC polynucleotides contained in the recombinant BAC vectors it is possible
CC to physically map a polynucleotide of mycobacterial origin in a
CC biological sample. The methods and vectors from the present invention are
CC useful in providing information for combating tuberculosis. It is
CC possible to compare genomes between different strains or species and
CC their non-pathogenic strains or species counterparts. ABQ62492 to
CC ABQ63228 and ABB81227 to ABB81230 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 230 BP; 39 A; 87 C; 59 G; 43 T; 0 U; 2 Other;
Query Match 52.7%; Score 21.6; DB 3; Length 230;
Best Local Similarity 72.2%; Pred. No. 8.1e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 6 TCGGATGTCAGTCCCTCATCGTCGCCGCCGCGG 41
DB 33 TCCGGATTCTGGGTTTCATCGTCGCCGCCGCGG 68

RESULT 66
ADQ54664
ID ADQ54664 standard; DNA; 562 BP.
XX
AC ADQ54664;
XX
DT 21-OCT-2004 (first entry)
XX
DE Novel canine microarray-related DNA sequence SeqID5966.
XX
KW canine microarray; drug screening; toxicity assay;
KW environmental pollutant; cellular response; gene expression profile;
KW toxic response; liver necrosis; fatty liver disease;
KW protein adduct formation; hepatitis; dog; ds.
XX
OS Canis familiaris.
XX
PN WO2004063324-A2.
XX
PD 29-JUL-2004.
XX
PF 05-MAY-2003; 2003WO-US013853.
XX
PR 03-MAY-2002; 2002US-0377240P.
XX
PA (GENE-) GENE LOGIC INC.
PA (PFIZ ) PFIZER PROD INC.
XX
PI Diggans JC, Porter M, Wei T;
XX WPI; 2004-561890/54.
XX
PT New isolated nucleic acid molecule, useful for drug screening and
PT toxicity assays or for assessing the impact, including toxicity, of a
PT compound, pharmaceutical agent or environmental pollutant on a cell or
PT living organism.
XX

PS Claim 1; SEQ ID NO 5966; 41pp; English.
XX
CC This invention is related to a novel isolated canine nucleic acid
CC sequences and the construction of canine microarrays containing a
CC significant portion of the canine genome. The isolated canine nucleic
CC acid sequences of the invention may be useful for drug screening and
CC toxicity assays. The invention is therefore useful for assessing the
CC impact, including toxicity, of a compound, pharmaceutical agent or
CC environmental pollutant on a cell or living organism. The methods are
CC useful for detecting genes that are up- or down-regulated in canines in a
CC disease state. The sequences are useful as diagnostic agents or markers
CC to detect a cellular response in a sample individually or as part of a
CC gene expression profile. It is also useful as a target for agents that
CC modulate gene expression or activity. The database is useful for
CC producing electronic Northern blots that allow the user to determine the cell
CC type or tissue in which a given gene is expressed and to allow
CC determination of the abundance or expression level of a given gene in a
CC particular tissue or cell. The methods are useful for determining the
CC similarity of a toxic response to one or more individual compounds. The
CC methods are useful for predicting at least one toxic response or the
CC likelihood that a compound or test agent will induce various specific
CC pathologies such as those of the liver (liver necrosis, fatty liver
CC disease, protein adduct formation or hepatitis), those of the kidney,
CC heart, brain or testes, or other pathologies associated with at least one
CC of the toxins. The methods are also useful for predicting or elucidating
CC the potential cellular pathways influenced, induced or modulated by the
CC compound or test agent due to the similarity of the expression profile
CC compared to the profile induced by a known toxin. The present sequence is
CC that of a canine DNA sequence which was claimed for use during the
CC production of a canine microarray of the invention.
XX
SQ Sequence 562 BP; 136 A; 177 C; 152 G; 96 T; 0 U; 1 Other;
Query Match 52.7%; Score 21.6; DB 13; Length 562;
Best Local Similarity 72.2%; Pred. No. 8.4e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCCTCATCGTCGCCGCCG 37
DB 298 AGCTCCGCCGCCCAAGTTCGCCAGCTCTGCGCCG 333

RESULT 67
ACL66884
ID ACL66884 standard; DNA; 1689 BP.
XX
AC ACL66884;
XX
DT 02-JUN-2005 (first entry)
XX
DE M. xanthus gene sequence, seq id 3347.
XX
KW Transgenic plant; DNA replication; gene regulation; gene expression;
KW gene; ds.
XX
OS Myxococcus xanthus.
XX
PN US6833447-B1.
XX
PD 21-DEC-2004.
XX
PF 10-JUL-2001; 2001US-00902540.
XX
PR 10-JUL-2000; 2000US-0217883P.
XX
PA (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX WPI; 2005-028716/03.
XX
PT New substantially purified Myxococcus xanthus nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT
```


Db	6088	CCTCAGGATGCTGCTCACTTAAGGCTGCCCGTAGC	6123	
RESULT 70				
ABQ81846/c				
ID	ABQ81846	standard; DNA; 349980 BP.		
XX	AC	ABQ81846;		
XX	XX	19-NOV-2002 (first entry)		
DE	XX	Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.		
XX	XX	Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;		
KW	XX	antidiarrheic; antibacterial; inhibitor of Salmonella; detection;		
KW	XX	identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;		
XX	XX	rotavirus; food composition; pharmaceutical composition; gene; ds.		
XX	OS	Bifidobacterium longum.		
OS	XX	Synthetic.		
XX	XX	EP1227152-A1.		
PN	XX	31-JUL-2002.		
XX	XX	30-JAN-2001; 2001EP-00102050.		
PF	XX	30-JAN-2001; 2001EP-00102050.		
XX	XX	(NEST) SOC PROD NESTLE SA.		
PA	XX	WPI; 2002-668397/72.		
DR	XX	Novel polynucleotide comprising Bifidobacterium genome sequence useful as		
PT	XX	a probe or primer for detecting and/or identifying Bifidobacterium longum		
PT	XX	in a biological sample.		
XX	XX	Disclosure; SEQ ID NO 1102; 80pp; English.		
PS	XX	The present invention describes a polynucleotide (I) comprising a		
CC	XX	sequence of a Bifidobacterium genome selected from the nucleotide		
CC	XX	sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at		
CC	XX	least 90% identity or which hybridises with the sequences given in		
CC	XX	ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding a		
CC	XX	fusion protein, comprising a sequence selected from 1097 sequences given		
CC	XX	in ABP65258 to ABP6354 ligated in frame to a polynucleotide encoding a		
CC	XX	heterologous polypeptide. (I) has antidiarrheic and antibacterial		
CC	XX	activities, and can be used as an inhibitor of Salmonella. (I) (which is		
CC	XX	a probe) is useful for the detection and/or identification of		
CC	XX	Bifidobacterium longum in a biological sample. A carrier containing the		
CC	XX	lactic acid bacterium Bifidobacterium longum NCC2705 (NCIM I-2618) can be		
CC	XX	used for preventing and/or treating diarrhoea brought about by pathogenic		
CC	XX	bacteria and/or rotavirus. The carrier is a food composition selected		
CC	XX	from milk, yogurt, curd, cheese, fermented milk, milk based fermented		
CC	XX	products, ice-creams, fermented cereal based products, milk based		
CC	XX	powders, infant formula, pet food or a pharmaceutical composition		
CC	XX	selected from tablets, liquid bacterial suspensions, dried oral		
CC	XX	supplement, wet oral supplement, dry tube feeding or wet tube feeding.		
CC	XX	(I) is useful in DNA arrays or chips to carry out analysis of the		
CC	XX	expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent		
CC	XX	Bifidobacterium related nucleotide sequences given in the Sequence		
CC	XX	Listing from the present invention but not mentioned further within the		
CC	XX	specification. N.B. the sequence data for this patent is not represented		
CC	XX	in the printed specification but is based on sequence information		
CC	XX	supplied by the European Patent Office		
XX	XX	Sequence 349980 BP; 69200 A; 103414 C; 105147 G; 72219 T; 0 U; 0 Other;		
QY	4	CCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGNCG	39	
Query Match	52.7%;	Score 21.6;	DB 6;	Length 349980;
Best Local Similarity	72.2%;	Pred. No. 1.1e+03;		
Matches	26;	Conservative 1;	Mismatches 9;	Indels 0; Gaps 0;
Db	6088	CCTCAGGATGCTGCTCACTTAAGGCTGCCCGTAGC	6123	
RESULT 71				
ABD06358				
ID	ABD06358	standard; DNA; 234 BP.		
XX	AC	ABD06358;		
XX	XX	29-JUL-2004 (first entry)		
DE	XX	Pseudomonas aeruginosa polynucleotide #4962.		
XX	XX	Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;		
KW	XX	antibacterial.		
XX	OS	Pseudomonas aeruginosa.		
OS	XX	US5551795-B1.		
PN	XX	22-APR-2003.		
PD	XX	18-FEB-1999; 99US-00252991.		
XX	XX	18-FEB-1998; 98US-0074788P.		
PF	XX	27-JUL-1998; 98US-0094190P.		
PR	XX	(GENO-) GENOME THERAPEUTICS CORP.		
XX	XX	Rubenfield MJ, Nolling J, Deloughery C, Bush D;		
PI	XX	WPI; 2003-615309/58.		
DR	XX	P-PSDB; ABO72787.		
XX	XX	Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,		
PT	XX	useful as molecular targets for diagnostics, prophylaxis and treatment of		
PT	XX	pathological conditions resulting from bacterial infection.		
XX	XX	Disclosure; SEQ ID NO 4962; 455pp; English.		
PS	XX	The invention relates to Pseudomonas aeruginosa polypeptides and the		
CC	XX	polynucleotides encoding them. The sequences are useful in diagnosis and		
CC	XX	therapy of pathological conditions, as molecular targets for diagnostics, and		
CC	XX	prophylaxis and treatment of pathological conditions resulting from a		
CC	XX	bacterial infection, for evaluating a compound, such as a polypeptide,		
CC	XX	for the ability to bind a P. aeruginosa nucleic acid, as components of		
CC	XX	effective antibacterial targets, as targets for antibacterial drugs,		
CC	XX	including anti-P. aeruginosa drugs, as templates for recombinant		
CC	XX	production of P. aeruginosa-derived peptides or polypeptides, as target		
CC	XX	components for diagnosis and/or treatment of P. aeruginosa-caused		
CC	XX	infection, and in detection of P. aeruginosa sequences or other sequences		
CC	XX	of Pseudomonas species using biochip technology. Sequences ABD01397-		
CC	XX	ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:		
CC	XX	The sequence data for this patent did not form part of the printed		
CC	XX	specification but was obtained in electronic format from USPTO at		
CC	XX	seqdata.uspto.gov/sequence.html		
XX	XX	Sequence 234 BP; 33 A; 76 C; 77 G; 48 T; 0 U; 0 Other;		
QY	3	GCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGNCGCG	41	
Query Match	52.2%;	Score 21.4;	DB 11;	Length 234;
Best Local Similarity	69.2%;	Pred. No. 9.4e+02;		
Matches	27;	Conservative 1;	Mismatches 11;	Indels 0; Gaps 0;
Db	6088	CCTCAGGATGCCAGTCCCTCATCGCTGGCCGCGNCGCG	131	
RESULT 72				
ABQ99123/c				
ID	ABQ99123	standard; DNA; 292 BP.		
XX	XX			

XX	ABX51132;	
AC		
XX	25-FEB-2003 (first entry)	
DT		
XX		
DE	Bovine EST associated with lactation/muscle/fat deposition #1061.	
XX		
KW	Bovine; ss; EST; expressed sequence tag; lactation; LMFD;	
KW	muscle deposition; fat deposition; genome mapping; gene identification;	
KW	gene analysis; cattle breeding.	
XX		
OS	Bos Taurus.	
XX		
PN	US2002137160-A1.	
XX		
PD	26-SEP-2002.	
XX		
PF	26-OCT-2001; 2001US-00983965.	
XX		
PR	17-DEC-1998; 98US-0113678P.	
PR	15-DEC-1999; 99US-00465231.	
XX		
PA	(BYAT/) BYATT J C.	
PA	(MATH/) MATHIALAGAN N.	
PA	(TAON/) TAO N.	
PA	(WARR/) WARREN W C.	
XX		
PI	Byatt JC, Mathialagan N, Tao N, Warren WC;	
XX		
DR	WPI; 2003-102386/09.	
XX		
PT	Purified nucleic acid molecules, useful for genome mapping, gene	
PT	identification and analysis, cattle breeding or preparation of constructs	
PT	for cattle gene expression and genetically improved cattle.	
XX		
PS	Claim 2; SEQ ID NO 1061; 38pp; English.	
XX		
CC	The invention relates to a purified nucleic acid molecule associated with	
CC	lactation or muscle and fat deposition (designated LMFD), derived from	
CC	cattle, and the LMFD nucleic acid can specifically hybridise to a second	
CC	nucleic acid molecule comprising any of 5912 nucleotide sequences,	
CC	appearing as ABX50072-ABX55983, or complements of them. Also included are	
CC	; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic	
CC	acid linked to a promoter and a 3' non- translated sequence that	
CC	functions in the cell to cause termination of transcription and addition	
CC	of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and	
CC	(2) determining a level or pattern of a molecule in a bovine cell or	
CC	tissue comprising: (a) incubating a marker nucleic acid (comprising any	
CC	of the 5912 nucleic acid sequences or its complement or fragment) with a	
CC	complementary nucleic acid molecule obtained from the bovine cell or	
CC	tissue, where hybridisation between the marker nucleic acid and the	
CC	complementary nucleic acid permits the detection of the molecule; and (b)	
CC	detecting the level or pattern of the complementary nucleic acid, where	
CC	the detection of the complementary nucleic acid is predictive of the	
CC	level or pattern of the molecule. The LMFD nucleic acid is used for	
CC	determining a level or pattern of a molecule in a bovine cell or tissue.	
CC	It is useful for genome mapping, gene identification and analysis, cattle	
CC	breeding, preparation of constructs for use in cattle gene expression, or	
CC	for genetically improving cattle. The present sequence is one of the 5912	
CC	bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present	
CC	sequence was not shown in the specification but was obtained in	
CC	electronic format from the USPTO web site:	
CC	seqdata.uspto.gov/sequence.html?docID=20020137160	
XX		
SQ	Sequence 381 BP; 80 A; 118 C; 111 G; 72 T; 0 U; 0 Other;	
	Query Match 52.2%; Score 21.4; DB 8; Length 381;	
	Best Local Similarity 69.2%; Pred No. 9,6e+02;	
	Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0	
QY	2 AGCTCTCGGATCCGAGTCCTCATCGTGGCCCGNCGC 40	
	261 AACACGCGAGACCACTGCCACTTGGCAGGCCCTGAAGC 223	
Db		

XX	
DT	29-JUL-2004 (first entry)
DE	Pseudomonas aeruginosa polynucleotide #11294.
KW	Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW	antibacterial.
OS	Pseudomonas aeruginosa.
XN	US6551795-B1.
FN	
PD	22-APR-2003.
XX	
PF	18-FEB-1999; 99US-00252991.
PR	18-FEB-1998; 98US-0074788P.
PT	27-JUL-1998; 98US-0094190P.
XX	(GENO-) GENOME THERAPEUTICS CORP.
PA	Rubenfield MJ, Nolling J, Deloughery C, Bush D;
PI	WI; 2003-615309/S8.
DR	P-PSDB; ABO79119.
DR	Noel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, of
PT	useful as molecular targets for diagnostics, prophylaxis and treatment of
PT	bathological conditions resulting from bacterial infection.
XX	Disclosure; SEQ ID NO 11294; 455pp; English.
XX	The invention relates to Pseudomonas aeruginosa polypeptides and the
CC	poleuleotides encoding them. The sequences are useful in diagnosis and
CC	therapy of pathological conditions, as molecular targets for diagnosis,
CC	prophylaxis and treatment of pathological conditions resulting from a
CC	bacterial infection, for evaluating a compound, such as a polypeptide,
CC	for the ability to bind a P. aeruginosa nucleic acid, as components of
CC	effective antibacterial targets, as targets for antibacterial drugs,
CC	including anti-P. aeruginosa drugs, as templates for recombinant
CC	production of P. aeruginosa-derived peptides or polypeptides, as target
CC	components for diagnosis and/or treatment of P. aeruginosa-caused
CC	infection, and in detection of P. aeruginosa sequences or other sequences
CC	of Pseudomonas species using biochip technology. Sequences AB001397-
ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:	
CC	The sequence data for this patent did not form part of the printed
CC	specification but was obtained in electronic format from USPTO at
seqdata.uspto.gov/sequence.html	
XX	
SQ	Sequence 501 BP; 60 A; 185 C; 182 G; 74 T; 0 U; 0 Other;
Query Match	52.2%; Score 21.4; DB 11; Length 501;
Best Local Similarity	77.4%; Pred. No. 9.8e+02;
Matches	24; Conservative 1; Mismatches 6; Indels 0; Gaps 0
OY	8 CGGATGCCAGTCCCTCATCGTCGTGGCCGC GCNC 38 : :
Dd	337 CGAATGCCAGTCCGCGC GTGGCCACG GC 307 : :
RESULT 81	
ACH78213/c	
ID	ACH78213 standard; DNA; 526 BP.
XX	
AC	ACH78213;
XX	
DT	29-JUL-2004 (first entry)
XX	Human genome derived single exon probe #11408.
XX	
KW	Human; probe; ss; gene expression; single exon probe; microarray;
KX	alternative splicing event; genomic alteration.
XX	

OS	Homo sapiens.
XX	
PN	US2003194704-A1.
XX	
XX	
PD	16-OCT-2003.
XX	
XX	
PF	03-APR-2002; 2002US-00029386.
XX	
PR	03-APR-2002; 2002US-00029386.
XX	
PA	(PENN/) PENN S G.
PA	(PENN/) RANK D R.
PA	(HANZ/) HANZEL D K.
XX	
PI	Penn SG, Rank DR, Hanzel DK;
XX	
XX	
DR	WPI; 2004-119264/12.
XX	
XX	
PT	New human genome-derived single exon nucleic acid probes useful for human
PT	gene expression analysis, for identifying or characterizing alternative
PT	splicing events, for assessing genomic alterations or as tools for
PT	surveying tissues.

Claim 15; SEQ ID NO 11408; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above). The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704

Sequence 526 BP; 82 A; 149 C; 222 G; 73 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 12; Length 526;
Best Local Similarity 69.2%; Pred. No. 9.8e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0

QY 2 AGCTCCGGATGCCAGTCCCTCATCGTCGCGCGGC 40
 ||||| |
Db 124 AGCTCCGGACTCCCTCCCTCCTCTGCGCGGCTC 86
 ||||| |

RESULT 82

```
ABA31177
ID ABA31177 standard; DNA; 572 BP.
XX
AC ABA31177;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #9643 for gene expression analysis in human heart cell sample.
XX
DE Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 1; SEQ ID NO 9643; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 572 BP; 116 A; 135 C; 187 G; 134 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 4; Length 572;
Best Local Similarity 69.2%; Pred. No. 9.8e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCTGCTGCGCCGCGCGC 41
Db 134 GCATTTGGATGTGCTGCTCCCGCAAGGCTGCGAGGCCACG 172

RESULT 83
AAK12507
ID AAK12507 standard; DNA; 572 BP.
XX
AC AAK12507;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 12498.
XX
```

```
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 12498; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 572 BP; 116 A; 135 C; 187 G; 134 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 4; Length 572;
Best Local Similarity 69.2%; Pred. No. 9.8e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCTGCTGCGCCGCGCGC 41
Db 134 GCATTTGGATGTGCTGCTCCCGCAAGGCTGCGAGGCCACG 172

RESULT 84
ADD68671/c
ID ADD68671 standard; DNA; 597 BP.
XX
AC ADD68671;
XX
DT 15-JAN-2004 (first entry)
XX
DE Murine DNA amplification-related DNA - SEQ ID 28.
XX PCR; DNA amplification; ds; mouse; murine.
XX
OS Mus sp.
XX
PN JP2002315583-A.
XX
PD 29-OCT-2002.
XX
PF 29-JUN-2001; 2001JP-00197813.
XX
PR 29-JUN-2000; 2000JP-00196242.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
```


Query Match 52.2%; Score 21.4; DB 11; Length 654;
Best Local Similarity 69.2%; Pred. No. 9.9e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
||| ||| ||| ||| ||| ||| ||| ||| : |||
Db 390 GCAACCGCAGGCCAGTTCTCGTCGTCGGCCAGCCAGCG 352

RESULT 87
ABD14229
ID ABD14229 standard; DNA; 738 BP.
XX
XX
AC ABD14229;
XX
XX
DT 29-JUL-2004 (first entry)
XX
XX
DE Pseudomonas aeruginosa polynucleotide #12833.
XX
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.

OS	<i>Pseudomonas aeruginosa</i> .
XX	
XX	US6551795-B1.
PN	
XX	22-APR-2003.
PD	

PF	18-FEB-1999;	99US-00252991.	
XX			
PF	18-FEB-1998;	98US-0074788P.	
XX	27-JUL-1998;	98US-0094190P.	
XX			
PA	(GENO-)	GENOME THERAPEUTICS CORP.	
XX			
PI	Rubenfield MJ, Nolling J, Deloughery C, Bush D;		
XX			
XX	WPI; 2003-615309/58.		
DR	P-PDB: A8080658.		
DR			

Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide.
 useful as molecular targets for diagnostics, prophylaxis and treatment of
 pathological conditions resulting from bacterial infection.

Disclosure; SEQ ID NO 12833; 455bp; English.

The invention relates to *Pseudomonas aeruginosa* polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs, as templates for recombinant production of *P. aeruginosa*-derived peptides or polypeptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused infection, and in detection of *P. aeruginosa* sequences or other sequences of *Pseudomonas* species using biochip technology. Sequences AB01397-ABD17967 represent *P. aeruginosa* polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html

```

Q      Sequence 738 BP; 126 A; 230 C; 254 G; 128 T; 0 U; 0 Other;

Query Match      52.2%; Score 21.4; DB 11; Length 738;
Best Local Similarity 69.2%; Pred. No. 9.9e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

```

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
 || ||| ||| ||| ||| ||| ||| ||| : |||
 Db 310 GCAACCGCAGGCCAGTTCCTCGTCCGCCAGCCAGCG 348

RESULT 88
ABD11508/C

ID ABD11508 standard; DNA; 816 BP.

AC ABD11508;

29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polynucleotide #10112.

AA Bacterial infection; gene; ds; *Pseudomonas aeruginosa* infection;
 KW antibacterial.
 KW

OS *Pseudomonas aeruginosa*.

AA
PN
US6551795-B1.

XX
PD 22-APR-2003.

AA
PF 18-FEB-1999; 99US-00252991.

AA
PR 18-FEB-1998: 98US-0074788P.

PR 27-JUL-1998; 9805-0094190P;
XX

FA (GENO-) GENOME THERAPEUTICS CORP.
XX

FI KUBENFIELD MW, NOTTING J, DETROUGNEY C, BUSH D,
XX

DR WPT; 2003-613309/38.
DR P-PSDB; ABO77937.

Novel isolated nucleic acid encoding Pseudomox

PT pathological conditions resulting from bacterial use as molecular targets for diagnostics, FI

PS Disclosure: SEQ ID NO 10112; 455pp; English.

The invention relates to *Pseudomonas aeruginosa* polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs, as templates for recombinant production of *P. aeruginosa*-derived peptides or polypeptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused infection, and in detection of *P. aeruginosa* sequences or other sequences of *Pseudomonas* species using biochip technology. Sequences ABD01397-ABD17967 represent *P. aeruginosa* polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html

Sequence 816 BP; 161 A; 299 C; 233 G; 123 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 11; Length 816;

BEST LOCAL SIMILARITY 69.2%; FREQ: NO. IE+VS;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41

Db 82 GCCACCTGATGCCAGGACAGCTTGACCGGCCTGGGCGG 44

RESULT 89

ABD11440/C
ID ABD11440 standard: DNA: 834 BP.

AC ABD11440:

W

DT 29-JUL-2004 (first entry)
XX Pseudomonas aeruginosa polynucleotide #10044.
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
KW Pseudomonas aeruginosa.
OS US6551795-B1.
XX 22-APR-2003.
XX 18-FEB-1999; 99US-00252991.
XX 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX (GENO-) GENOME THERAPEUTICS CORP.
PA Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX P-PSDB; ABO77869.
DR Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX Disclosure; SEQ ID NO 10044; 455pp; English.
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX Sequence 834 BP; 159 A; 298 C; 239 G; 138 T; 0 U; 0 Other;
SQ Query Match 52.2%; Score 21.4; DB 11; Length 834;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 3 GCCTCGGATGCCAGTCCCTCATCGCTGCGCCGCGCG 41
DB 749 GCCACCTGATGCCAGGACAGCTTGACCGGCTGGCGCG 711
RESULT 90
ABD11189
ID ABD11189 standard; DNA; 909 BP.
XX ABD11189;
AC ABD11189;
XX 29-JUL-2004 (first entry)
DT Pseudomonas aeruginosa polynucleotide #9793.
XX Pseudomonas aeruginosa.
DE Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
KW Pseudomonas aeruginosa.
OS

XX US6551795-B1.
XX 22-APR-2003.
XX 18-FEB-1999; 99US-00252991.
XX 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX (GENO-) GENOME THERAPEUTICS CORP.
PA Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX P-PSDB; ABO77618.
DR Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX Disclosure; SEQ ID NO 9793; 455pp; English.
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX Sequence 909 BP; 144 A; 267 C; 318 G; 180 T; 0 U; 0 Other;
SQ Query Match 52.2%; Score 21.4; DB 11; Length 909;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 3 GCCTCGGATGCCAGTCCCTCATCGCTGCGCCGCGCG 41
DB 275 GCCACCTGATGCCAGGACAGCTTGACCGGCTGGCGCG 313
RESULT 91
ABD14344/c
ID ABD14344 standard; DNA; 966 BP.
XX ABD14344;
AC ABD14344;
XX 29-JUL-2004 (first entry)
DT Pseudomonas aeruginosa polynucleotide #12948.
XX Pseudomonas aeruginosa.
DE Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
KW Pseudomonas aeruginosa.
OS US6551795-B1.
XX 22-APR-2003.
XX 18-FEB-1999; 99US-00252991.
PR 18-FEB-1998; 98US-0074788P.
XX

PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
XX P-PSDB; ABO60773.
XX
PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide, of
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 12948; 455pp; English.
XX
CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-*P. aeruginosa* drugs, as templates for recombinant
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
CC infection, and in detection of *P. aeruginosa* sequences or other sequences
CC of *Pseudomonas* species using biochip technology. Sequences ABD01397-
CC ABD17967 represent *P. aeruginosa* polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX Sequence 966 BP; 168 A; 333 C; 298 G; 167 T; 0 U; 0 Other;
SQ
Query Match 52.2%; Score 21.4; DB 11; Length 966;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 3 GCTCTCGGATGCCAGTCCCTCATCGCTGCGCCGCGCGCG 41
DB 604 GCAACCGCAGCGAGTCTCTCTCGTCTCGCCAGCCAGCG 566
RESULT 92
ADT47081/c
ID ADT47081 standard; cDNA; 1236 BP.
XX
AC ADT47081;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #21832.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 45519; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 1236 BP; 167 A; 426 C; 446 G; 197 T; 0 U; 0 Other;
SQ
Query Match 52.2%; Score 21.4; DB 13; Length 1236;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 3 GCTCTCGGATGCCAGTCCCTCATCGCTGCGCCGCGCGCG 41
DB 476 GCTCTCGGATGCCAGAGGCTCATCGCCGCTCCAGGTGCG 438
RESULT 93
ADA48031/c
ID ADA48031 standard; DNA; 1305 BP.
XX
AC ADA48031;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene conferring disease resistance in plants.
XX
XX disease resistance; pathogen tolerance; plant pathogen; da; gene; plant.
XX
XX *Oryza sativa*.
XX
XX WO2003000906-A2.
XX
XX 03-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-IB002453.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX 26-SEP-2001; 2001US-0352277P.
XX 22-MAR-2002; 2002US-0366535P.
XX

XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Katagiri F, Krepis J, Provart N, Ricke D, Zhu T;
XX WPI: 2003-184052/18.
DR P-PSDB; ADA48032.
XX
XX New polynucleotide comprising a plant nucleotide sequence having an open
PT reading frame that encodes a polypeptide associated with disease
PT resistance, useful for conferring resistance or tolerance to a plant
PT pathogen.
XX
XX Claim 1; SEQ ID NO 101; 299pp; English.
PS
XX
XX The invention relates to a novel isolated polynucleotide comprising a
CC plant nucleotide sequence having an open reading frame that encodes a
CC polypeptide associated with disease resistance or its fragment having
CC substantially the same activity as the full-length polypeptide. The
CC polynucleotide of the invention is useful for conferring resistance or
CC tolerance to a plant pathogen. The present sequence represents a gene
CC conferring disease resistance used in the invention.
XX
SQ Sequence 1305 BP; 225 A; 356 C; 553 G; 170 T; 0 U; 1 Other;
Query Match 52.2%; Score 21.4; DB 9; Length 1305;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCG 41
DB 276 GCCACGAGTGCACCGCGTCAACCGCTGCGCGTCCCG 238
RESULT 94
ADE07095/c
ID ADE07095 standard; DNA; 1329 BP.
XX
AC ADE07095;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel coding sequence (useful for identifying genetic disorders) #161.
XX novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder; gene; ds.
XX Unidentified.
OS
XX WO2003054152-A2.
PN
XX 03-JUL-2003.
PD
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX WPI: 2003-569235/53.
DR P-PSDB; ADE08006.

XX New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
XX Claim 1; SEQ ID NO 161; 1177pp; English.
PS
XX
XX The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present DNA sequence represents a gene of the
CC invention.
XX
SQ Sequence 1329 BP; 234 A; 379 C; 456 G; 260 T; 0 U; 0 Other;
Query Match 52.2%; Score 21.4; DB 10; Length 1329;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 2 AGCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCG 40
DB 380 AGCCTCCGGCTCCCTCCCTCCCTCCCTCCCTCCCTCC 342
RESULT 95
ADU40252/c
ID ADU40252 standard; cDNA; 1329 BP.
XX
AC ADU40252;
XX
DT 27-JAN-2005 (first entry)
XX
DE Novel human polynucleotide seq id 37.
XX
DE
KW cytostatic; antianemic; immunosuppressive; neuroprotective;
KW antirheumatic; antiarthritic; muscular; osteopathic; vulnerary;
KW antiulcer; antiinflammatory; CNS; nootropic; antiparkinsonian;
KW anticonvulsant; cerebroprotective; vasotropic; gene therapy;
KW gene mapping; forensic; mutation identification; biodiversity; cancer;
KW haematopoiesis; myeloid cell disorder; lymphoid cell disorder;
KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW myasthenia gravis; tissue growth; tissue regeneration; tissue repair;
KW tissue replacement; burn; incision; ulcer; osteoporosis; osteoarthritis;
KW bone degenerative disorder; periodontal disease; nervous system disease;
KW neuropathy; mechanical disorder; traumatic disorder; nerve injury;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; Shy-Drager syndrome; stroke; gene; ss;
KW human.
XX
XX Homo sapiens.
OS
XX US2004219521-A1.
PN
XX
XX 04-NOV-2004.
PD
XX
PF 22-APR-2002; 2002US-00128558.
XX
XX 21-JAN-2000; 2000US-00488725.
PR 25-JAN-2000; 2000US-00491404.
PR 25-APR-2000; 2000US-0052317.
PR 22-DEC-2000; 2000WO-US035017.
PR 25-JAN-2001; 2001WO-US002623.
PR 05-FEB-2001; 2001WO-US003800.
PR 26-FEB-2001; 2001WO-US004927.
PR 05-MAR-2001; 2001WO-US004941.
PR 30-MAR-2001; 2001WO-US008631.
PR 18-APR-2001; 2001WO-US008656.
PR 11-DEC-2001; 2001US-0339453P.
XX
XX (TANG/) TANG Y T.
PA


```
XX PF 15-AUG-2003; 2003WO-US026073.
XX XX
XX PR 15-AUG-2002; 2002US-0404311P.
XX XX
XX PA (FUNC-) FUNCTIONAL GENETICS INC.
XX XX
XX PI Li L, Aghdasi B;
XX XX
XX DR WPI; 2004-269214/25.
XX XX
XX XX
XX PT New purified mammalian rapamycin resistance and tumorigenesis (RapR7)
XX PT protein, useful for diagnosing and/or treating diseases or conditions
XX PT associated with rapamycin resistance, cancer and tumorigenesis.
XX XX
XX PS Disclosure; SEQ ID NO 19; 128pp; English.
XX XX
XX CC The present invention describes a purified mammalian rapamycin resistance
XX CC and tumorigenesis (RapR7) protein. RapR7 has cytostatic activity.
XX CC Methods and compositions of the present invention are useful for the
XX CC diagnosis and/or treatment of diseases or conditions associated with
XX CC rapamycin resistance, cancer and tumorigenesis, and for identifying
XX CC agents for treating these conditions. The present sequence represents a
XX CC human RapR7 regulatory region nucleotide sequence, which is used in the
XX CC exemplification of the present invention.
XX XX
XX SQ Sequence 1440 BP; 216 A; 460 C; 519 G; 245 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 12; Length 1440;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCGC 41
    ||||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1029 GCCCGCGCGCGCGCGCCCTCATCGCTGCGCGCCGCGCGC 991

RESULT 98
ABQ91417
ID ABQ91417 standard; DNA; 1470 BP.
AC ABQ91417;
XX XX
XX DT 01-OCT-2002 (first entry)
XX XX
XX DE M. capsulatus gene #1402 for DNA array.
XX XX
XX KW Micro array; gene; ds; differential expression; gene expression.
XX OS Methylococcus capsulatus.
XX XX
XX PN WO200255655-A2.
XX XX
XX PD 18-JUL-2002.
XX XX
XX PF 14-JAN-2002; 2002WO-NO000019.
XX XX
XX PR 12-JAN-2001; 2001NO-00000235.
XX PR 12-JAN-2001; 2001NO-00000239.
XX XX
XX PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.
XX PA (TIGR-) TIGR.
XX XX
XX PI Birkeland NK, Eidhammer I, Jonassen I, Jensen HB, Lien T;
XX PI Lillehaug JR, Lossius I, Eisen JA, Fraser CM, Durkin AS;
XX PI Salzberg SL;
XX XX
XX DR WPI; 2002-557818/59.
XX XX
XX PT Novel DNA array useful for determining differential expression of
XX PT Methylococcus capsulatus genes, comprises polynucleotides or
XX PT oligonucleotides representative for a selective number of Methylococcus
XX PT capsulatus genes.
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XX PS Claim 14; Page 556-557; 678pp; English.
XX CC
XX CC The invention relates to a novel DNA array giving a representation of a
XX CC number of Methylococcus capsulatus genes. The method of the invention is
XX CC useful for determination of the differential expression of the genes of
XX CC M. capsulatus, and for studying gene expression on a genomic scale and in
XX CC gene expression assays of M. capsulatus genes. The sequences shown in
XX CC ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
XX CC invention
XX XX
XX SQ Sequence 1470 BP; 252 A; 460 C; 477 G; 281 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 6; Length 1470;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCGC 40
    ||||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86 AGCGCGCGCGACTCGACCTCAACGCTGCGCGCGCGC 124

RESULT 99
ABL19573
ID ABL19573 standard; DNA; 1861 BP.
XX XX
XX AC ABL19573;
XX XX
XX DT 26-MAR-2002 (first entry)
XX XX
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 10192.
XX XX
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical; gene; ds.
XX OS Drosophila melanogaster.
XX XX
XX PN WO200171042-A2.
XX XX
XX PD 27-SEP-2001.
XX XX
XX PF 23-MAR-2001; 2001WO-US009231.
XX XX
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX XX
XX PA (PEKE ) PE CORP NY.
XX XX
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX XX
XX DR WPI; 2001-656860/75.
XX XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX PT interactions.
XX XX
XX PS Claim 1; SEQ ID NO 10192; 21pp + Sequence Listing; English.
XX XX
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX CC ABB72072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 1861 BP; 525 A; 495 C; 510 G; 331 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 4; Length 1861;
Best Local Similarity 69.2%; Pred. No. 1e+03;
```

Job time : 301 secs

Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGNCG 39
||| | ||||| ||||| :
Db 1589 AACCCAGGATGCCAGTTCCTCAAGGGTGGCCCAATTG 1627

RESULT 100
ACL36154
ID ACL36154 standard; cDNA; 2000 BP.
XX
AC ACL36154;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice stress-regulated promoter SEQ ID NO:14717.
XX
KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;
XX agriculture.
XX
OS Oryza sativa.
XX
PN WO2003008540-A2.
XX
PD 30-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX
XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
PS Claim 48; SEQ ID NO 14717; 89pp; English.
XX

XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX

SQ Sequence 2000 BP; 412 A; 709 C; 524 G; 354 T; 0 U; 1 Other;

Query Match 52.2%; Score 21.4; DB 11; Length 2000;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGNCGG 41
||| | ||||| ||||| :
Db 1098 GCCACAGCTGCCACCGCTCACCCGCTGCCGCTCCCG 1136

Search completed: May 9, 2006, 22:23:40

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: May 9, 2006, 22:17:45 ; Search time 1878 Seconds
(without alignments)
1021.443 Million cell updates/sec
Title: US-09-904-968a-1_N3336_COPY_3300_3340
Perfect score: 41
Sequence: 1 aagctcccgatgccagtc.....tcctgctggccgncgcg 41
Scoring table: IDENTITY NUCDX
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries
Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_ges1:*
10: gb_ges2:*
11: gb_ges3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		ID	Description
		Match	Length		
C 1	39.4	96.1	340	9	AQ939774 NR5-118R
C 2	28.4	69.3	702	9	BZ892025 Hmi2_0104
C 3	24.8	60.5	611	8	DN393531 LTB3934-0
C 4	24.4	59.5	690	10	CG190773 PUIILD25TD
C 5	24.2	59.0	890	2	BG772871 602721069
C 6	24	58.5	445	7	CO336372 ENL2413_5
C 7	24	58.5	555	5	BQ384615 NISC_mm07
C 8	24	58.5	745	10	CNS020XK
C 9	24	58.5	806	5	BU279692 603865894
C 10	23.8	58.0	1101	10	CNS000K2
C 11	23.6	57.6	356	9	BH841209 Drosophil
C 12	23.6	57.6	584	10	BH841209 TC3-55C20
C 13	23.6	57.6	646	8	CX775930 UI-EH-HG2
C 14	23.6	57.6	727	3	BI888178 ZF637-1-0
C 15	23.6	57.6	730	8	CX774191 UI-EH-HG1
C 16	23.6	57.6	884	10	AG848813 Oryza sat
C 17	23.6	57.6	917	3	BI662946 603286312
C 18	23.4	57.1	483	7	CO983269 GM89018A2
C 19	23.4	57.1	576	6	CF246184 TGEStzy15
C 20	23.4	57.1	1209	8	DN684120 CXK34-A07
C 21	23.4	57.1	1404	8	DN655453 CEC17-B09
C 22	23.2	56.6	374	5	BY278985 BY278985

96	22.4	54.6	415	3	BW721516	BW721516 UI-E-E01-	C 169	22	53.7	624	10	CW026783	CW026783 104_253
97	22.4	54.6	482	2	BG717495	BG717495 602689259	C 170	22	53.7	633	2	BE410885	BE410885 601303506
98	22.4	54.6	554	5	BQ785316	BQ785316 saq76a07	C 171	22	53.7	633	11	CNS0710Q	AL424320 T7 end of
99	22.4	54.6	638	10	CW579372	CW579372 OA_ABa010	C 172	22	53.7	635	2	BI064629	BI064629 pglfn.pk0
100	22.4	54.6	680	10	AG104213	AG104213 Pan_trosl	C 173	22	53.7	641	2	CG037953	CG037953 PUK8H96TD
101	22.4	54.6	692	10	CW592639	CW592639 OA_ABa012	C 174	22	53.7	642	9	BZ779785	BZ779785 i134611.g
102	22.4	54.6	727	9	AZ074798	AZ074798 RPCI-23-4	C 175	22	53.7	647	2	BE386619	BE386619 601274315
103	22.4	54.6	737	10	CZ722561	CZ722561 OC_Ba004	C 176	22	53.7	675	5	BU393876	BU393876 603512776
104	22.4	54.6	753	10	CZ726194	CZ726194 OC_Ba005	C 177	22	53.7	688	8	DN256838	Meso02807
105	22.4	54.6	759	3	BI967604	BI967604 GMB30002B	C 178	22	53.7	688	8	DR006928	TC106643
106	22.4	54.6	771	10	CL542062	CL542062 OB_Ba006	C 179	22	53.7	693	6	CA415230	UI-H-EUI-
107	22.4	54.6	791	1	AL765898	AL765898 wh66h06.x	C 180	22	53.7	704	3	BP450095	BP450095
108	22.4	54.6	798	3	BI825415	BI825415 603072344	C 181	22	53.7	709	10	CL819350	OR_CBa003
109	22.4	54.6	821	7	CO796485	CO796485 AGENCOURT	C 182	22	53.7	718	2	BE390186	601286191
110	22.4	54.6	901	8	DN784286	DN784286 92288392	C 183	22	53.7	720	8	CV804593	AGENCOURT
111	22.4	54.6	902	9	BZ553902	BZ553902 Pacsl-60	C 184	22	53.7	728	7	CK359451	AGENCOURT
112	22.4	54.6	989	9	CZ222573	CZ222573 CH261-48E	C 185	22	53.7	733	8	DR081743	RTFEP11_3
113	22.4	54.6	1034	2	BE866354	BE866354 601678814	C 186	22	53.7	737	2	BG760245	BG760245 602716644
114	22.4	54.6	1166	6	CD500566	CD500566 CDA45-G03	C 187	22	53.7	743	2	BG427686	602500144
115	22.2	54.1	387	10	CZ394778	CZ394778 ZMWB0174	C 188	22	53.7	758	3	BP441623	BP441623
116	22.2	54.1	654	6	CA680933	CA680933 wIm24.pk0	C 189	22	53.7	765	8	DN124579	DN124579 1125493
117	22.2	54.1	661	6	CD924532	CD924532 G750_113G	C 190	22	53.7	773	7	CK7711392	959664_MA
118	22.2	54.1	675	7	CO121308	CO121308 GR_EB02H	C 191	22	53.7	778	8	DR081806	RTFEP11_3
119	22.2	54.1	677	10	CG234435	CG234435 OGVCU866TH	C 192	22	53.7	783	7	CK597420	AGENCOURT
120	22.2	54.1	689	6	CD893289	CD893289 G118_123F	C 193	22	53.7	783	10	CZ528157	SRAA-aac5
121	22.2	54.1	695	6	CD927723	CD927723 GR45_102P	C 194	22	53.7	798	7	CK603037	AGENCOURT
122	22.2	54.1	712	6	CD454178	CD454178 WHE0987-0	C 195	22	53.7	800	9	AQ864214	nbebo022N
123	22.2	54.1	724	6	CD869974	CD869974 AZ02_113C	C 196	22	53.7	816	2	BE733889	601568350
124	22.2	54.1	769	7	CO442891	CO442891 MZCCL1005	C 197	22	53.7	831	2	BE727035	601563705
125	22.2	54.1	805	5	BX453231	BX453231 BX453231	C 198	22	53.7	831	2	BE379548	BE379548 601238164
126	22.2	54.1	869	5	BX444778	BX444778 BX444778	C 199	22	53.7	873	10	AG878594	Oryza sat
127	22.2	54.1	869	10	CL901826	CL901826 CSHC1201	C 200	22	53.7	874	2	BG474208	602516820
128	22.2	54.1	966	2	BF203427	BF203427 601865857	C 201	22	53.7	911	5	BX354894	BX354894
129	22.2	54.1	1378	3	BM905928	BM905928 AGENCOURT	C 202	22	53.7	922	2	BG764905	602737342
130	22	53.7	121	9	BZ591412	BZ591412 3590_1_84	C 203	22	53.7	924	5	BQ948154	BQ948154 AGENCOURT
131	22	53.7	200	8	D84460	D84460 D84460 Porc	C 204	22	53.7	936	10	CL502260	CL502260 SAIL_70_F
132	22	53.7	235	2	BF818549	BF818549 MR3-CI018	C 205	22	53.7	939	2	BG766730	602743175
133	22	53.7	259	2	BF713700	BF713700 ESTPBL276	C 206	22	53.7	940	2	BG766674	602739958
134	22	53.7	293	7	CO991983	CO991983 UMC-pdgen	C 207	22	53.7	948	2	BG331308	602432036
135	22	53.7	296	1	AI569263	AI569263 ttt42f05.x	C 208	22	53.7	970	5	BUS57844	AGENCOURT
136	22	53.7	298	3	BF949304	BF949304 BF949304	C 209	22	53.7	978	5	BX449417	BX449417
137	22	53.7	314	7	CN257514	CN257514 170004243	C 210	22	53.7	1030	5	BUS57719	AGENCOURT
138	22	53.7	319	11	DE116312	DE116312 Oryzias l	C 211	22	53.7	1089	5	BX841390	BX841390
139	22	53.7	344	1	AI833890	AI833890 605096G08	C 212	22	53.7	1153	2	BG330655	602430060
140	22	53.7	351	2	BI223040	BI223040 602943373	C 213	22	53.7	1194	2	BG330027	602429790
141	22	53.7	351	2	BE501829	BE501829 hw35G06.x	C 214	22	53.7	1204	5	BUI45784	AGENCOURT
142	22	53.7	351	2	BE501849	BE501849 hw36a06.x	C 215	22	53.7	1497	10	CL973192	CL973192 OsIFCC042
143	22	53.7	363	6	CB212298	CB212298 OML02578	C 216	22	53.7	2423	4	AF318366	Homo sapi
144	22	53.7	369	3	BM659181	BM659181 ITU0602653	C 217	21.8	53.2	152	6	CF615655	CES014044
145	22	53.7	400	9	BH758990	BH758990 013 5 T7	C 218	21.8	53.2	185	9	CG970216	CG970216 ZUAD525TH
146	22	53.7	401	3	BM847402	BM847402 K-EST0126	C 219	21.8	53.2	212	8	FL13632	FL13632 HSFIG075 St
147	22	53.7	404	10	CG464579	CG464579 KRIBB_2D	C 220	21.8	53.2	275	10	CZ333013	CZ333013 ZMMBFC0041
148	22	53.7	406	9	AQ017724	AQ017724 CIT-HSPF-2	C 221	21.8	53.2	301	9	CC181170	CC181170 JsaIBAC_0
149	22	53.7	428	6	CF226963	CF226963 IH089 sub	C 222	21.8	53.2	280	10	CL316143	CL316143 ZMMBFC050
150	22	53.7	431	9	BZ913711	BZ913711 CH240_54N	C 223	21.8	53.2	349	7	CF965417	CF965417 10998r8ic
151	22	53.7	468	6	CF648588	CF648588 3530_1_56	C 224	21.8	53.2	355	9	CG979211	CG979211 ZUAF377TH
152	22	53.7	491	6	CB205983	CB205983 OML00263	C 225	21.8	53.2	380	9	AQ852358	LMAJFVL_1
153	22	53.7	520	5	BU074427	BU074427 im75f03.x	C 226	21.8	53.2	404	9	CG930910	CG930910 ZMMBFC054
154	22	53.7	522	1	AI995067	AI995067 701501658	C 227	21.8	53.2	426	5	BY504611	BY504611
155	22	53.7	548	2	BI211309	BI211309 IPL_59 B0	C 228	21.8	53.2	465	6	CF308748	CF308748
156	22	53.7	551	3	BQ246302	BQ246302 TabI5013F	C 229	21.8	53.2	476	9	BH900639	BH900639 Octb0181
157	22	53.7	551	11	CR839827	CR839827 GR0AAA8BG	C 230	21.8	53.2	483	5	BW964069	BW964069
158	22	53.7	559	2	BG362665	BG362665 sac07b03	C 231	21.8	53.2	491	2	BI076018	BI076018
159	22	53.7	568	6	CD877766	CD877766 AZ04_101A	C 232	21.8	53.2	503	7	CK008657	CK008657 26259r8ic
160	22	53.7	575	1	AJ449183	AJ449183 AJ449183	C 233	21.8	53.2	505	7	BI211383	BI211383
161	22	53.7	575	3	BM440722	BM440722 pgr1n.pk0	C 234	21.8	53.2	520	7	CN432728	CN432728
162	22	53.7	582	1	AJ274024	AJ274024 AJ274024	C 235	21.8	53.2	526	6	CB441818	CB441818
163	22	53.7	585	1	AV523351	AV523351 AV523351	C 236	21.8	53.2	551	2	BE683491	BE683491 183294_MA
164	22	53.7	616	10	CAW307597	CAW307597 104_795_1	C 237	21.8	53.2	553	1	AA696508	AA696508 CM07807_5
165	22	53.7	616	1	AJ450894	AJ450894 AJ450894	C 238	21.8	53.2	579	6	CB617041	CB617041 3529_1_67
166	22	53.7	621	5	BX671154	BX671154 BX671154	C 239	21.8	53.2	579	8	DN215609	DN215609 MEST971_C
167	22	53.7	624	5	BX671378	BX671378 BX671378	C 240	21.8	53.2	593	7	CO889267	CO889267 BovGen_17
168	22	53.7	624	6	CD214780	CD214780 pgtm2n.pk0	C 241	21.8	53.2	600	5	BX0901538	BX0901538

[illegible]

```
388 21.6 52.7 707 8 DN745300 GI-CF-209
389 21.6 52.7 715 5 BX861274
390 21.6 52.7 718 8 BX861274
391 21.6 52.7 721 8 BQ750888
392 21.6 52.7 721 11 BQ750888
393 21.6 52.7 726 5 BX305013
394 21.6 52.7 732 6 CO249789
395 21.6 52.7 734 6 CA500056
396 21.6 52.7 735 6 CA800066
397 21.6 52.7 742 5 BX859070
398 21.6 52.7 743 7 CR367877
399 21.6 52.7 749 2 BE659880
400 21.6 52.7 750 7 CR367234
401 21.6 52.7 753 7 CR368280
402 21.6 52.7 754 5 BX880804
403 21.6 52.7 754 7 CR366178
404 21.6 52.7 755 8 CX702411
405 21.6 52.7 766 8 CX702042
406 21.6 52.7 771 5 BX879765
407 21.6 52.7 773 5 BX913656
408 21.6 52.7 787 6 CB169889
409 21.6 52.7 811 7 CR363328
410 21.6 52.7 831 11 CNS04937
411 21.6 52.7 837 8 CX702136
412 21.6 52.7 876 3 BI951111
413 21.6 52.7 909 5 BQ647220
414 21.6 52.7 965 5 BQ960212
415 21.6 52.7 973 2 BG704332
416 21.6 52.7 992 5 BX428794
417 21.6 52.7 1054 3 BM562329
418 21.6 52.7 1083 8 DR150985
419 21.6 52.7 1096 11 CNS06R3Q
420 21.6 52.7 1174 5 BQ98019
421 21.6 52.7 1683 3 BM550161
422 21.6 52.7 1718 3 BM477352
423 21.6 52.7 3095 4 BC051240
424 21.6 52.7 132 8 DN155128
425 21.4 52.2 161 6 CB394113
426 21.4 52.2 168 1 AA895494
427 21.4 52.2 192 7 CR537202
428 21.4 52.2 307 1 AW015190
429 21.4 52.2 316 7 CO778035
430 21.4 52.2 328 1 AA450647
431 21.4 52.2 330 1 AU093949
432 21.4 52.2 331 1 AI867834
433 21.4 52.2 340 5 BY045091
434 21.4 52.2 359 5 W34032
435 21.4 52.2 367 8 BF775989
436 21.4 52.2 378 2 BE428065
437 21.4 52.2 378 2 BE428414
438 21.4 52.2 385 6 CD531207
439 21.4 52.2 388 5 BU785612
440 21.4 52.2 391 7 CK074479
441 21.4 52.2 395 6 CA648703
442 21.4 52.2 399 8 CX620883
443 21.4 52.2 400 1 AL364430
444 21.4 52.2 405 9 CE205796
445 21.4 52.2 408 1 AI121642
446 21.4 52.2 434 1 AJ612119
447 21.4 52.2 434 5 BX511680
448 21.4 52.2 435 6 BX511680
449 21.4 52.2 436 6 CA640445
450 21.4 52.2 436 9 CE164404
451 21.4 52.2 437 1 AA797791
452 21.4 52.2 439 1 AA620244
453 21.4 52.2 446 1 AA529473
454 21.4 52.2 446 10 CW617838
455 21.4 52.2 450 5 BQ459319
456 21.4 52.2 455 5 BY490206
457 21.4 52.2 455 7 CK834994
458 21.4 52.2 457 3 BJ757841
459 21.4 52.2 461 10 C2696047
460 21.4 52.2 462 1 AI316608
```

```
461 21.4 52.2 473 1 AA059965
462 21.4 52.2 475 9 BZ351204
463 21.4 52.2 477 3 BI674742
464 21.4 52.2 480 7 CN449423
465 21.4 52.2 488 6 CD906816
466 21.4 52.2 489 3 BPI49818
467 21.4 52.2 493 10 CW034680
468 21.4 52.2 496 7 CN671566
469 21.4 52.2 498 3 BI830382
470 21.4 52.2 501 2 BE219383
471 21.4 52.2 501 7 CF984174
472 21.4 52.2 503 2 BF443144
473 21.4 52.2 505 10 CL195402
474 21.4 52.2 506 6 CB783367
475 21.4 52.2 511 10 CW575705
476 21.4 52.2 516 2 BE926700
477 21.4 52.2 516 3 BM125744
478 21.4 52.2 516 3 BM125744
479 21.4 52.2 525 6 CA065029
480 21.4 52.2 525 6 CA065105
481 21.4 52.2 529 5 BQ462644
482 21.4 52.2 530 7 CV043920
483 21.4 52.2 532 7 CO598811
484 21.4 52.2 535 3 BM630654
485 21.4 52.2 542 5 BQ553736
486 21.4 52.2 543 7 CK309078
487 21.4 52.2 544 1 AI292468
488 21.4 52.2 553 2 BF618790
489 21.4 52.2 554 1 AM653994
490 21.4 52.2 556 3 BM255475
491 21.4 52.2 561 7 CK332540
492 21.4 52.2 563 2 BE594382
493 21.4 52.2 564 2 BG047966
494 21.4 52.2 564 6 CA359548
495 21.4 52.2 564 7 CK310598
496 21.4 52.2 564 6 CA086375
497 21.4 52.2 574 2 BE592199
498 21.4 52.2 580 10 CZ313421
499 21.4 52.2 581 10 CZ301795
500 21.4 52.2 587 11 CR892938
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ALIGNMENTS

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RESULT 1
AQ939774/c
LOCUS NRS-1178 Human NotI clones Homo sapiens genomic, genomic survey
DEFINITION NRS-1178 Human NotI clones Homo sapiens genomic, genomic survey
ACCESSION AQ939774.1 GI:7216152
VERSION AQ939774.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homindae; Homo.
REFERENCE 1 (bases 1 to 340)
AUTHORS Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovsky,V.V.,
Xie,L., Muravenko,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N.,
Li,J., Protodopov,A., Kashuba,V., Ernberg,I., Winberg,G. and
Wanstedt,C.
TITLE NotI clones in the analysis of the human genome
JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)
PUBMED 10710430
COMMENT Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf.Podowski@cgkr.ki.se
```



```

FEATURES
  source
    Class: NotI site.
    Location/Qualifiers
      1..340
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        /clone_lib="Human NotI clones"
ORIGIN
  Query Match      96.1%; Score 39.4; DB 9; Length 340;
  Best Local Similarity 95.1%; Pred. No. 0.016;
  Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCCTCGGATGCCAGTCCCTCATCGTGGCCGCGCGC 41
    |||||
Db 236 AAGCCTCGGATGCCAGTCCCTCATCGTGGCTGGCTGGCG 196

RESULT 2
BZ892025
LOCUS
DEFINITION
  Hml2_0104.xl_011.ab1 Hm pUC18 Library Haloarcula marismortui ATCC
ACCESSION
  BZ892025
VERSION
  BZ892025.1 GI:33342658
KEYWORDS
  GSS.
SOURCE
  Haloarcula marismortui ATCC 43049
ORGANISM
  Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
  Halobacteriaceae; Haloarcula.
REFERENCE
  1 (bases 1 to 702)
AUTHORS
  Goo,Y., Roach,J., Glusman,G., Baliga,N.S., Deutsch,K., Pan,M.,
  DasSarma,S., Ng,W.V. and Hood,L.
TITLE
  Low-pass Sequencing for Microbial Comparative Genomics
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Goo Y
  Institute for Systems Biology
  1441 North 34th Street, Seattle, WA 98103, USA
  Tel: 206 732 1412
  Fax: 206 732 1299
  Email: ygoo@systemsbiology.org
  Seq primer: M13 forward
  Class: shotgun.
FEATURES
  source
    Location/Qualifiers
      1..702
        /organism="Haloarcula marismortui ATCC 43049"
        /mol_type="genomic DNA"
        /strain="ATCC 43049"
        /db_xref="taxon:272569"
        /clone_lib="Hm pUC18 Library"
        /note="Vector: pUC18; Site 1; SmaI; A shotgun library was
        constructed from Haloarcula marismortui genomic DNA using
        pUC18/SmaI/BAP plasmid"
ORIGIN
  Query Match      69.3%; Score 28.4; DB 9; Length 702;
  Best Local Similarity 81.6%; Pred. No. 61;
  Matches 31; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGTGGCCGCGCGC 40
    |||||
Db 311 GCCTCCGAAGCGGTCTCTCATCGTCAACGCGCGC 348

RESULT 3
DN393531/c
LOCUS
DEFINITION
  LIB3934-056-A1-K1-F1 LIB3934 Canis familiaris cDNA clone
ACCESSION
  DN393531
VERSION
  DN393531.1 GI:60574752
KEYWORDS
  EST.
SOURCE
  Canis familiaris (dog)
  Location/Qualifiers
    1..611
      /organism="Canis familiaris"
      /mol_type="mRNA"
      /strain="beagle"
      /db_xref="taxon:9615"
      /clone="CLN12937122"
      /tissue_type="brain"
      /lab_host="DH10B"
      /clone_lib="LIB3934"
      /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; brain
      from normal dog"
ORIGIN
  Query Match      60.5%; Score 24.8; DB 8; Length 611;
  Best Local Similarity 77.8%; Pred. No. 9e+02;
  Matches 28; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGTGGCCGCGC 38
    |||||
Db 160 GCCTCTGTGTCGCCGCCCAACGCTGCCCGGCC 125

RESULT 4
CG190773/c
LOCUS
DEFINITION
  PUILD25TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0608E02,
  genomic survey sequence.
ACCESSION
  CG190773
VERSION
  CG190773.1 GI:34081834
KEYWORDS
  GSS.
SOURCE
  Zea mays
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
  1 (bases 1 to 690)
  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
  Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
  Benner,J.
  Maize Genomics Consortium
  Unpublished (2003)
  Other GSSs: PUILD25TB
  Contact: Cathy Whitelaw
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
  Seq primer: TF
  Class: sheared ends.
FEATURES
  source
    Location/Qualifiers
      1..690
        /organism="Zea mays"
        /mol_type="genomic DNA"
        /strain="B73"
        /db_xref="taxon:4577"
        /clone="ZMMBTa0608E02"
        /clone_lib="ZM 0.6 1.0 KB"
        /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
        Cot selected genomic DNA library"
ORIGIN

```



```

/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:5049408"
/sex="female"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC Ov1"
/notes="Organ: ovary; Vector: pCMV-SPORT6; Site 1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.0 kb. Constructed by Life Technologies."

```

ORIGIN

```

Query Match      58.5%; Score 24; DB 5; Length 555;
Best Local Similarity 72.5%; Pred. No. 1.6e+03;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

```

```

QY 2 AGCTCCGGATGCGAGTCCCTCATCGTGGCCGCGCG 41
|||||

```

```

Db 43 AGCAGCGGTGCGACGACCCACCGACGCCGCGCG 4
|||||

```

RESULT 8

```

CNS020KX AL206826.1 GI:7865645 linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
153F20 of library G from Tetraodon nigroviridis, genomic survey
sequence.

```

```

ACCESSION AL206826
VERSION AL206826.1
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae.

```

REFERENCE

```

AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fzimes,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
PUBMED 10835645
AUTHORS

```

```

2 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Fzimes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
PUBMED 10899143

```

REFERENCE

```

3 (bases 1 to 745)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

```

```

COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

```

FEATURES

```

Location/Qualifiers
1..745
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="153F20"
/clone_lib="G"
/notes="Genoscope sequence ID : COAG153DC10SP1
end : PUC-Ori"

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ORIGIN

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Query Match      58.5%; Score 24; DB 10; Length 745;
Best Local Similarity 72.5%; Pred. No. 1.6e+03;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

```

```

QY 2 AGCTCCGGATGCGAGTCCCTCATCGTGGCCGCGCG 41
|||||

```

```

Db 591 AGCATCCAGTCCAGTCCGTCCTCCCAAGCTCAGCGCG 552
|||||

```

RESULT 9

```

BU279692/c 603865894F1 CSEQCHN54 Gallus gallus cdna clone CHEST884124 5', mRNA
sequence.

```

```

ACCESSION BU279692
VERSION BU279692.1
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

```

```

Eukaryota; Aves; Neognathae; Galliformes; Phasianidae;
Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.

```

REFERENCE

```

AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

```

FEATURES

```

Location/Qualifiers
1..806
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton line 151"
/db_xref="taxon:9031"
/clone="CHEST884124"
/sex="Female"
/tissue_type="not cerebrum or cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN54"
/notes="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

```

ORIGIN

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Query Match      58.5%; Score 24; DB 5; Length 806;
Best Local Similarity 72.5%; Pred. No. 1.7e+03;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

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QY 1 AAGCTTCGGATGCCAGTCCCTCATCGTGGCCGCGCG 40
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```

```

Db 782 AAGGCTGCTGCTGCTTAACCTCAACACTGGCCGCGCAGC 743
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```

```

RESULT 10
CNS000K2
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR02P13 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL058270
VERSION
AL058270.1 GI:4930724
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
AUTHORS
Direct Submission
TITLE
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
FEATURES
source
1..1101
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR02P13"
/clone_lib="RPCI-98"
/note="end : T7"
ORIGIN
Query Match 58.0%; Score 23.8; DB 10; Length 1101;
Best Local Similarity 77.1%; Pred. No. 2e+03;
Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 4 CTCCTCGGATTCAGTCCCTCATCGTCGCGCCGNC 38
|||||
Db 629 CTCCTCGGATTCAGTCCCTCATCGTCGCGCCGNC 663
|||||
RESULT 11
BH841209/c
LOCUS
DEFINITION
BH841209.TP TC3 Trypanosoma cruzi genomic clone TC3-55C20, genomic
survey sequence.
ACCESSION
BH841209
VERSION
BH841209.1 GI:21408424
KEYWORDS
GSS.
SOURCE
Trypanosoma cruzi
ORGANISM
Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 356)
REFERENCE
Mylers,P.J., Aggarwal,G., Fazelinia,G., Mack,J., Marty,A.,
Munden,H., Nelson,S., Pentony,M., Rinta,J., Robertson,L.,
Seyler,A., Siek,E., Stuart,K., Vogt,C., Worthey,E., El-Sayed,N.M.,
Ghedini,E. and Andersson,B.
Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing
TITLE
1..356
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR02P13"
/clone_lib="RPCI-98"
/note="end : T7"
ORIGIN
Query Match 58.0%; Score 23.8; DB 10; Length 1101;
Best Local Similarity 77.1%; Pred. No. 2e+03;
Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 4 CTCCTCGGATTCAGTCCCTCATCGTCGCGCCGNC 38
|||||
Db 629 CTCCTCGGATTCAGTCCCTCATCGTCGCGCCGNC 663
|||||
RESULT 12
CE771255/c
LOCUS
DEFINITION
CE771255
ACCESSION
CE771255
VERSION
CE771255.1 GI:37112019
KEYWORDS
GSS.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 584)
REFERENCE
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Deicher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE
JOURNAL
PUBMED
14512627
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..584
/organism="Canis familiaris"
JOURNAL
COMMENT
Other GSSs: TC3-55C20.TV
Contact: Peter Myler
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109, USA
Tel: 206 284 8846
Fax: 206 284 0313
Email: mylerpj@sbri.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1..356
/organism="Trypanosoma cruzi"
/mol_type="genomic DNA"
/strains="CL Brener"
/db_xref="taxon:5693"
/clone="TC3-55C20"
/clone_lib="TC3"
/note="Vector: pBelobAC11; Site 1: Hin dIII; Constructed
for Uppsala University by Marie-Christine Le Paslier in
the Laboratory of Denis Le Paslier at the Centre d'Etude
du Polymorphisme Humain (CEPH), Paris, France. Briefly,
Trypanosoma cruzi CL-Brener agarose embedded DNA (obtained
from Dr. Franco da Silveira) was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBelobAC11 digested with Hin dIII. The average insert
size is 100 kb. Total clone coverage: approx. 33 X the
haploid genome."
ORIGIN
Query Match 57.6%; Score 23.6; DB 9; Length 356;
Best Local Similarity 73.7%; Pred. No. 2.1e+03;
Matches 28; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 3 GCCTCCGATGCCAGTCCTCATCGTCGCGCCGNC 40
|||||
Db 88 GCCCTCGAAGCAGTCCTCAAAACGCTGCGCCGCGC 51
|||||
RESULT 13
CE771255
LOCUS
DEFINITION
CE771255
ACCESSION
CE771255
VERSION
CE771255.1 GI:37112019
KEYWORDS
GSS.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 584)
REFERENCE
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Deicher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE
JOURNAL
PUBMED
14512627
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..584
/organism="Canis familiaris"

```

```

/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BetXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 57.6%; Score 23.6; DB 10; Length 584;
Best Local Similarity 73.7%; Pred. No. 2.2e+03;
Matches 28; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCGAGTCCTCATCGCTGCGCCCGCGCCG 40
|||||
Db 394 GCCTCTGGATACAAATCCATCATCATCTGCCGAGGGCTC 357

RESULT 13
CX775930
LOCUS
DEFINITION
CX775930 646 bp mRNA linear EST 25-JAN-2005
UI-EH-HG2-aas-p-12-0-UI.81 UI-EH-HG2 Emiliana huxleyi cDNA clone
CX775930
ACCESSION
CX775930.1 GI:58186283
VERSION
EST.
KEYWORDS
Emiliana huxleyi
ORGANISM
Emiliana huxleyi
Eukaryota; Haptophyceae; Isochrysidales; Emiliana.
REFERENCE
1 (bases 1 to 646)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalisation and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
PUBMED
889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Provasoli-Guillard National Center for Culture
of Marine Phytoplankton (CCMP)
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/dinoflagellate.html
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
1..646
/organism="Emiliana huxleyi"
/mol_type="mRNA"
/strain="CCMP 371"
/db_xref="taxon:2903"
/clone="UI-EH-HG2-aas-p-12-0-UI"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-EH-HG2"
/notes="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoR I; Site 2: Not I; UI-EH-HG2 is a
normalized library derived from UI-EH-HG1. The library was
constructed and normalized according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GAAGGCTAGT. Tissue was obtained from the
Provasoli-Guillard National Center for Culture of Marine

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Phytoplankton (CCMP).
TAG_TISSUE=Emiliana huxleyi coccolithophorid
TAG_LIB=UI-EH-HG2
TAG_SEQ=GAAGGCTAGT"

ORIGIN
Query Match 57.6%; Score 23.6; DB 8; Length 646;
Best Local Similarity 73.7%; Pred. No. 2.2e+03;
Matches 28; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCGAGTCCTCATCGCTGCGCCCGCGCCG 40
|||||
Db 129 GCCAATGAAGCCGCGCCTCGTGGCTGCTCGCGCGC 166

RESULT 14
BI888178/c
LOCUS
DEFINITION
ZF637-1-002433 Zebrafish shield stage whole embryo cDNA library
MPMGp637 Zebrafish shield stage whole embryo cDNA library
MPMGp637_10022;MPMGp63702210 5',
mRNA sequence.
BI888178
ACCESSION
BI888178.1 GI:16095449
VERSION
EST.
KEYWORDS
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 727)
Clark,M., Aanstad,P., Hennig,S., Johnson,S.L. and Lehrach,H.
EST sequencing of a zebrafish shield stage cDNA library normalised
by oligonucleotide fingerprinting
Unpublished (2001)
JOURNAL
COMMENT
Contact: Hennig S
Laboraty 123, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Inhnstr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
fingerprinting
High quality sequence stop: 727.
Location/Qualifiers
1..727
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="MPMGp637_10022;MPMGp63702210"
/tissue_type="whole embryo"
/dev_stages="shield stage, 6 hrs post-fertilisation"
/lab_host="E.coli, XL1 blue MRF"
/clone_lib="Zebrafish shield stage whole embryo cDNA
library MPMGP637"
/notes="Vector: pSport1; Site 1: NotI; Site 2: SalI;
oligo-dT-NotI primed, SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"

ORIGIN
Query Match 57.6%; Score 23.6; DB 3; Length 727;
Best Local Similarity 73.7%; Pred. No. 2.2e+03;
Matches 28; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 2 AGCCTCCGATGCCAGTCCTCATCGCTGCGCCCGCGCG 39
|||||
Db 650 AACCCCGGCTGACCGCCCTCATCGCTGCGCAGGGCG 613

RESULT 15
CX774191
LOCUS
CX774191 730 bp mRNA linear EST 25-JAN-2005

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ORIGIN
Query Match          57.6%   Score 23.6; DB 8; Length 730;
Best Local Similarity 73.7%   Pred. No. 2.2e+03;
Matches 28; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy  3  GCCTCCGGATGCCAGTCCTCATCGCTGGCCCGGCGC 40
      |||  |||  |||  |||  |||  |||  |||  |||
Db   104 GCCAATGGAGAGCCGCCCTCGTGGTGGTCCGGCCGC 141

RESULT 16
AG848813
LOCUS      AG848813          884 bp      DNA      linear      GSS 03-NOV-2004
DEFINITION  Oryza sativa (indica cultivar-group) genomic DNA, BAC end sequence,
            BAC clone:K0108G11 R, genomic survey sequence.

```

```

ORIGIN
Query Match 57.6%; Score 23.6; DB 10; Length 884;
Best Local Similarity 73.7%; Pred. No. 2.2e+03;
Matches 28; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 3 GCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCC 40
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 GCGCGCGCGCGCATCCCTCATCCGCGCGCGCGCC 681

RESULT 17
BI662946
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Mammalian Gene Collection (MGC)

```

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc..
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAMI1812 row: h column: 03
 High quality sequence stop: 369.
 Location/Qualifiers
 1. .917
 /organism="Mus musculus"
 /mol type="mRNA"

/strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5320370"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH108"
 /clone_lib="NCI_CGAP Mam6"
 /notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 57.6%; Score 23.6; DB 3; Length 917;
 Best Local Similarity 73.7%; Pred. No. 2.2e+03;
 Matches 28; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCTCTCGGATGCGAGTCCTCATCGCTGGCCGCGCCG 40
 ||||| ||| ||||| ||||| ||||| ||||| :|||
 Db 510 GCTCTCTTTCGACGACCTCAGCGCTGGCCGCGCCG 547

RESULT 18
CO983269/c

LOCUS GM89018A2B01.r1 Gm-r1089 Glycine max cDNA clone Gm-r1089-6578 3,
 mRNA sequence.

ACCESSION CO983269.1 GI:51341952

VERSION EST.

KEYWORDS Glycine max (soybean)

SOURCE Glycine max

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE

AUTHORS 1 (bases 1 to 483)
 Vodkin,L., Shoemaker,R., Keim,P., Polacco,J.C., Retzel,E.,
 Khanna,A., Shealy,R., Clough,S., Thibaud-Nissen,F., Coryell,V.,
 Expelding,J., Gonzalez,D.O., Stromvik,M., Rodriguez-Huete,A.M.,
 Schweitzer,P., Gong,G. and Liu,L.
 A Functional Genomics Program for Soybean (NSF 9872565) (2004)
 Unpublished (2004)
 Other ESTs: BM893189 corresponding to Gm-c1069-3072 (5')
 Contact: Vodkin, L.O., PI, A Functional Genomics Program for
 Soybean (NSF 9872565)
 Lewin, H. A., Director, Keck Center for Comparative and Functional
 Genomics
 University of Illinois
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
 Tel: (217) 244-6147
 Fax: (217) 333-4582
 Email: l-vodkin@uiuc.edu

Seq primer: 5'-TTTTTTTTTTTTTTTTT(A/C/G)-3'
 High quality sequence stop: 483.
 Location/Qualifiers
 1..483
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="Gm-r1089-6578"
 /clone_lib="Gm-r1089"
 /note="The library Gm-r1089 is a sequence-driven, reracked
 set of 9,216 low redundancy clones selected from 38
 different cDNA libraries constructed from various tissues
 and stages of development of soybean including 973 cDNAs
 from germinating cotyledons(source library Gm-c1069,
 Gm-c1076, and Gm-c1077); 1,465 cDNAs from various tissue
 and organ systems of the adult plant; 476 cDNAs from adult
 stem tissue (source library Gm-c1062); 1340 cDNAs from
 tissue culture derived somatic embryos (source libraries

FEATURES

Source

ORIGIN

Query Match 57.1%; Score 23.4; DB 7; Length 483;
 Best Local Similarity 70.7%; Pred. No. 2.5e+03;
 Matches 29; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCTCGGATGCCAGTCCCTCATCGCTGGCCGCGCGCG 41
 ||||| ||||| ||||| ||||| ||||| ||||| :|||

Db 266 AGGCCACCGGATTCCTCTCTCTCCGCGCGCTGCGCG 226

RESULT 19

CF246184/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Gm-c1036 and Gm-c1075); 2918 cDNAs from hypocotyls or
 young seedlings; 742 cDNAs from germinating seedlings,
 shoot tips, or leaves exposed to various stresses(source
 libraries Gm-c1065, Gm-c1066, and Gm-c1068); 839 cDNAs
 from young leaves or hypocotyls exposed to bacterial and
 fungal pathogens (source libraries Gm-c1072, Gm-c1073,
 Gm-c1074; and Gm-c1084); and 463 from roots of young
 plants grown in hydroponic media without phosphate (source
 library Gm-c1087). The 5' ESTs of the source clones from
 the different libraries were used to select singletons, or
 a representative of each contig, which were reracked to
 form library Gm-r1089 and the cDNA clones of the reracked
 Gm-r1089 library were then sequenced at the 3' end. The
 unigene selection and 3' sequencing was funded by NSF
 Plant Genome project #9872565
 (http://soybeanomics.cropsci.uiuc.edu/) as part of
 creation of a low redundancy soybean cDNA set. The source
 cDNA libraries were constructed by the laboratories of
 Lila Vodkin, University of Illinois, Randy Shoemaker, Iowa
 State University, and Paul Keim, Northern Arizona
 University as part of the Public EST project.
 http://129.186.26.94/soybeanest.html. The contig analysis
 to select unique genes was performed by the laboratory of
 Ernest Retzel, Center for Computational Genomics and
 Bioinformatics, University of Minnesota,
 http://web.ahc.umn.edu/biodata/nsfscj/. Reracking and 3'
 sequencing were conducted by services of the University of
 Illinois Keck Center for Comparative and Functional
 Genomics http://www.biotech.uiuc.edu/keck.htm. Note: The
 corresponding 5' EST from each clone in the Gm-r1089
 library is listed in the 'OTHER EST' field. The detailed
 information on the source library for each clone can also
 be obtained by referring to the clone ID of the original
 cDNA library that is also listed under 'OTHER EST'."

CF246184 576 bp mRNA linear EST 07-AUG-2003
 TgESTyi59e09.y1 TgMAS Tachyzoite cDNA library Toxoplasma gondii
 cDNA clone TgBSTyi59e09.y1 5', mRNA sequence.

CF246184

EST.

TOXOPLASMA GONDII

TOXOPLASMA GONDII

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Sarcocystidae; Toxoplasma.

1 (bases 1 to 576)

Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,

Clifton,S., Pape,D., Martin,J., Wyllie,T., Dante,M., Marra,M.,

Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,

Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,

Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.

Toxoplasma EST Project

Unpublished (2001)

Contact: Clifton, S.

Toxoplasma EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: toxo@watson.wustl.edu

Contact David Sibley (toxoset@borcim.wustl.edu) for further

/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CEC"

/notes=vector: Express 1: Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGAGCGCCGCTT)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa.q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems:
<http://www.openbiosystems.com/stickleback>

ORIGIN

Query Match 57.1%; Score 23.4; DB 8; Length 1404;
Best Local Similarity 70.7%; Pred. No. 2.7e+03;
Matches 29; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCGGATCGCATCTCATCTGCGCGCGCGCG 41

DB 742 AAGTCCCGCGCTCAAGTCTCCGTCGTCGCGCGCGCGCG 702

RESULT 22

BY278985/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY278985 374 bp mRNA linear EST 11-DEC-2002
BY278985 RIKEN full-length enriched, visual cortex Mus musculus
cDNA clone K430335006 5', mRNA sequence.

BY278985

BY278985.1 GI:26469322

EST

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Mus;

(bases 1 to 374)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,

Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schornbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,

Batalov,S., Beisel,K.W., Blake,J.A., Brad,D., Brusic,V.,

Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,

Garcinich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,

Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,

Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,

Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,

Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,

Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,

Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,

Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,

Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,

Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,

Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,

Arakawa,I., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,

Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,

Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,

TITLE

JOURNAL

PUBMED

COMMENT

Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-resesc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hiroosawa,Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

1..374

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="K430335006"

/tissue_type="visual cortex"

/clone_lib="RIKEN full-length enriched, visual cortex"

ORIGIN

Query Match

Best Local Similarity

Matches 27; Conservative

1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GCCTCGGATCGCATCTCATCTGCGCGCGCGNC 38

DB 55 GTCTCATATCGGTCGTCGTCGTCGTCGTCGCGCC 20

RESULT 23

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 608)

EST

Ambystoma mexicanum (axolotl)

Ambystoma mexicanum

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;

Ambystoma

1 (bases 1 to 608)

CN039111 608 bp mRNA linear EST 29-MAR-2004
nm_30_m13_t3_Mach Ambystoma mexicanum cDNA, mRNA sequence.

CN039111

CN039111.1 GI:45809482

EST

Ambystoma mexicanum (axolotl)

Ambystoma mexicanum

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;

Ambystoma

1 (bases 1 to 608)

AUTHORS Putta,S., Smith,J.J., Walker,J.A., Rondet,M., Weisrock,D., Monaghan,J., Samuels,A.K., Kump,K., King,D.C., Maness,N.J., Habermann,B., Tanaka,E., Bryant,S.V., Gardiner,D.M., Parichy,D.M. and Voss,S.R.

TITLE From biomedicine to natural history research: EST resources for ambystomatid salamanders

JOURNAL BMC Genomics 5 (1), 54 (2004)

PUBMED 15310388

COMMENT Contact: SR Voss

Department of Biology
University of Kentucky
TH Morgan Building, Lexington, KY 40506, USA
Tel: 859 257 9888
Fax: 859 257 1717

Email: svoss@uky.edu

The EST is quality trimmed at the ends with a 20 base window and quality threshold of 15 (phred quality score). Please visit <http://salamander.uky.edu> For any information (trace, quality files etc) regarding this EST.

FEATURES Location/Qualifiers

1..608
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Limb Blastema and Proximal Limb Tissue"
collected from larvae on days 1-6 of regeneration"
/clone_lib="Match"

ORIGIN

Query Match 56.6%; Score 23.2; DB 7; Length 608;
Best Local Similarity 75.0%; Pred. No. 3e+03;
Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 CTCGCGATGCCAGTCCCTCATCGCTGCGCCCGGCG 39

Db 215 CCTCGGCTTCAGTACTTCACCACTTGCCCGTCG 180

RESULT 24

CO701815/c

LOCUS DG32-214a13 DG32-liver Canis familiaris cDNA 3', mRNA linear EST 26-JUL-2004

DEFINITION Dog arrayTAG cDNA clone collection

ACCESSION CO701815

VERSION CO701815.1 GI:50650483

KEYWORDS EST.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 709)

AUTHORS Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,

Henrich,J. and Loebbert,R.

TITLE Dog arrayTAG cDNA clone collection

JOURNAL Unpublished (2004)

COMMENT Contact: Thomas Schlueter

LiOn Bioscience AG

Walldorferstrasse 98, D-69123 Heidelberg, Germany

Tel: +49 6221 4038 150

Fax: +49 6221 4038 290

Email: Thomas.Schlueter@lionbioscience.com.

FEATURES Location/Qualifiers

1..709
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="liver"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG32-liver"
/note="Organ: liver; Vector: Dog pBluescript LION"

ORIGIN

Query Match 56.6%; Score 23.2; DB 7; Length 799;

Best Local Similarity 75.0%; Pred. No. 3e+03;

Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNC 38

Db 171 GCCTCCGTCTGCTGTCTCTCCCTCCCGCGCGCGCTC 206

Query Match 56.6%; Score 23.2; DB 7; Length 709;
Best Local Similarity 75.0%; Pred. No. 3e+03; 8; Indels 0; Gaps 0;
Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGCTTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGN 37

Db 684 AGCTTCCGGCCCCCAAGTTCCTCCAGCTCTGCGCCGCT 649

RESULT 25

CO931079

LOCUS AGENCOURT_30433863 NIH_ZGC_14 Danio rerio cDNA clone IMAGE:7405062
5', mRNA sequence.

ACCESSION CO931079

VERSION CO931079.1 GI:51285756

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 799)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: ggapbs-remail.nih.gov

Tissue Procurement: John Ngai, Nancy Freeman, NIDCD

cDNA Library Preparation: Dr. Sumio Sugano

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM15602 row: j column: 04

High quality sequence start: 9

High quality sequence stop: 148.

FEATURES Location/Qualifiers

1..799

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:7405062"

/tissue_type="olfactory epithelium"

/lab_host="DH10B Tona"

/clone_lib="NIH_ZGC_14"

/note="Organ: olfactory epithelium; Vector: pME18S-FL3;

Site 1: DraIII; Site 2: DraIII; 1st strand cDNA was primed

with an oligo(dT) primer

[GCGGTGAAGACGGCTATGCGCTTTTTTTTTTTTTTTT];

double-stranded cDNA was ligated to a DraIII adaptor

[GGCCUACUGG], digested and directionally cloned into

distinct DraIII sites of the pME18S-FL3. Library was size

selected for 1.0 kb, with a average insert size of ~1.2kb.

Library constructed by Yutaka Suzuki (University of Tokyo

Institute of Medical Science). Custom primers recommended

for sequencing: 5' end primer 5'-GGATGTTGCTTTACTTCTA-3'

and 3' end primer 5'-CGACTGCGCTCGACACA-3'. Note: This

is a Zebrafish Gene Collection (ZGC) library"

ORIGIN

RESULT 26
 BX408897
 LOCUS
 DEFINITION BX408897 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA
 clone CSODH007YC09 5-PRIME, mRNA sequence.
 ACCESSION BX408897
 VERSION BX408897.2 GI:46951017
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 13, 2003 this sequence version replaced gi:30656780.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 994.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?S=CS08AA013ZC12_CS01244_1&c=994.f.
 Location/Qualifiers
 1. .903
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODH007YC09"
 /tissue_type="T CELLS (JURKAT CELL LINE)"
 /cell_line="JURKAT CELL LINE"
 /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

FEATURES

source

RESULT 27
 CC377365
 LOCUS
 DEFINITION FUHMX92TB ZM 0.6-1.0 KB Zea mays genomic clone ZMMBta487P16,
 genomic survey sequence.
 ACCESSION CC377365
 VERSION CC377365.1 GI:30850982
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE
 AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and

ORIGIN

Query Match 56.6%; Score 23.2; DB 5; Length 903;
 Best Local Similarity 75.0%; Pred. No. 3e+03;
 Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATCCGATCCCTCATCGCTGCGCCGCGCGC 40
 |||||
 Db 35 CTCGGATCCGATCCCTCATCGCTGCGCCGCGCGC 70
 |||||

RESULT 27
 CC377365
 LOCUS
 DEFINITION FUHMX92TB ZM 0.6-1.0 KB Zea mays genomic clone ZMMBta487P16,
 genomic survey sequence.
 ACCESSION CC377365
 VERSION CC377365.1 GI:30850982
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE
 AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and

TITLE
 JOURNAL
 COMMENT

Bennetzen, J.
 Maize Genomics Consortium
 Unpublished (2003)
 Other_GSSs: FUHMX92TD
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TR
 Class: sheared ends.
 Location/Qualifiers
 1. .177
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBta487P16"
 /clone_lib="ZM 0.6-1.0 KB"
 /note="Vector: pCR4-TOPO; Site:1: EcoRI; 0.6-1.0 kb high
 CoT selected genomic DNA library"

FEATURES

source

Query Match 56.1%; Score 23; DB 9; Length 177;
 Best Local Similarity 71.8%; Pred. No. 3.3e+03;
 Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCGGATCCGATCCCTCATCGCTGCGCCGCGCGC 41
 |||||
 Db 124 GCCTCGGATCCGATCCCTCATCGCTGCGCCGCGCGC 162
 |||||

ORIGIN

RESULT 28
 CC604446
 LOCUS
 DEFINITION OGCD86TM ZM 0.7-1.5 KB Zea mays genomic clone ZMMBma0146P04,
 genomic survey sequence.
 ACCESSION CC604446
 VERSION CC604446.1 GI:31965867
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE
 AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other_GSSs: OGCD86TC
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TR
 Class: methylation filtered.
 Location/Qualifiers
 1. .234
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBma0146P04"
 /clone_lib="ZM 0.7-1.5 KB"
 /note="Vector: pBCSK-; Site:1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"

FEATURES

source

Query Match 56.6%; Score 23.2; DB 5; Length 903;
 Best Local Similarity 75.0%; Pred. No. 3e+03;
 Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATCCGATCCCTCATCGCTGCGCCGCGCGC 40
 |||||
 Db 35 CTCGGATCCGATCCCTCATCGCTGCGCCGCGCGC 70
 |||||

ORIGIN

Query Match 56.1%; Score 23; DB 9; Length 234;
 Best Local Similarity 71.8%; Pred. No. 3.3e+03;
 Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCAGTCCCTCATCTGCGCCGCGCGCG 41
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 91 GCCTTCGGCCACCAAGTCTCTCTGCGCGCGAGCGCG 129

RESULT 29
 CC604439/c
 LOCUS CGCDB86TC_ZM_0.7_1.5_KB_Zea_mays genomic clone ZMMBma0146P04, 257 bp DNA linear GSS 18-JUN-2003
 DEFINITION genomic survey sequence.

ACCESSION CC604439
 VERSION CC604439.1 GI:31965860
 KEYWORDS GSS.
 SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 257)

AUTHORS

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: OGCD896TM

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

FEATURES

source

1..257

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMMBma0146P04"

/clone_lib="ZM_0.7_1.5_KB"

/note="Vector: pBCKS-; Site 1: HincII; 0.7-1.5 kb"

/methylation filtered genomic DNA library"

ORIGIN

Query Match 56.1%; Score 23; DB 9; Length 257;
 Best Local Similarity 71.8%; Pred. No. 3.3e+03;
 Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCAGTCCCTCATCTGCGCCGCGCGCG 41
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 130 GCCTTCGGCCACCAAGTCTCTCTGCGCGCGAGCGCG 92

RESULT 30
 CW120817
 LOCUS CW120817 526 bp DNA linear GSS 29-OCT-2004
 DEFINITION 104_498_11109551_148_34555_090 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11109551, genomic survey sequence.

ACCESSION CW120817

VERSION CW120817.1 GI:54813364

KEYWORDS GSS.

SOURCE Sorghum bicolor (sorghum)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 526)

AUTHORS

Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
 Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
 McMenamy, J., Smith, M., Roe, B.A., Wiley, G., Korff, I.F.,
 Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddalo, J.A. and
 Martienssen, R.A.

Sorghum genome sequencing by methylation filtration

PLoS Biol. 3 (1), e13 (2005)

15660154

Contact: Bedell JA

Orion Genomics, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6979

Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: 498 row: h column: 23

Seq primer: SWfor Forward

Class: methylation filtered

High quality sequence stop: 526.

FEATURES

source

1..526

/organism="Sorghum bicolor"

/mol_type="genomic DNA"

/cultivar="ATx623"

/db_xref="taxon:4558"

/clone="11109551"

/clone_lib="Sorghum methylation filtered library (LibID:

104)"

/note="Organ: leaf; Vector: pBCKS(-); Site 1: HincII; DNA

prepared from purified nuclei was randomly sheared,

end-repaired, size fractionated to enrich for the 0.5 to 5

kb fraction, ligated into HincII-digested pBCKS(-) vector

and electroporated into E. coli cells. This is a

methylation filtered library."

ORIGIN

Query Match 56.1%; Score 23; DB 10; Length 526;
 Best Local Similarity 71.8%; Pred. No. 3.4e+03;
 Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCAGTCCCTCATCTGCGCCGCGCGCG 41
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 92 GCCTCCGGCAGGAGACCCGCATCTGTCTCGGCGCG 130

RESULT 31

CG264881

LOCUS

DEFINITION

OG5CJ96TC_ZM_0.7_1.5_KB_Zea_mays genomic clone ZMMBma0830024, genomic survey sequence.

ACCESSION

CG264881

VERSION

CG264881.1 GI:34177022

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 577)

REFERENCE

AUTHORS

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

1..577

```

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0830024"
/clone_lib="ZM 0.7 1.5 KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match          56.1%; Score 23; DB 10; Length 577;
Best Local Similarity 71.8%; Pred. No. 3.4e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 28 GCCTCCGGCCACGATCTCTCGTCCGCGCGGCGCGCG 66

RESULT 32
CD974061/c
LOCUS
DEFINITION
QAE41c05.yg QAE Zea mays cDNA clone QAE41c05, mRNA sequence.
ACCESSION
CD974061
VERSION
CD974061.1 GI:32834383
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 638)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.inbio.gen.fr).
Location/Qualifiers
1..638
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QAE41c05"
/tissue_type="pericarp"
/clone_lib="QAE"

ORIGIN
Query Match          56.1%; Score 23; DB 6; Length 638;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 39
||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 41 AGGGCTCCAAATGCCAGTCCCTCGCGCGCGCGCGCGCTCG 3

RESULT 33
CC658573
LOCUS
DEFINITION
OGUGT39TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBma0436H06,
genomic survey sequence.
ACCESSION
CC658573.1 GI:32062011
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 704)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2002)
Contact: Genoplante
Genoplante
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
Location/Qualifiers
1..704
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0436H06"

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 643)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGUGT39TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
Location/Qualifiers
1..643
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0436H06"
/clone_lib="ZM 0.7 1.5 KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match          56.1%; Score 23; DB 9; Length 643;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 349 GCCTCCGGCAGGAGACCGCATCTGTGTCTCGCGCGCG 387

RESULT 34
BZ539634/c
LOCUS
DEFINITION
OGAEW36TC ZM2 0.7 1.5 KB Zea mays genomic clone ZMMBma0045F23,
genomic survey sequence.
ACCESSION
BZ539634
VERSION
BZ539634.1 GI:27088070
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 704)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
Location/Qualifiers
1..704
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0045F23"

```

/clone lib="ZM2 0.7 1.5 KB"
/note="Vector: pBSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 56.1%; Score 23; DB 9; Length 704;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 GCCTCGGCGCACAGTTCCTCGTCCGCGCGACGACGCG 497

RESULT 35

DR817309
LOCUS ZM_BFB0050U17.r ZM_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005
DEFINITION DR817309
ACCESSION DR817309.1 GI:71436259
VERSION EST.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 707)
Kim.H., Collura,K., Wisotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wang,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0050 row: J column: 17.
Location/Qualifiers
1. .707
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B TI phage reesistant"
/clone_lib="ZM_BFB"

FEATURES

source

/note="Vector: PCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones, for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 day aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 day whole seed; 11. 12 day endosperm and
embryo; 12. 17 day endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high

density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 56.1%; Score 23; DB 8; Length 707;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 273 GCCTCGGCGCACAGTTCCTCGTCCGCGCGACGACGCG 311

RESULT 36

BU358886/c
LOCUS 603477535F1 CSEQCHN71 Gallus gallus cDNA clone ChEST363f10 5', mRNA linear EST 28-NOV-2002
DEFINITION BU358886
ACCESSION BU358886
VERSION BU358886.1 GI:25866887
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 727)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392

COMMENT

Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

Location/Qualifiers
1. .727
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST363f10"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSEQCHN71"
/note="Organ: hearts; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 56.1%; Score 23; DB 5; Length 727;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGCG 40
||||| ||||| ||||| ||||| ||||| ||||| |||||

[illegible]

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.

FEATURES

source
1. .794
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0325K14"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBGSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 56.1%; Score 23; DB 9; Length 794;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 3 GCCTCGGATGCAGTCCCTCATCGTGGCCGCGCGCG 41
|||||
Db 255 GCCTCGGCCACAGTTCCTCGTCCGCGGACGACGCG 217
|||||

RESULT 40

CC684604
LOCUS CC684604
DEFINITION OGUGA96TH ZM 0.7 1.5_KB Zea mays genomic clone ZMMBMA0432023,
genomic survey sequence.
ACCESSION CC684604
VERSION CC684604.1 GI:32089380
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 808)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGUGA96TV
Contact: Cathy Whitelaw

TITLE
JOURNAL
COMMENT

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.

FEATURES

source
1. .808
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0432023"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBGSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 56.1%; Score 23; DB 9; Length 808;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 3 GCCTCGGATGCAGTCCCTCATCGTGGCCGCGCGCG 41
|||||

Db 284 GCCTTCGGCCACAGTTCCTCGTCCGCGGACGACGCG 322
|||||

RESULT 41

CG267676/c
LOCUS CG267676
DEFINITION OG2CD60TV ZM 0.7 1.5_KB Zea mays genomic clone ZMMBMA0760J24,
genomic survey sequence.
ACCESSION CG267676
VERSION CG267676.1 GI:34179817
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 816)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG2CD60TH
Contact: Cathy Whitelaw

TITLE
JOURNAL
COMMENT

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.

FEATURES

source
1. .816
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0760J24"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBGSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 56.1%; Score 23; DB 10; Length 816;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 3 GCCTCGGATGCAGTCCCTCATCGTGGCCGCGCGCG 41
|||||
Db 95 GCCTTCGGCCACAGTTCCTCGTCCGCGGACGACGCG 57
|||||

RESULT 42

BZ733090
LOCUS BZ733090
DEFINITION OGFAO64TM ZM 0.7 1.5_KB Zea mays genomic clone ZMMBMA0240L07,
genomic survey sequence.
ACCESSION BZ733090
VERSION BZ733090.1 GI:28708619
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 822)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGFAO64TC

ORIGIN

Query Match 56.1%; Score 23; DB 9; Length 808;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 3 GCCTCGGATGCAGTCCCTCATCGTGGCCGCGCGCG 41
|||||

Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers

FEATURES

1. .822
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0240L07"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 56.1%; Score 23; DB 9; Length 822;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCTCGGATGCCAGTCCTCTATCGTGGCCCGGCGC 40
Db 747 ATCTCGGCGAGCGGTGCGCGAGCGGTGCGGCGCGC 785

RESULT 43

CG382101/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CG382101
CG382101
CG382101.1 GI:34299368
GSS.

Zea mays
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 871)

REFERENCE

AUTHORS
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG1CG74TH
Contact: Cathy Whitelaw

TITLE

JOURNAL
COMMENT

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers

FEATURES

1. .871
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0729N03"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 56.1%; Score 23; DB 10; Length 871;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY

3 GCCTCGGATGCCAGTCCTCTATCGTGGCCCGGCGC 41
Db 747 GCCTCGGCCACCACTCTCTCTGTCGCGGCGGACGCG 709

RESULT 44

CG252385
LOCUS

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CG252385
CG252385.1 GI:34154475
GSS.

Zea mays
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 894)

REFERENCE

AUTHORS
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG1DO01TH
Contact: Cathy Whitelaw

TITLE

JOURNAL
COMMENT

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers

FEATURES

1. .894
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0738A01"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 56.1%; Score 23; DB 10; Length 894;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCTCTATCGTGGCCCGGCGC 41
Db 96 GCCTCGGCCACCACTCTCTCTGTCGCGGCGGACGCG 134

RESULT 45

BI331393/c
LOCUS

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI331393
BI331393.1 GI:15016050
EST.

Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 897)

REFERENCE

AUTHORS
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

BI331393
602983383F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5136021 5',
mRNA sequence.

Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11334 row: f column: 22
High quality sequence stop: 724.
Location/Qualifiers
1. 857
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5136021"
/lab_host="DH10B (TI phage-resistant)"
/clone_l1b="NCI CGAP Li9"
/notes="Organ: liver;
Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

FEATURES source

ORIGIN

```

Query Match      56.1%; Score 23; DB 3; Length 897;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    |||||
Db 716 GCCCTCCGGATGCCGGTCCACCAACCTGGGCGCATCGCG 678
    |||||

```

RESULT	46
CG347976	
LOCUS	CG347976
DEFINITION	OGYCH43TV ZM_0.7.1.5.KB Zea mays genomic clone ZMMBma078TH14, genomic survey sequence.
ACCESSION	CG347976
VERSION	CG347976.1
KEYWORDS	GI:34265242
SOURCE	GSS.
ORGANISM	Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 915) Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Robbins,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nurnberg,A., Buddman,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002) Other GSSs: OGYCH43TH Contact: Cathy Whitelaw
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

FEATURES
SOURCE

```

source
/organism="Zea mays"
/ntype="genomic DNA"
/strain="873"
/db_xref="taxon:4577"
/clone="ZMMBm0787H14"
/clone.lib="ZM 0 7 1.5_KB"
/note=vector: pCSK+; Site I: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library

```

ORIGIN

Query Match	56.1%; Score 23; DB 10; Length 915;
Best Local Similarity	71.8%; Pred. No. 3.5e+03;
Matches	28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
Qy	3 GCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 41
Db	101 GCCTCCGGCGAGGAGACCCGCATCTGTCTCGCGCGC 139
RESULT 47	
CC693275	
LOCUS	CG693275 959 bp DNA linear GSS 19-JUN-2003
DEFINITION	OGUBP87TV ZM 0.7-1.5 KB Zea mays genomic clone ZMMBMA0402006, genomic survey sequence.
ACCESSION	CC693275
VERSION	CC693275.1 GI:32098051
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE	Consortium for Maize Genomics
JOURNAL	Unpublished (2002)
COMMENT	Other GSSs: OGUBP87TH Contact: Cathy Whitelaw TIGR
FEATURES	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TP Class: methylation filtered. Location/Qualifiers 1..959 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZMMBMA0402006" /clone_lib="ZM 0.7-1.5 KB" /note="Vector: pBCSk-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"
ORIGIN	
Query Match	56.1%; Score 23; DB 9; Length 959;
Best Local Similarity	71.8%; Pred. No. 3.5e+03;
Matches	28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
Qy	3 GCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 41
Db	325 GCCTTCGCCACCAAGTTCTCTCGTGGCGGCGACGCGC 363
RESULT 48	
BG024956	
LOCUS	BG024956 995 bp mRNA linear EST 24-JAN-2001
DEFINITION	602275931F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4363975 5', mRNA sequence.
ACCESSION	BG024956
VERSION	BG024956.1 GI:12411064
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	NIH-MGC http://mqc.nci.nih.gov/ .


```

DEFINITION AGENCOURT_8468872 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6308419
5' mRNA sequence.
ACCESSION BQ712863
VERSION BQ712863.1 GI:21851762
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1415)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13727 row: h column: 20
High quality sequence start: 60
High quality sequence stop: 286.
FEATURES
source
location/Qualifiers
1..1415
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6308419"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_129"
/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
Site 1: EcorV; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 2.2 kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 56.1%; Score 23; DB 5; Length 1415;
Best Local Similarity 71.8%; Pred. No. 3.6e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCTCTATCGCTGCCGCGGCG 41
||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 677 GCCCGCGTCCGCTTCTGTGCTGCTGCGCGGCGCG 715

RESULT 52
AQ581777/c 112 bp DNA linear GSS 07-JUN-1999
LOCUS RPCI-11-433H17.TJ RPCI-11 Homo sapiens genomic clone
DEFINITION RPCI-11-433H17, genomic survey sequence.
ACCESSION AQ581777
VERSION AQ581777.1 GI:5008887
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 112)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Venter, J.C.
AUTHORS Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
MAP Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: RPCI-11-433H17.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research

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9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
FEATURES
source
location/Qualifiers
1..112
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7666072"
/db_xref="taxon:9606"
/clone="RPCI-11-433H17"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
RPCI11 Human Male BAC Library"

ORIGIN
Query Match 55.6%; Score 22.8; DB 9; Length 112;
Best Local Similarity 79.4%; Pred. No. 3.7e+03;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGCTTCGGATGCCAGTCCCTCATCGCTGGGCC 34
||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 34 AGGCCTCTGGATGCTGCTGCTGCCAAGTCTCTGGCCC 1

RESULT 53
BH229820 283 bp DNA linear GSS 08-NOV-2001
LOCUS BH229820 survey sequence.
DEFINITION 1006154F07.x1 1006 - RescueMu Grid G Zea mays genomic, genomic
ACCESSION BH229820
VERSION BH229820.1 GI:16832264
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 283)
Walbot,V.
AUTHORS Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Place: 1006154 row: 17
Class: transposon-tagged.
FEATURES
source
location/Qualifiers
1..283
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1006 - RescueMu Grid G"

```


Qy 5 CTCGGATGCCAGTCCCTCATCGCTGCCCGGCGCG 41
 Db 328 CACCGGATCTTGTCTTCATCGCTGCCCGGCGCTCG 292

RESULT 58
 CF836753/c
 LOCUS
 DEFINITION
 Citrus sinensis CDNA clone CS_P8A03106, mRNA sequence.
 CF836753
 CF836753.1 GI:38052405
 EST.
 Citrus sinensis
 Citrus sinensis

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

CONTACT: Timothy Close
 Department of Botany & Plant Sciences, University of California
 Riverside, CA, 92521-0124
 Tel: 9097873318
 Fax: 9097874437
 Email: timothy.close@ucr.edu
 Seq primer: T7.

FEATURES
 source
 1..359
 Location/Qualifiers
 /organism="Citrus sinensis"
 /mol_type="mRNA"
 /cultivar="Parent Washington Navel"
 /db_xref="taxon:2711"
 /clone="CS_P8A03106"
 /tissue_type="Shoot meristem"
 /dev_stage="10 year old trees"
 /lab_host="E. coli TUC121"
 /clone_lib="Washington Navel Orange Shoot Meristem cDNA
 Library"

/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI; Site 2: XhoI; Parent Washington Navel
 Orange trees on Troyer rootstock (UCR 16K) were the source
 of tissue. Trees, at UC Riverside Agricultural Operations,
 were planted October 12, 1992. In each of 17 reps one tree
 on Troyer rootstock was initially treated with Enzone, one
 with Alliette and Nemacure, and one was left untreated.
 These treatments were discontinued in 1998. At the time of
 sampling, there were differences in the apparent health
 and size of the trees on Troyer rootstock. Fall-flush
 shoots were sampled in early November 2002 to minimize the
 number of floral shoot meristems. Federici and Mu (Roose
 lab) harvested meristems only from trees that appeared to
 be healthy and had a large number of young shoot tips on
 the day of collection. The average weight of a meristem
 was about 2 mg. Federici noted that there were quite a few
 insects and signs of insect damage to the shoot tips.
 Mealy bugs, thrips and aphids were observed, plus a few
 very tiny fast moving insects that may have been mites or
 crawler stage of scale (although Federici did not see any
 mature scale). It was not difficult to avoid collecting
 most of these because they were easy to see with the
 dissecting microscope. It was harder to exclude the frass.
 Some frass was definitely retained in the samples. Tissues
 were snap frozen and then stored at -80C until further
 processing. Fenton (Close lab) purified RNA by the phenol
 method described in J. Japanese Soc. Hort. Sci. 1996. 64
 (4): 809-814, purified poly(A) mRNA using a PolyAtrack
 mRNA Isolation System IV (Promega), produced a primary

cDNA library using a lambda ZAP XR cDNA Synthesis Kit
 (Stratagene), then mass-excised one million pfu from the
 primary library to produce a phagemid population.
 Phagemids were plated, plasmid DNA purified, cDNA clones
 archived, and DNA sequences determined bi-directionally
 using an ABI3730 at the Arizona Genomics Institute,
 University of Arizona (Kim, Kudrna, Wing, Yu).
 Chromatogram files were downloaded by FTP to UC Riverside
 (by Close), then processed at UC Riverside (by Wanamaker,
 Close lab) using the HarvEST pipeline
 (http://harvest.ucr.edu) to remove vector and cloning
 oligo sequences and various contaminants, and to trim to a
 high quality region. Sequences that retained a phred 17
 region of at least 100 bases were deposited to GenBank."

ORIGIN

Query Match 55.1%; Score 22.6; DB 7; Length 359;
 Best Local Similarity 73.0%; Pred. No. 4.5e+03;
 Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 5 CTCGGATGCCAGTCCCTCATCGCTGCCCGGCGCG 41
 Db 339 CCGCGATCTTGTCTTCATCGCTGCCCGGCGCTCG 303

RESULT 59
 BW865890/c
 LOCUS
 DEFINITION
 Amphioxus Branchiostoma floridae cDNA library,
 neurula whole animal Branchiostoma floridae cDNA clone bbne078n04
 5', mRNA sequence.
 BW865890
 BW865890.1 GI:66480567
 EST.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

CONTACT: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 1..361
 /organism="Branchiostoma floridae"
 /mol_type="mRNA"
 /db_xref="taxon:7739"
 /clone="bbne078n04"
 /tissue_type="whole animal"
 /dev_stage="neurula"
 /clone_lib="Amphioxus Branchiostoma floridae unpublished
 cDNA library, neurula whole animal"

FEATURES

source
 1..361
 /organism="Branchiostoma floridae"
 /mol_type="mRNA"
 /db_xref="taxon:7739"
 /clone="bbne078n04"
 /tissue_type="whole animal"
 /dev_stage="neurula"
 /clone_lib="Amphioxus Branchiostoma floridae unpublished
 cDNA library, neurula whole animal"

ORIGIN

Query Match 55.1%; Score 22.6; DB 5; Length 361;
 Best Local Similarity 73.0%; Pred. No. 4.5e+03;
 Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 4 CTCGGATGCCAGTCCCTCATCGCTGCCCGGCGCG 40
 Db 215 CCACCGGTGCCAGTCCCTCATCGCTGCCCGGCGCTCG 179

RESULT 60
 CF836754
 LOCUS

CF836754 361 bp mRNA linear EST 30-OCT-2003

```

DEFINITION      UCRC03_03106_r Washington Navel Orange Shoot Meristem cDNA Library
ACCESSION      Citrus sinensis cDNA clone CS_Pea03106, mRNA sequence.
VERSION        CF836754
KEYWORDS       EST.
SOURCE         Citrus sinensis
ORGANISM       Citrus sinensis
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; eurosids I; Sapindales; Rutaceae; Citrus.
TITLE          1 (bases 1 to 361)
JOURNAL        Close,I.O., Roose,M.L., Federici,C.P., Mu,L., Fenton,R.D.,
COMMENT        Wanamaker,S., Kim,H.R., Kudrna,D., Wing,R. and Yu,Y.
                Development of EST Resources and New Genetic Markers for California
                Citrus - Washington Navel Orange Shoot Meristem
                Unpublished (2003)
                Contact: Timothy Close
                Department of Botany & Plant Sciences, University of California
                Riverside, CA, 92521-0124
                Tel: 9097873318
                Fax: 9097874437
                Email: timothy.close@ucr.edu
                Seq primer: T3.
                Location/Qualifiers
                  1. 361
                   /organism="Citrus sinensis"
                   /mol_type="mRNA"
                   /cultivar="Parent Washington Navel"
                   /db_xref="taxon:2711"
                   /clone="CS_Pea03106"
                   /tissue_type="Shoot meristem"
                   /dev_stage="10 year old trees"
                   /lab_host="E. coli TJC121"
                   /clone_lib="Washington Navel Orange Shoot Meristem cDNA
                   Library"
                   /note="vector: Lambda Uni-ZAP XR, excised phagemid;
                   Site 1: EcoRI; Site 2: XhoI; Parent Washington Navel
                   Orange trees on Troyer rootstock (UCR 16K) were the source
                   of tissue. Trees, at UC Riverside Agricultural Operations,
                   were planted October 12, 1992. In each of 17 reps one tree
                   on Troyer rootstock was initially treated with Enzone, one
                   with Alliette and Nemacure, and one was left untreated.
                   These treatments were discontinued in 1998. At the time of
                   sampling, there were differences in the apparent health
                   and size of the trees on Troyer rootstock. Fall-flush
                   shoots were sampled in early November 2002 to minimize the
                   number of floral shoot meristems. Federici and Mu (Roose
                   lab) harvested meristems only from trees that appeared to
                   be healthy and had a large number of young shoot tips on
                   the day of collection. The average weight of a meristem
                   was about 2 mg. Federici noted that there were quite a few
                   insects and signs of insect damage to the shoot tips.
                   Mealy bugs, thrips and aphids were observed, plus a few
                   very tiny fast moving insects that may have been mites or
                   crawler stage of scale (although Federici did not see any
                   mature scale). It was not difficult to avoid collecting
                   most of these because they were easy to see with the
                   dissecting microscope. It was harder to exclude the frass.
                   Some frass was definitely retained in the samples. Tissues
                   were snap frozen and then stored at -80C until further
                   processing. Fenton (Close lab) purified RNA by the phenol
                   method described in J. Japanese Soc. Hort. Sci. 1996. 64
                   (4): 809-814, purified poly(A) mRNA using a PolyATtract
                   mRNA Isolation System IV (Promega), produced a primary
                   cDNA library using a lambda ZAP XR cDNA Synthesis Kit
                   (Stratagene), then mass-excised one million pfu from the
                   primary library to produce a phagemid population.
                   Phagemids were plated, plasmid DNA purified, cDNA clones
                   archived, and DNA sequences determined bi-directionally
                   using an ABI3730 at the Arizona Genomics Institute,
                   University of Arizona (Kim, Kudrna, Wing, Yu).
                   Chromatogram files were downloaded by FTP to UC Riverside
                   (by Close), then processed at UC Riverside (by Wanamaker,

```

Close lab) using the HarvEST pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to
high quality region. Sequences that retained a phred 17
region of at least 100 bases were deposited to GenBank."

```

ORIGIN
Query Match      55.1%; Score 22.6; DB 7; Length 361;
Best Local Similarity 73.0%; Pred.No. 4.5e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy   5 CTCGGATGCCAGTCCCTCATCGCTGCGCCCGNGCGG 41
    | ||||| | ||||| ||||| ||||| : |||||
Db  21 CACCGGATTCTTGTCCTTCATCGGTGC GGCGCCTCG 57

RESULT 61
DN957603
LOCUS          368 bp mRNA linear EST 09-MAY-2005
DEFINITION     USDA-FP/ARO_13433 Star Ruby grapefruit hot water-treated flavado
                Citrus x paradisi cDNA clone Hw-01_D05 5', mRNA sequence.
ACCESSION      DN957603
VERSION        DN957603.1 GI:63104337
KEYWORDS       EST.
SOURCE         Citrus x paradisi
ORGANISM       Citrus x paradisi
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Sapindales; Rutaceae; Citrus.
REFERENCE      1 (bases 1 to 368)
AUTHORS        McCollum,T.G., Maul,P. and Porat,R.
TITLE          Expressed Sequence Tags (ESTs) from Flavado of Star Ruby grapefruit
                after hot water treatment
JOURNAL        Unpublished (2005)
COMMENT        Contact: McCollum, T.G.
                US Horticultural Research Laboratory
                USDA, ARS
                2001 S. Rock Road, Ft. Pierce, FL 34945, USA
                Tel: 561-462-5836
                Fax: 561-462-5986
                Email: gmccollum@ushrl.ars.usda.gov
Seq primer: T3 Primer.
                Location/Qualifiers
                ..368
                /organism="Citrus x paradisi"
                /mol_type="mRNA"
                /db_xref="taxon:37656"
                /clone="Hw-01_D05"
                /tissue_type="flavado"
                /dev_stage="mature fruit"
                /lab_host="SOLR"
                /clone_lib="Star Ruby grapefruit hot water-treated
                flavado"
                /notes="Organ: fruit; Vector: pBluescript II SK+; Site_1:
                EcoRI; Site 2: XhoI; Standard library construction
                protocols from Stratagene cDNA synthesis kit (Cat No.
                200401-5) and Uni-ZAP XR vector kit (Cat No. 237211)"

ORIGIN
Query Match      55.1%; Score 22.6; DB 8; Length 368;
Best Local Similarity 73.0%; Pred.No. 4.5e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy   5 CTCGGATGCCAGTCCCTCATCGCTGCGCCCGNGCGG 41
    | ||||| | ||||| ||||| ||||| : |||||
Db  242 CACCGGATTCTTGTCCTTCATCGGTGC GGCGCCTCG 278

RESULT 62
COL179529
LOCUS          369 bp mRNA linear EST 18-JUN-2004
DEFINITION     COL179529 Sprieme Exelixis Flytag CK01 pcDNA-SK+ Drosophila
                melanogaster cDNA clone EK059641 5, mRNA sequence.
```



```

ACCESSION      COL179529
VERSION        COL179529.1  GI:48952410
KEYWORDS
SOURCE
ORGANISM       Drosophila melanogaster (fruit fly)
               Drosophila melanogaster
               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
               Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 369)
AUTHORS        Kopcynski, C., Platt, D., Campbell, J., Muzong, C., Laufer, A.,
               Peterson, E. and Swimmer, C.
TITLE          Exelixis FlyTag EST Project CK01 Library
JOURNAL        Unpublished (2004)
COMMENT        Contact: Stapleton, M.
               BDGP
               Lawrence Berkeley National Lab
               One Cyclotron Rd, Berkeley, CA 94720, USA
               Fax: 510 486 6798
               Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
               Plate: EK.596 row: D column: 5
               High quality sequence stop: 368.
               Location/Qualifiers
               1. .369
               /organism="Drosophila melanogaster"
               /mol_type="mRNA"
               /db_xref="taxon:7227"
               /clone_lib="Exelixis FlyTag CK01 pCDNA-SKs"
               /note="Organ: mixed stage embryos, imaginal disks, and
               adult heads; Vector: pCDNA-SK+; Site 1: NotI; Site 2:
               XhoI; Random primed, normalized library from mixed stage
               embryos, imaginal disks, and adult heads."

ORIGIN
Query Match      55.1%; Score 22.6; DB 7; Length 369;
Best Local Similarity 73.0%; Pred. No. 4.5e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      3  GCCTCGGATGCCAGTCCCTCATCGTGGCCGCGCG 39
         ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      105 GTCTCGGATGCCACACCCACAGCGCTGGATGGCG 141

RESULT 63
LOCUS      AQ191651/c
DEFINITION HS_3225_B1_G10_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3225 Col=19 Row=N, genomic survey
            sequence.
ACCESSION  AQ191651
VERSION     AQ191651.1  GI:3590273
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 379)
AUTHORS     Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
            Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
            Hood, L.
TITLE       Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED     10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector

```

```

Plate: 3225 row: N column: 19
Class: BAC ends
High quality sequence stop: 379.
Location/Qualifiers
1. .379
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Plate=3225 Col=19 Row=N"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN
Query Match      55.1%; Score 22.6; DB 9; Length 379;
Best Local Similarity 73.0%; Pred. No. 4.6e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      1  AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCGCGN 37
         ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      113 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCG 77

RESULT 64
LOCUS      AI711336/c
DEFINITION  UI-R-AA1-zv-h-08-0-UI.s1 UI-R-AA1 Rattus norvegicus cDNA clone
            UI-R-AA1-zv-h-08-0-UI 3', mRNA sequence.
ACCESSION  AI711336
VERSION     AI711336.1  GI:5001112
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE   1 (bases 1 to 414)
AUTHORS     Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
PUBMED     8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            normalized arium at 16.5 dpc library cDNA Library Preparation:
            M.B. Soares Lab Clone distribution: clones will be available
            through Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
Location/Qualifiers
1. 414
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AA1-zv-h-08-0-UI"
/dev stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-AA1"
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-AA1
library is a normalized library constructed from 16.5 dpc

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TAG_LIB=UI-R-A
TAG_SFO=GATTC"

ORIGIN

Query Match 55.1%; Score 22.6; DB 1; Length 414;
Best Local Similarity 73.0%; Pred. No. 4.6e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 2 AGCCTCCGGATGCCAGTCCCTCATCTGCTGGCCCGGNC 38
Db 309 AGCCTACAGATGCCCTCCCCCAGCTCTGGCTGGGCC 273

RESULT 65	CA728594	LOCUS	CA728594	604 bp	mrna	linear	EST 26-NOV-2002
DEFINITION	wdilc.pk005.o7 wdilc Triticum aestivum cdna clone wdilc.pk005.o7 5' end, mRNA sequence.						

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CA728594	CA728594.1	GI:25450584	EST	
			Triticum aestivum (bread wheat)	
			Triticum aestivum	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.	

REFERENCE
AUTHORS
1 (bases 1 to 604)
Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.

TITLE	JOURNAL
DuPont Wheat CDNA Sequence	Unpublished (2002)

COMMENT

Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Scr primer: M13

FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10

```

/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref=taxon:4565"
/clone="wdilc.pk005.07"
/tissue_type="inflorescence"
/lab_host="DH10B"
/clone_lib="wdilc"
/note=vector: pbluescript SK
xhoI; Wheat ('Triticum aestivum
inflorescence +/- 4 cm")

```

ORIGIN

Query Match 55.1%; Score 22.6; DB 6; Length 604;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
|||||
Dh 207 CCTCCGGATCCCGGCCCAAGTCCGCCCGCGGTGCG 243
|||||

RESULT 66	CC763987	624 bp	DNA	linear	GSS 27-JUN-2003
CC763987/c					
LOCUS					
DEFINITION	CH240 41B8.TV	CHORI-240	Bos taurus	genomic clone	CH240 41B8.

genomic survey sequence.

ACCESSION	CC763987
VERSION	CC763987.1
KEYWORDS	GI:32310485 GSS.

SOURCE
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE

Bachman, S., Green, S., Campos, E. J., Benson, L. D., Edwards, J., Liu, L., Womack, J. E., de Jong, P. J., and Lewin, H. A.

TITLE Bovine BAC end sequences from CHORI-240 library

**JOURNAL
COMMENT**

Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@email.cho.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderinginformation.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by University of Illinois at Urbana-Champaign, USA with funds provided by grant No. AG202-34480-11828 from USDA-CRREBS and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative).

Plate: 41 row:

FEATURES source

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/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_41B8"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC.3
Hereford bull Li Domino 9
library (Male) produced b

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ORIGIN

Query Match	55.1%	Score 22.6;	DB 9;	Length 624;
Best Local Similarity	73.0%;	Pred. No. 4.7e+03;		
Matches 27: Conservative	1: Mismatches 9;	Indels 0;	Gaps 0;	

Qy

2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGC 38
||| || | | | | | | | | | | | | | | | | :
Db

478 AGCGGCCACATTCCAGAACCCTCATCCCTGGCCTGGGC 442

RESULT 67
BI765915/9

LOCUS	BI755915	625 bp	linear	EST 25-SEP-2001
DEFINITION	603046189f1 NTH_MGC_l16 Homo sapiens cdna clone IMAGE:5186231 5', mRNA sequence.			

ACCESSION BI765915

VERSION BI765915.1 GI:15757493

KEYWORDS EST.

SOURCE	Homo sapiens (human)
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99	99
100	100

ORGANISM Homo sapiens

Eukaryota; Metazoa;

Mammalia; Eutheria;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 625)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM11465 row: b column: 24
 High quality sequence stop: 625.

FEATURES

source

1. 625
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5186231"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 116"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SF0R16; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.1%; Score 22.6; DB 3; Length 625;
 Best Local Similarity 73.0%; Pred. No. 4.7e+03;
 Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 QY 5 CTCGGATCCGATCCCTCATCGTCGCCGCGCGG 41
 Db 109 CGCCGATTCCTGCTCTGCTGGTGGCGCCGCCGCG 73

RESULT 68

DN621129/c

LOCUS

DEFINITION

UCRCS11_06E15_f Parent Washington Navel Orange Scale-Infested Rind

cDNA Library UCRCS11 Citrus sinensis cDNA clone CS_WED0006E15, mRNA

sequence.

DN621129

DN621129.1 GI:61690229

EST.

Citrus sinensis

Citrus sinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

Rosids; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 658)

Close, T.J., Roose, M.L., Federici, C.F., Mandal, J., Fenton, R.D.,

Luck, R., Forster, L., Morse, J., Flores, P., Wanmaker, S., Kim, H.R.,

Kudrna, D., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,

Muller, C. and Wing, R.

Development of EST Resources and New Genetic Markers for California

Citrus - Parent Washington Navel Orange Scale-Infested Rind cDNA

Library UCRCS11

Unpublished (2005)

Contact: Timothy J. Close

Department of Botany & Plant Sciences

University of California

Riverside, CA 92521-0124, USA

Tel: 909-787-3318

TITLE

JOURNAL

COMMENT

Fax: 909-787-4437

Email: timothy.close@ucr.edu

Seq primer: T7.

FEATURES

source

Location/Qualifiers

1. 658
 /organism="Citrus sinensis"
 /mol_type="mRNA"
 /cultivar="Parent Washington Navel"
 /db_xref="taxon:2711"
 /clone="CS_WED0006E15"
 /tissue_type="Flavado, albedo, some red scale"
 /dev_stage="12 year old trees"
 /lab_host="E. coli TG121"
 /clone_lib="Parent Washington Navel Orange Scale-Infested Rind cDNA Library UCRCS11"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site_1: EcoRI; Site_2: XhoI; In cooperation with Dr.
 Robert Luck and Dr. Joseph Morse, Department of
 Entomology, University of California Riverside, navel
 orange fruit was infested with red scale (Aonidiella
 aurantii [Maskell]). Dr. Luck's technician, Lisa Forster,
 maintained colonies of red scale. Dr. Morse's technician,
 Paul Flores, cleaned and infested the fruit, bagged the
 fruit after the crawlers had time to settle, then
 harvested the fruit at the early second instar and late
 third instar phases of the insect. Claire Federici (Dr.
 Mikeal Roose's lab) cleaned off most of the insects (some
 remained firmly attached), cut the peel, then froze and
 scored at -80°C. The trees used for this set of samples
 were growing in field 16K of the University of California
 Citrus Experiment Station. This was the same field from
 which the tissue was collected for the navel shoot
 meristems and the peel for citrus thrips, Scirtothrips
 citri (Moulton). The trees were planted 12 October 1992.
 The scion was Parent navel. The trees used for infesting
 with red scale all had Troyer rootstock. Three different
 trees were used for each of the two infestations, a total
 of 6 trees. This experiment did not take place according
 to the original schedule because the red scale colony
 became infested with mites, so too few insects were
 available to infest the fruit on the date originally
 planned. The plan had been to infest on or about June 30
 and August 13. Instead the infestation dates were August
 30 and September 27, 2004. Because this took us into the
 cool weather of fall, the insects applied on the second
 infestation date took about three times as long to develop
 to the same stage as the insects applied on the first
 infestation date. The insects were reared on lemons.
 Before infesting the fruit on the trees, Paul Flores
 cleaned the peel and checked to make sure it was not
 already infested. He placed about 200 crawler stage
 insects on the fruit using a soft paintbrush. After the
 crawlers had a day to move around and find a spot to
 attach, Paul placed a very fine mesh drawing bag over
 the fruit to exclude predators and parasitoids of the
 scale. Bags were left in place for the duration of the
 field development period and also covered control fruit.
 Paul Flores infested fruit on 30 August and 1 September
 2004 after cleaning the fruit on August 27. On 21
 September the first set of red scale infested fruit were
 sampled. He brought Claire Federici 15 infested fruit and
 12 uninfested control fruit. The insects were at the early
 second instar. The controls had been cleaned and bagged at
 the same time as inoculated ones, but had no scale
 introduced. The infestation was heavy, so the insects were
 not well separated on the fruit. A razor blade was used to
 slice off the flavado with about half the thickness of the
 albedo included. The peel from only the stem half of the
 fruit was used because that was where the insects were
 most concentrated. The insects were impossible to wash off
 without severely damaging the peel; each fruit was washed
 with water and a sponge or bottlebrush and wiped dry with
 a paper towel before cutting it, but many of the insects

to the same stage as the insects applied on the first infestation date. The insects were reared on lemons. Before infesting the fruit on the trees, Paul Flores cleaned the peel and checked to make sure it was not already infested. He placed about 200 crawler stage insects on the fruit using a soft paintbrush. After the crawlers had a day to move around and find a spot to attach, Paul placed a very fine mesh drawing bag over the fruit to exclude predators and parasitoids of the scale. Bags were left in place for the duration of the field development period and also covered control fruit. Paul Flores infested fruit on 30 August and 1 September 2004 after cleaning the fruit on August 27. On 21 September the first set of red scale infested fruit were sampled. He brought Claire Federici 15 infested fruit and 12 uninfested control fruit. The insects were at the early second instar. The controls had been cleaned and bagged at the same time as inoculated ones, but had no scale introduced. The infestation was heavy, so the insects were not well separated on the fruit. A razor blade was used to slice off the flavedo with about half the thickness of the albedo included. The peel from only the stem half of the fruit was used because that was where the insects were most concentrated. The insects were impossible to wash off without severely damaging the peel; each fruit was washed with water and a sponge or bottlebrush and wiped dry with a paper towel before cutting it, but many of the insects were still intact and were included in the sample. The pulp had color but the fruit rind was still green. The peel from each half fruit was bagged separately in foil packets, and pressed between sheets of dry ice to freeze. All packets were placed in a paper bag with the date and information about 'control' or 'infested' written on the bag, and then placed at -80oC. The second sampling date from the first infestation was 11 October. Paul brought 19 infested and 9 uninfested fruit to Claire. These were all set up on 30 August. The insects were at the late third instar. Mikeal Roose's advice was to prepare three bulks of each, 5 infested and 3 uninfested fruit per bulk. The remaining four infested fruit were infested to a lesser degree and were discarded. Washing was done as before and the peel from each fruit frozen between sheets of aluminum foil pressed between sheets of dry ice. There were quite a lot of adhering insects in the frozen rind. After it was frozen, the peel from 3 uninfested or 5 infested fruit were pooled in a foil packet, then stored at -80oC. The pulp had color but the rind was mostly green. However, there was a little color developing on some fruit around the insects. The third sampling date was 2 December. Paul brought the first fruit from the second infestation, which were set up on September 27 or 28. He brought 15 infested and 10 uninfested fruit. Claire cut and froze them as before, making three pools of 5 infested fruit and three pools of 3 uninfested fruit. The control fruit all had green at the stem end, mostly about 1/4 of the circumference from stem to blossom end, but one fruit was green all over. The infested fruit were almost fully orange, with only a small amount of the surface still green, approximately the size of a quarter coin. Paul said it would be at least a month, probably 6 weeks or even more before the insects reach the late third instar, so this was the final sample for the cDNA library due to time constraints for EST sequencing. Mandal and Fenton (Close lab) purified RNA by the phenol method described in J. Japanese Soc. Hort. Sci. 1996. 64 (4): 809-814, purified poly(A) mRNA using PolyAT Tract mRNA Isolation Kit (Promega), produced a primary cDNA library using a lambda ZAP XR cDNA Synthesis Kit (Stratagene), then mass-excised 1 million pfu from the primary library to produce a phagemid population. The library was made from a mixture of RNA from each of the three treatments such that approximately equal amounts of early second instar and late third instar RNA were used. Phagemids were plated,

plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute (Kim, Kudrna, Collura, Wiesoteki, Byrne, Stum, Smart, Muller, Wing). Chromatogram files were downloaded by FTP by Close, then processed by Wanmaker (Close lab) using the HarVest pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were assembled, then chimeras were removed following manual inspection of assemblies (Wanmaker, Close, Roose). Sequences that survived all removal steps were submitted to GenBank. Clones from this library are archived at the Arizona Genomics Institute (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Query Match 55.1%; Score 22.6; DB 8; Length 677;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGCTGGCCGCGCGG 41
Db 640 CACCGATTCTTGCTCTCATCGCTGGCCGCGCTCG 676

RESULT 70
BJ213473/c

LOCUS BJ213473.1

DEFINITION BJ213473 Y. Ogiwara unpublished cDNA library, Wh Triticum aestivum

ACCESSION BJ213473

VERSION BJ213473.1 GI:19953031

KEYWORDS EST

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 684)
Ogiwara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadaasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .684
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="wh22j06"
/tissue_type="spike at meiosis"
/dev_stages="Feekes' scale 9"
/clone_lib="Y. Ogiwara unpublished cDNA library, Wh"

FEATURES
source

ORIGIN

Query Match 55.1%; Score 22.6; DB 3; Length 684;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCTTCGGATGCCAGTCCCTCATCGCTGGCCGCGG 37
Db 217 AGGCTTCGGCTGCCACCGCTCATCTGTGCGCCGTGA 181

RESULT 71
CK193871

```

LOCUS          CK193871          688 bp      mRNA      linear      EST 08-DEC-2003
DEFINITION     FGAS002290 Triticum aestivum FGAS: Library 3 Gate 6 Triticum
aestivum cDNA, mRNA sequence.
ACCESSION      CK193871
VERSION        CK193871.1  GI:39556261
KEYWORDS       EST.
SOURCE         Triticum aestivum (bread wheat)
ORGANISM       Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
REFERENCE      1 (bases 1 to 688)
AUTHORS        Allard,F., Crosby,W.L., Danyluk,J., Eudes,P., Frick,M., Gaudet,D.,
Genewein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroché,A.,
Links,M.G., McCarthy,E.B., Monroy,A., Muzak,I., Nilsson,D.,
Penniket,C., Roach,J.L. and Sarhan,F.
TITLE          Functional Genomics of Abiotic Stress In Wheat and Canola Crops
JOURNAL        Unpublished (2003)
COMMENT        Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas.est@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [101..612].
Plate: L3C102 row: B column: 04.
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                    /note="Organ: Root; Vector: pCMV.SPORT6; Root tissue from
control, cold-acclimated and salt stressed wheat cultivar
Norstar. 7 mRNA populations were combined before
constructing the library; 7 day non-acclimated roots, 1,
23, and 53 days cold-acclimated at 4C, and 30 minutes, 3
hours and 6 hours treated roots with 200mM NaCl.
Non-acclimated and cold-acclimated plants were grown in
vermiculite while salt stressed plant were grown
hydroponically. First strand synthesis in this library was
done in the presence of methylated dCTP thereby protecting
from internal cleavage with NotI."

ORIGIN
Query Match      55.1%; Score 22.6; DB 7; Length 688;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      4  CTCCTGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
      ||||| ||||| ||||| ||||| ||||| |||||
DB      313 CCTCCGATCCCGCCACGTCGCGCGCGGTCGC 349

RESULT 72
LOCUS          CC677627          694 bp      DNA      linear      GSS 19-JUN-2003
DEFINITION     OGMAZ38TH_ZM_0.7_1.5_KB_Zea_mays genomic clone ZMMBMA0332G04,
genomic survey sequence.
ACCESSION      CC677627
VERSION        CC677627.1  GI:32082403
KEYWORDS       GSS.
SOURCE         Zea mays
ORGANISM       Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 694)
AUTHORS        Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE          Consortium for Maize Genomics
JOURNAL        Unpublished (2002)
COMMENT        Other_GSSs: OGMAZ38TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: 1F
Class: methylation filtered.
Location/Qualifiers
                 1..694
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /strain="B73"
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methylation filtered genomic DNA library"

ORIGIN
Query Match      55.1%; Score 22.6; DB 9; Length 694;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      5  CTCCTGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 41
      ||||| ||||| ||||| ||||| ||||| |||||
DB      109 CCCCGCTCGCGTGGCGCATCGCGGACCCCGCGC 145

RESULT 73
LOCUS          CC677636/c          694 bp      DNA      linear      GSS 19-JUN-2003
DEFINITION     OGMAZ38TV_ZM_0.7_1.5_KB_Zea_mays genomic clone ZMMBMA0332G04,
genomic survey sequence.
ACCESSION      CC677636
VERSION        CC677636.1  GI:32082412
KEYWORDS       GSS.
SOURCE         Zea mays
ORGANISM       Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 694)
AUTHORS        Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE          Consortium for Maize Genomics
JOURNAL        Unpublished (2002)
COMMENT        Other_GSSs: OGMAZ38TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: 1F
Class: methylation filtered.
Location/Qualifiers
                 1..694
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /strain="B73"
                    /db_xref="taxon:4577"
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                    /clone_lib="ZM 0.7 1.5_KB"
                    /note="Vector: pBcSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

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ORIGIN methylation filtered genomic DNA library"

Query Match 55.1%; Score 22.6; DB 9; Length 694;
 Best Local Similarity 73.0%; Pred. No. 4.7e+03;
 Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTCGCCGCGCGCG 41
 Db 586 CCCGGCTCGCGTGGCGCATCGCCGACCCGCGCG 550

RESULT 74
 BZ647470 710 bp DNA linear GSS 29-JAN-2003
 LOCUS OGAMY51TC ZM 0.7 1.5_KB Zea mays genomic clone ZMMBPa0098105,
 DEFINITION genomic survey sequence.

ACCESSION BZ647470 GI:28110429
 VERSION BZ647470.1
 KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 710)

White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: OGAMY51TM

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

1. .710

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone_lib="ZM 0.7 1.5_KB"

/notes="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

Query Match 55.1%; Score 22.6; DB 9; Length 710;

Best Local Similarity 73.0%; Pred. No. 4.7e+03;

Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTCGCCGCGCGCG 41

Db 138 CCCGGCTCGCGTGGCGCATCGCCGACCCGCGCG 174

RESULT 75
 CC972022 710 bp DNA linear GSS 18-AUG-2003
 LOCUS ZUADS49TV ZM 3.0 4.0_KB Zea mays genomic clone ZMMBPa0036101,
 DEFINITION genomic survey sequence.

ACCESSION CC972022

VERSION CC972022.1

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 710)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: ZUADS49TH

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: sheared ends.

Location/Qualifiers

1. .710

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone_lib="ZMMBPa0036101"

/clone_lib="ZM 3.0 4.0_KB"

/notes="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'

genomic DNA library"

Query Match 55.1%; Score 22.6; DB 9; Length 710;

Best Local Similarity 73.0%; Pred. No. 4.7e+03;

Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTCGCCGCGCGCG 41

Db 637 CCCGGCTCGCGTGGCGCATCGCCGACCCGCGCG 601

RESULT 76

CG325313/c

LOCUS

DEFINITION

ACCESSION

CG325313

VERSION

CG325313.1

KEYWORDS

GSS

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 710)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

1. .710

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone_lib="ZMMBPa0036101"

/clone_lib="ZM 0.7 1.5_KB"

/notes="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

Query Match 55.1%; Score 22.6; DB 10; Length 710;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 5 CTCGGATCCAGTCCTCATCGCTGGCCGCGCG 41
Db 245 CCCCCTCCGGTGGCGATCGCGACCCCGCGCG 209

RESULT 77
DN621099/c
LOCUS
DEFINITION
UCRS11_06D23_f Parent Washington Navel Orange Scale-Infested Rind
cDNA Library UCRS11 Citrus sinensis cDNA clone CS_WED0006D23, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
DN621099.1 GI:61690199
EST.
Citrus sinensis
Citrus sinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE
AUTHORS
Close, T.J., Roose, M.L., Federici, C.F., Mandal, J., Fenton, R.D.,
Luck, R., Forster, L., Morse, J., Flores, P., Wananaker, S., Kim, H.R.,
Kudrna, D., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,
Muller, C. and Wing, R.

TITLE
Development of EST Resources and New Genetic Markers for California
Citrus - Parent Washington Navel Orange Scale-Infested Rind cDNA
Library UCRS11

JOURNAL
COMMENT
Contact: Timothy J. Close
Department of Botany & Plant Sciences
University of California
Riverside, CA 92521-0124, USA
Tel: 909-787-3318
Fax: 909-787-4437
Email: timothy.close@ucr.edu
Seq primer: T7.

FEATURES
source
1..718
/organism="Citrus sinensis"
/mol_type="mRNA"
/cultivar="Parent Washington Navel"
/db_xref="taxon:2711"
/clone="CS_WED0006D23"
/tissue_type="Flavedo, albedo, some red scale"
/dev_stage="12 year old trees"
/lab_host="E. coli TJCl21"
/clone_lib="Parent Washington Navel Orange Scale-Infested
Rind cDNA Library UCRS11"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; in cooperation with Dr.
Robert Luck and Dr. Joseph Morse, Department of
Entomology, University of California Riverside, navel
orange fruit was infested with red scale (Aonidiella
aurantii [Maskell]). Dr. Luck's technician, Lisa Forster,
maintained colonies of red scale. Dr. Morse's technician,
Paul Flores, cleaned and infested the fruit, bagged the
fruit after the crawlers had time to settle, then
harvested the fruit at the early second instar and late
third instar phases of the insect. Claire Federici (Dr.
Mikeal Roose's lab) cleaned off most of the insects (some
remained firmly attached), cut the peel, then froze and
scored at -80oC. The trees used for this set of samples
were growing in field 16K of the University of California
Citrus Experiment Station. This was the same field from
which the tissue was collected for the navel shoot
meristems and the peel for citrus thrips, Scirtothrips

citri [Moulton]. The trees were planted 12 October 1992.
The scion was Parent navel. The trees used for infesting
with red scale all had Troyer rootstock. Three different
trees were used for each of the two infestations, a total
of 6 trees. This experiment did not take place according
to the original schedule because the red scale colony
became infested with mites, so too few insects were
available to infest the fruit on the date originally
planned. The plan had been to infest on or about June 30
and August 13. Instead the infestation dates were August
30 and September 27, 2004. Because this took us into the
cool weather of fall, the insects applied on the second
infestation date took about three times as long to develop
to the same stage as the insects applied on the first
infestation date. The insects were reared on lemons.
Before infesting the fruit on the trees, Paul Flores
cleaned the peel and checked to make sure it was not
already infested. He placed about 200 crawler stage
insects on the fruit using a soft paintbrush. After the
crawlers had a day to move around and find a spot to
attach, Paul placed a very fine mesh drawstring bag over
the fruit to exclude predators and parasitoids of the
scale. Bags were left in place for the duration of the
field development period and also covered control fruit.
Paul Flores infested fruit on 30 August and 1 September
2004 after cleaning the fruit on August 27. On 21
September the first set of red scale infested fruit were
sampled. He brought Claire Federici 15 infested fruit and
12 uninfested control fruit. The insects were at the early
second instar. The controls had been cleaned and bagged at
the same time as inoculated ones, but had no scale
introduced. The infestation was heavy, so the insects were
not well separated on the fruit. A razor blade was used to
slice off the flavedo with about half the thickness of the
albedo included. The peel from only the stem half of the
fruit was used because that was where the insects were
most concentrated. The insects were impossible to wash off
without severely damaging the peel; each fruit was washed
with water and a sponge or bottlebrush and wiped dry with
a paper towel before cutting it, but many of the insects
were still intact and were included in the sample. The
pulp had color but the fruit rind was still green. The
peel from each half fruit was bagged separately in foil
packets, and pressed between sheets of dry ice to freeze.
All packets were placed in a paper bag with the date and
information about 'control' or 'infested' written on the
bag, and then placed at -80oC. The second sampling date
from the first infestation was 11 October. Paul brought 19
infested and 9 uninfested fruit to Claire. These were all
set up on 30 August. The insects were at the late third
instar. Mikeal Roose's advice was to prepare three bulks
of each, 5 infested and 3 uninfested fruit per bulk. The
remaining four infested fruit were infested to a lesser
degree and were discarded. Washing was done as before and
the peel from each fruit frozen between sheets of aluminum
foil pressed between sheets of dry ice. There were quite a
lot of adhering insects in the frozen rind. After it was
frozen, the peel from 3 uninfested or 5 infested fruit
were pooled in a foil packet, then stored at -80oC. The
pulp had color but the rind was mostly green. However,
there was a little color developing on some fruit around
the insects. The third sampling date was 2 December. Paul
brought the first fruit from the second infestation, which
were set up on September 27 or 28. He brought 15 infested
and 10 uninfested fruit. Claire cut and froze them as
before, making three pools of 5 infested fruit and three
pools of 3 uninfested fruit. The control fruit all had
green at the stem end, mostly about 1/4 of the
circumference from stem to blossom end, but one fruit was
green all over. The infested fruit were almost fully
orange, with only a small amount of the surface still
green, approximately the size of a quarter coin. Paul said
it would be at least a month, probably 6 weeks or even

bag, and then placed at -80oC. The second sampling date from the first infestation was 11 October. Paul brought 19 infested and 9 uninfested fruit to Claire. These were all set up on 30 August. The insects were at the late third instar. Mikel Rose's advice was to prepare three bulks of each, 5 infested and 3 uninfested fruit per bulk. The remaining four infested fruit were infested to a lesser degree and were discarded. Washing was done as before and the peel from each fruit frozen between sheets of aluminum foil pressed between sheets of dry ice. There were quite a lot of adhering insects in the frozen rind. After it was frozen, the peel from 3 uninfested or 5 infested fruit were pooled in a foil packet, then stored at -80oC. The pulp had color but the rind was mostly green. However, there was a little color developing on some fruit around the insects. The third sampling date was 2 December. Paul brought the first fruit from the second infestation, which were set up on September 27 or 28. He brought 15 infested and 10 uninfested fruit. Claire cut and froze them as before, making three pools of 5 infested fruit and three pools of 3 uninfested fruit. The control fruit all had green at the stem end, mostly about 1/4 of the circumference from stem to blossom end, but one fruit was green all over. The infested fruit were almost fully orange, with only a small amount of the surface still green, approximately the size of a quarter coin. Paul said it would be at least a month, probably 6 weeks or even more before the insects reach the late third instar, so this was the final sample for the cDNA library due to time constraints for EST sequencing. Mandal and Fenton (Close lab) purified RNA by the phenol method described in Japanese Soc. Hort. Sci. 1996. 64 (4): 803-814, purified poly(A) mRNA using PolyAT Tract mRNA Isolation Kit (Promega), produced a primary cDNA library using a lambda ZAP XR cDNA Synthesis Kit (Stratagene), then mass-excised 1 million pfu from the primary library to produce a phagemid population. The library was made from a mixture of RNA from each of the three treatments such that approximately equal amounts of early second instar and late third instar RNA were used. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute (Kim, Kudrna, Collura, Wiscotski, Byrne, Stum, Smart, Muller, Wing). Chromatogram files were downloaded by FTP by Close, then processed by Wanmaker (Close lab) using the HarVEST pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were assembled, then chimeras were removed following manual inspection of assemblies (Wanmaker, Close, Roose). Sequences that survived all removal steps were submitted to GenBank. Clones from this library are archived at the Arizona Genomics Institute (<http://www.genome.arizona.edu/orders/>)."

ORIGIN

Query Match 55.1%; Score 22.6; DB 8; Length 729;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCTCATCGTCGGCCGCGCGG 41
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 290 CACCGATTCTTGTCTTCATCGTGGCGCGCTCG 254

RESULT 79

BZ647476/c
LOCUS
DEFINITION
BZ647476 732 bp DNA linear GSS 29-JAN-2003
genomic survey sequence.
ACCESSION
BZ647476
VERSION
BZ647476.1 GI:28110442

KEYWORDS

SOURCE
ORGANISM

GSS.
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 732)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

TITLE

JOURNAL

COMMENT

Other GSSs: OGAMY51TC

Contact: Cathy Whitelaw

TIGR

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Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: methylation filtered.

Location/Qualifiers

1. .732

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone_lib="ZM 0.7 1.5 KB"

/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

FEATURES

source

ORIGIN

Query Match 55.1%; Score 22.6; DB 9; Length 732;

Best Local Similarity 73.0%; Pred. No. 4.7e+03;

Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCTCATCGTCGGCCGCGCGG 41
| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 691 CCCCGCTCCGCTCGCGCATCGCCGCCCGCGG 655

RESULT 80

BX389571/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX389571 739 bp mRNA linear EST 28-APR-2004
BX389571 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI033YG11 5-PRIME, mRNA sequence.

BX389571

BX389571.2 GI:46834850

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 739)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30461244.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

5547.r,

and it belongs to a clone representative of this cluster. For more

information about this cluster and the virtual cDNA, see

http://www.genoscope.cns.fr/cdna?s=CS0BAF0252C04_AF02332_3&c=5547.r


```

REFERENCE
1 (bases 1 to 804)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1144 row: o column: 08
High quality sequence stop: 682.

FEATURES
Location/Qualifiers
1..804
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294879"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 83"
/Note="Organ: Prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccatcgcc); Site 2: SfiI
(ggcatcatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGCGCGCGCGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
```

ORIGIN

```

Query Match 55.1%; Score 22.6; DB 2; Length 804;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGN 37
|||||
Db 768 AAACCTGGGATCCCGACCATCATCCGGATCCCGT 732
|||||

RESULT 84
CG257472 862 bp DNA linear GSS 25-AUG-2003
LOCUS OGWF043TH_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMA0567G13,
DEFINITION genomic survey sequence.
ACCESSION CG257472
VERSION CG257472.1 GI:34163986
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 862)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGWF043TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
```

Class: methylation filtered.

```

FEATURES
Location/Qualifiers
1..867
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0443D13"
/clone_lib="ZM_0.7_1.5_KB"
/Note="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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ORIGIN

```

Query Match 55.1%; Score 22.6; DB 9; Length 867;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
|||||
Db 622 CCCCCTGCTGCGTGGCGCATCGCCGACCCCGCG 658
|||||

RESULT 86
CG257472 862 bp DNA linear GSS 19-JUN-2003
LOCUS OGUF013TH_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMA0443D13,
DEFINITION genomic survey sequence.
ACCESSION CG257472
VERSION CG257472.1 GI:32108221
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 867)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
```

Class: methylation filtered.

```

FEATURES
Location/Qualifiers
1..867
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0443D13"
/clone_lib="ZM_0.7_1.5_KB"
/Note="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
```

ORIGIN

```

Query Match 55.1%; Score 22.6; DB 9; Length 867;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
|||||
Db 622 CCCCCTGCTGCGTGGCGCATCGCCGACCCCGCG 658
|||||

RESULT 86
CG257472 862 bp DNA linear GSS 19-MAR-2004
LOCUS CK934035
```

```

DEFINITION CGP1004542 B11 Developing fruit peel at 38 DAFB Citrus sinensis
              cDNA clone_F38DAB10001_IVF_B11 5', mRNA sequence.
ACCESSION   CK934035
VERSION     CK934035.1 GI:45447233
KEYWORDS    EST.
SOURCE      Citrus sinensis
ORGANISM    Citrus sinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Sapindales; Rutaceae; Citrus.
REFERENCE   1 (bases 1 to 881)
AUTHORS     Uratsu S., Baek J., Leslie A., Xu J., Cook D. and Dandekar A.
TITLE       Analysis of peel specific genes in Citrus (2004)
JOURNAL     Unpublished (2004)
COMMENT     Contact: Abhaya Dandekar, PhD
            CAES Genome Facility
            UC Davis, Department of Pomology
            One Shields Ave, Davis, CA 95616, USA
            Tel: 530 752 7784
            Fax: 530 752 8502
            Email: andandekar@ucdavis.edu
            Seq primer: WSC-F-TCCGAGATCTGGACGAGC.
FEATURES    Location/Qualifiers
             1..881
                /organism="Citrus sinensis"
                /mol_type="mRNA"
                /cultivar="Washington navel orange"
                /db_xref="taxon:2711"
                /clone="P38DAB10001_IVF_B11"
                /sex="Hermaphrodite"
                /cell_type="Peel/Rind"
                /dev_stage="Young fruit sample-collected June 17, 2003"
                /lab_host="XL10-Gold"
                /clone_lib="Developing fruit peel at 38 DAFB"
                /note="Organ: Fruit; Vector: pTriplex2; Site 1: Sf1A;
                Site 2: Sf1B; Developing citrus fruits were harvested
                from trees growing in the 'Citrus variety collection' in
                the Wolfkill experimental orchard located in Winters,
                California (USA). Fruit was collected on June 17, 2003,
                between 8 to 9 am and stored at 4C. The entire peel
                (including both flavedo and albedo) was used to isolate
                RNA using Trizol reagent from Invitrogen. The cDNA library
                was constructed using the SMART cDNA library kit
                (Clontech). The primary library was en masse evicted and
                plasmid DNA containing the cDNA library was isolated from
                the resultant bacterial population. Plasmid DNA was then
                transformed into ultra competent E coli cells (XL10 Gold;
                Stratagene). Transformants were plated out on Q-trays
                (2000 cfu/tray), picked using a Qbot and archived in 384
                well dishes."
ORIGIN
Query Match      55.1%; Score 22.6; DB 7; Length 881;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCGAGTCCCTCATCGCTGCCCGGCGG 41
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 724 CACCGATTTCTTGTCTCTATCGTGGCGCGGCTCG 760

RESULT 87
BQ962268
LOCUS       BQ962268
DEFINITION AGENCOURT_10051616 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6500626
            5', mRNA sequence.
ACCESSION   BQ962268
VERSION     BQ962268.1 GI:22377746
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```

```

Hominidae; Homo.
1 (bases 1 to 888)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14053 row: m column: 11
High quality sequence stop: 603.
FEATURES    Location/Qualifiers
             1..888
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6500626"
                /tissue_type="leiomyosarcoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 71"
                /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
                Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 2.1 kb."
ORIGIN
Query Match      55.1%; Score 22.6; DB 5; Length 888;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 4 CTCGGATGCGAGTCCCTCATCGCTGCCCGGCGG 40
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 595 CTTCGTGTTCGGGTGCCTCACCTCTGGCCAGGTGC 631

RESULT 88
BX379356
LOCUS       BX379356
DEFINITION BX379356 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DT033YG11 3-PRIME, mRNA sequence.
ACCESSION   BX379356
VERSION     BX379356.2 GI:46617172
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1 (bases 1 to 892)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30450754.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5547.r,
and it belongs to a clone representative of this cluster. For more
information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/cdna?e=CS0D1033AD06NP1&c=5547.r.
FEATURES    Location/Qualifiers
             1..892
                /organism="Homo sapiens"

```


Plate: 1007083 column: 31
Class: transposon-tagged.

FEATURES

source

Location/Qualifiers
1. .312
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"

/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI, Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription web units. For more information on RescueMu, go to the site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 54.6%; Score 22.4; DB 9; Length 312;
Best Local Similarity 70.0%; Pred. No. 5.2e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCGAGTCCCTCATCGTCGCCCGGCGG 41
|||||
DB 209 AGCTCCGGGCTCCAGTCCCTCATCGTCGCCCGGATCCCG 170
|||||

RESULT 92

DN148717/c

LOCUS

DEFINITION 4936 G06 G06 Switchgrass leaf cDNA library Panicum virgatum cDNA
clone 4936_G06_G06, mRNA sequence.

ACCESSION DN148717.1 GI:59869568

VERSION

KEYWORDS

SOURCE

ORGANISM

Panicum virgatum (switchgrass)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Paniceae; Panicum.

1 (bases 1 to 373)
Tobias, C.M., Twigg, P., Hayden, D.M., Fladseth, M.R., Vivian, L.A.,
Chow, E.K. and Sarath, G.

An EST survey of Switchgrass: a C4 perennial grass
Unpublished (2005)

JOURNAL

COMMENT

Contact: Tobias CM
Genomics and Gene Discovery Unit
USDA, Agricultural Research Service, Western Regional Research
Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 510 559-6172
Fax: 510 559-5818
Email: ctobias@pw.usda.gov

The phred basecalling program was used to call bases and identify
the high scoring region using the -trim_alt '' and trim cutoff 0.01
options. Vector sequences have been removed using the program
cross_match.
Seq primer: M13 reverse.

FEATURES

source

Location/Qualifiers
1. .373
/organism="Panicum virgatum"
/mol_type="mRNA"
/cultivar="Kanolow"
/db_xref="taxon:38727"
/clone="4936_G06_G06"

/dev_stage="immature tillers"
/lab_host="E. coli DH5alpha"
/clone_lib="Switchgrass leaf cDNA library"
/note="Organ: Leaf; Vector: pSPORT1; Site 1: SalI; Site 2:
NotI; Switchgrass cv. Kanlow plants were grown from seed
in a greenhouse in potting soil. Immature tillers were
collected randomly. Leaf tissue was flash frozen in liquid
nitrogen. The tissue was prepared by Gautam Sarath, USDA,
ARS, Wheat Forage and Sorghum Research Unit, U. Nebraska,
Lincoln. Total RNA and poly(A) RNA were prepared, cDNA
synthesized, and directionally ligated into pSPORT1 by
Paul Twigg, Biology Department, U. Nebraska Kearney,
Kearney, NE. Plasmid DNA preparations and DNA sequencing
were performed in the laboratory of CM Tobias."

ORIGIN

Query Match 54.6%; Score 22.4; DB 8; Length 373;
Best Local Similarity 70.0%; Pred. No. 5.3e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCGAGTCCCTCATCGTCGCCCGGCGG 41
|||||
DB 254 AGCTTCTCAGGCCAGTCTTCTCGGAGGCCGCGG 215
|||||

RESULT 93

CF808758

LOCUS

DEFINITION

CF808758 382 bp mRNA linear EST 15-APR-2004
pBH039XD06f USDA-IPAFS:Expression of Phytophthora sojae genes
during infection and propagation Glycine max cDNA clone sHB039D06
5, mRNA sequence.

ACCESSION CF808758.1 GI:37997169

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

1 (bases 1 to 382)
Tyler, B.
Tyler, B. Not Published
Unpublished (2003)
Contact: Tyler B
Tyler lab
VBI
1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtylev@vt.edu
PCR Primers
FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 039 row: D column: 06
Seq primer: BK reverse primer
High quality sequence stop: 382.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers
1. .382
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Harosoy"
/db_xref="taxon:3847"
/clone="sHB039D06"
/tissue_type="Phytophthora sojae-infected hypocotyl"
/cell_lines="Phytophthora sojae culture P6497"
/dev_stage="48 hr. post infection stage"
/clone_lib="USDA-IPAFS:Expression of Phytophthora sojae
genes during infection and propagation"
/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI"

ORIGIN

Query Match 54.6%; Score 22.4; DB 6; Length 382;
Best Local Similarity 70.0%; Pred. No. 5.3e+03;

	Matches	28;	Conservative	1;	Mismatches	11;	Indels	0;	Gaps	0;
Qy	1	AAGCCTCCGATGCCATTCCTCATTCGCTGGCCCGCNC	40							
Db	302	AGGCACCGGATTCTCTCTTCCTTCCTCGCGGCCTGGCGC	341							

RESULT_94	EST 01-APR-2002
AU055771/c	
LOCUS	409 bp mRNA linear
DEFINITION	Oryza sativa mature leaf Nipponbare Oryza sativa (japonica cultivar-group) cDNA clone S20046.1A, mRNA sequence.

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AU055771	AU055771.1	GI:4714654	EST.	
			Oryza sativa (japonica cultivar-group)	
			Oryza sativa (japonica cultivar-group)	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.	

REFERENCE	1 (bases 1 to 409)
AUTHORS	Yamamoto,K. and Sasaki,T.
TITLE	Rice cDNA from mature leaf
JOURNAL	Unpublished (1999)
COMMENT	Contact: Takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan Tel: 81-298-38-7441 Fax: 81-298-38-7468 Email: tsasaki@abf.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/ PROJECT = 'RGP'

```

FEATURES
source
Location/Qualifiers
1..409
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clones="S20046_1A"
/tissue_type="mature leaf"
/clone_lib="Oryza sativa mature leaf Nipponbare"

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ORIGIN
Query Match 54.6%; Score 22.4; DB 1; Length 409;
Best Local Similarity 70.0%; Pred. No. 5.3e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AGCCTCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
|||||
Db 248 AGCCTCGGATGCAAGTACCCATGGCGGTGGTGGTG 209
|||||

RESULT 95	BG790807	LOCUS	BG790807	414 bp	mRNA	linear	EST 22-JUL-2004
DEFINITION	sae70c07.y1 Gm-cl064 Glycine max cDNA clone GENOME SYSTEMS CLONE						
	ID: Gm-cl064-3566 5' similar to TR:080915 080915 T19C21.15 PROTEIN.						
	; mRNA sequence.						

ACCESSION	BC790807
VERSION	BC790807.1
KEYWORDS	GI:14126369
SOURCE	EST.
ORGANISM	Glycine max (soybean)
	Glycine max
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryotophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
AUTHORS
1. (bases 1 to 414)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

TITLE	JOURNAL	COMMENT
-------	---------	---------

McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Putative full length read vector to vector length is 417 this clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com).

FEATURES

```

1. 414
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1064-3566"
/tissue_type="seedling epicotyls"
/dev_stage="2 week old"
/lab_host="DH10B"
/clone_lib="Gm-c1064"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from the epicotyls of 2 week old seedling for the cultivar Williams. The seedlings were germinated in a growth chamber, excised above the soil level, and the plants were placed in a 100 ppm solution of auxin for 24 hours prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

```

ORIGIN

```
Query Match      54.6%; Score 22.4; DB 2; Length 414;
Best Local Similarity 70.0%; Pred. No. 5.3e+03;
Matches 28: Conservative 1; Mismatches 11; Indels 0; Gaps 0;
```

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
||| ||||| ||| ||| ||| ||||| : |||
pb 330 AGGCCACGGATTCCTTCCTTCCTCCGGGSCCTGCCGC 369

RESULT 96

BW721516		415 bp	mRNA	linear	EST 01-MAR-2002
OCUGS					
DEFINITION	UI-E-E01-aic-o-13-0-UI.r1		UI-E-E01 Homo sapiens cDNA clone		
	UI-E-E01-aic-o-13-0-UI.5'		mRNA sequence.		

ACCESSION BM721516
VERSION BM721516.1 GI:19041480
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

Coordinated Laboratory for Computational Genomics

University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES

source
1. .415
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EQ1-aic-o-13-0-UI"
/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EQ1"
/note="Organ: eye; Vector: p7773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EQ1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGGATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN
Query Match 54.6%; Score 22.4; DB 3; Length 415;
Best Local Similarity 70.0%; Pred. No. 5.3e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCCGGAGTCCAGTCCCTCATCGCTGGCGCGCGCGC 40
|||||
Db 253 AAGACGACGACTGCTGCGCCCTCTCGCTACCCCTGCCGC 292
|||||

RESULT 97
BG717495
LOCUS
DEFINITION
602869259F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4821519 5', mRNA sequence.
BG717495
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 482)

REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10728 row: f column: 16
High quality sequence stop: 441.

FEATURES

source
1. .482
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4821519"
/lab_host="DH10B"
/clone_lib="NIH MGC 97"
/note="Organ: Testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTN-3', size-selected for average insert size 2.2 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 54.6%; Score 22.4; DB 2; Length 482;
Best Local Similarity 70.0%; Pred. No. 5.4e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 1 AAGCTCCGGAGTCCAGTCCCTCATCGCTGGCGCGCGCGC 40
|||||
Db 270 AAGACGACGACTGCTGCGCCCTCTCGCTACCCCTGCCGC 309
|||||

RESULT 98

BQ785316
LOCUS
DEFINITION
BQ785316
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 554)

ACCESSION
BQ785316
VERSION
BQ785316.1 GI:21993788
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)

REFERENCE

AUTHORS
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McGann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 422.

FEATURES

Location/Qualifiers

```

source
1. .54
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/clones="SOYBEAN CLONE ID: Gm-cl076-5414"
/tissue_type="wounded cotyledons"
/dev_stage="11 day old seedlings"
/lab_host="DH10B"
/clone_lib="Gm-cl076"
/notes="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from 11 day old seedlings treated with that were treated
with 2 ugs/ml of a crude glucan elicitor preparation
isolated from the mycelial walls of Phytophthora sojae.
The library was prepared using the Stratagene pBluescript
II SK(+) library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with an XhoI restriction site. EcoRI
adaptors were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into E.coli ElectroMax DH10B host cells. Plant
material was provided by Michael G. Hahn (Complex
Carbohydrate Research Center, University of Georgia) and
the library was constructed by Anu Khanna (Lila Vodkin
lab, University of Illinois)."

ORIGIN

Query Match      54.6%; Score 22.4; DB 5; Length 554;
Best Local Similarity 70.0%; Pred. No. 5.4e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy      1  AAGCTTCGGATGCCAGTCCCTCATCGCTGCGCGGCGC 40
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      238 AGGCCACGGATTCTCTCTCTCTCTCGCGGCGCTGCCG 277

RESULT 99
CW579372
LOCUS
DEFINITION
OA_Aba0109B01.r OA_Aba Oryza australiensis genomic clone
CW579372
CW579372.1 GI:54465170
GSS.
Oryza australiensis
Oryza australiensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 638)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
Unpublished (2004)
OWAP Project
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0109 row: B column: 01
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
Location/Qualifiers
1. .638
/organism="Oryza australiensis"

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Wed May 10 09:39:48 2006

09-904-968a-1_n3336-3300_3340.dx.rst

Page 47

Search completed: May 9, 2006, 22:55:13
Job time : 1917 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 22:18:30 ; Search time 144 Seconds
(without alignments)
506.111 Million cell updates/sec

Title: US-09-904-968A-1_N3336_COPY_3300_3340

Perfect score: 41

Sequence: 1 aagctccgagtcagctcc.....tcactgctgcccgcgncgcg 41

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/prodata/1/ina/1_COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5_COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/H_COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq.*
- 7: /cgn2_6/prodata/1/ina/PP_COMB.seq.*
- 8: /cgn2_6/prodata/1/ina/RE_COMB.seq.*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	41	100.0	31571	2	US-08-323-443B-1
C 2	41	100.0	53526	3	US-08-658-136-2
C 3	41	100.0	53577	3	US-08-658-136-1
C 4	41	100.0	53577	3	US-08-460-215A-1
C 5	24.6	60.0	1424	3	US-09-902-540-3125
C 6	24.6	60.0	15268	3	US-09-902-540-1142
C 7	22.6	55.1	369	3	US-09-270-767-7807
C 8	22.6	55.1	369	3	US-09-270-767-23089
C 9	22.4	54.6	1269	3	US-09-252-991A-3470
C 10	22.4	54.6	227390	3	US-09-949-016-12201
C 11	22.4	54.6	227390	3	US-09-949-016-13365
C 12	22	53.7	1281	3	US-09-902-540-7196
C 13	22	53.7	6430	3	US-09-902-540-669
C 14	22	53.7	8559	3	US-09-949-016-13412
C 15	22	53.7	59252	3	US-09-949-016-12150
C 16	22	53.7	59252	3	US-09-949-016-12150
C 17	21.8	53.2	289	3	US-09-313-294A-4625
C 18	21.8	53.2	687	3	US-09-902-540-8880
C 19	21.8	53.2	10528	3	US-09-902-540-945
C 20	21.6	52.7	230	3	US-09-060-756-422
C 21	21.6	52.7	230	3	US-09-670-314-422
C 22	21.6	52.7	1689	3	US-09-902-540-3347
C 23	21.6	52.7	18537	3	US-09-902-540-1157
C 24	21.4	52.2	234	3	US-09-252-991A-4962
C 25	21.4	52.2	234	3	US-09-252-991A-4962
C 26	21.4	52.2	234	3	US-09-252-991A-4962
C 27	21.4	52.2	234	3	US-09-252-991A-4962
C 28	21.4	52.2	234	3	US-09-252-991A-4962
C 29	21.4	52.2	234	3	US-09-252-991A-4962
C 30	21.4	52.2	234	3	US-09-252-991A-4962
C 31	21.4	52.2	234	3	US-09-252-991A-4962
C 32	21.4	52.2	234	3	US-09-252-991A-4962
C 33	21.4	52.2	234	3	US-09-252-991A-4962
C 34	21.4	52.2	234	3	US-09-252-991A-4962
C 35	21.4	52.2	234	3	US-09-252-991A-4962
C 36	21.4	52.2	234	3	US-09-252-991A-4962
C 37	21.4	52.2	234	3	US-09-252-991A-4962
C 38	21.4	52.2	234	3	US-09-252-991A-4962
C 39	21.4	52.2	234	3	US-09-252-991A-4962
C 40	21.2	51.7	4403765	3	US-09-103-840A-2
C 41	21.2	51.7	4411529	3	US-09-103-840A-2
C 42	21	51.2	420	3	US-09-252-991A-13290
C 43	21	51.2	624	3	US-09-252-991A-12674
C 44	21	51.2	747	3	US-09-758-759-112
C 45	21	51.2	929	3	US-09-533-559-7620
C 46	21	51.2	972	3	US-09-909-796-11
C 47	21	51.2	1139	3	US-09-909-796-11
C 48	21	51.2	1146	3	US-09-252-991A-12818
C 49	21	51.2	1362	3	US-09-902-540-8360
C 50	21	51.2	1737	3	US-09-902-540-5562
C 51	21	51.2	1845	3	US-09-252-991A-13124
C 52	21	51.2	2185	3	US-10-104-047-556
C 53	21	51.2	2421	3	US-09-902-540-5156
C 54	21	51.2	7628	3	US-09-902-540-875
C 55	21	51.2	23673	3	US-09-773-816-1
C 56	21	51.2	29559	3	US-09-902-540-1254
C 57	21	51.2	41170	3	US-09-902-540-1367
C 58	21	51.2	67386	3	US-09-949-016-16519
C 59	21	51.2	109519	3	US-09-758-759-1
C 60	21	51.2	146095	3	US-09-949-016-13872
C 61	21	51.2	146104	3	US-09-949-016-13239
C 62	20.8	50.7	570	3	US-09-902-540-5941
C 63	20.8	50.7	682	3	US-08-796-792-1
C 64	20.8	50.7	682	3	US-09-491-795-1
C 65	20.8	50.7	958	3	US-09-902-540-1394
C 66	20.8	50.7	1134	3	US-09-342-681C-15
C 67	20.8	50.7	1661	3	US-09-342-681C-3
C 68	20.8	50.7	15073	3	US-09-949-016-15673
C 69	20.8	50.7	97195	3	US-09-949-016-12212
C 70	20.8	50.7	97196	3	US-09-949-016-16971
C 71	20.8	50.7	225127	3	US-09-949-016-16480
C 72	20.6	50.2	744	3	US-09-902-540-6444
C 73	20.6	50.2	777	3	US-09-902-540-3367
C 74	20.6	50.2	927	3	US-09-758-759-201
C 75	20.6	50.2	1347	3	US-09-724-797-43
C 76	20.6	50.2	12152	3	US-09-758-759-182
C 77	20.6	50.2	12865	3	US-09-902-540-1158
C 78	20.6	50.2	17125	3	US-09-902-540-1048
C 79	20.4	49.8	399	3	US-09-847-960-7
C 80	20.4	49.8	420	3	US-09-266-965-27
C 81	20.4	49.8	430	3	US-09-847-960-8
C 82	20.4	49.8	533	3	US-09-847-960-1
C 83	20.4	49.8	549	3	US-09-252-991A-1469
C 84	20.4	49.8	601	3	US-09-949-016-46393
C 85	20.4	49.8	672	3	US-09-902-540-8798
C 86	20.4	49.8	708	3	US-09-902-540-1910
C 87	20.4	49.8	1056	3	US-09-252-991A-1419
C 88	20.4	49.8	1143	3	US-09-902-540-9099
C 89	20.4	49.8	1410	3	US-09-252-991A-1239
C 90	20.4	49.8	1417	3	US-09-199-737-3
C 91	20.4	49.8	1431	3	US-09-058-333A-3
C 92	20.4	49.8	1431	3	US-09-252-991A-1316
C 93	20.4	49.8	1593	3	US-09-252-991A-1519
C 94	20.4	49.8	1881	3	US-09-489-039A-5942
C 95	20.4	49.8	2187	3	US-09-127-219B-2
C 96	20.4	49.8	2263	3	US-09-595-549-1
C 97	20.4	49.8	2712	3	US-09-252-991A-1366

98	20.4	49.8	2733	3	US-09-799-451-480	Sequence 480, App	171	19.8	48.3	2058	3	US-08-470-588-1	Sequence 1, Appli
99	20.4	49.8	4080	3	US-09-016-434-1326	Sequence 1326, Ap	c 172	19.8	48.3	2459	3	US-09-973-278-842	Sequence 842, App
100	20.4	49.8	5445	3	US-09-023-655-1319	Sequence 1319, Ap	c 173	19.8	48.3	2460	3	US-09-973-278-845	Sequence 845, App
101	20.4	49.8	5645	3	US-09-949-002-8	Sequence 8, Appli	c 174	19.8	48.3	2461	3	US-09-902-540-1867	Sequence 1867, Ap
102	20.4	49.8	5681	3	US-09-919-172-58	Sequence 58, Appl	c 175	19.8	48.3	2541	3	US-09-902-540-8123	Sequence 8123, Ap
103	20.4	49.8	5933	3	US-09-919-172-23	Sequence 23, Appl	c 176	19.8	48.3	2809	3	US-09-949-016-3722	Sequence 3722, Ap
104	20.4	49.8	6014	3	US-09-949-002-199	Sequence 199, App	c 177	19.8	48.3	2809	3	US-09-949-016-3723	Sequence 3723, Ap
105	20.4	49.8	10096	3	US-09-902-540-935	Sequence 935, App	c 178	19.8	48.3	2820	3	US-09-976-594-367	Sequence 367, App
c 106	20.4	49.8	10318	3	US-09-902-540-973	Sequence 973, App	c 179	19.8	48.3	3171	3	US-09-079-812E-1	Sequence 1, Appli
c 107	20.4	49.8	10521	3	US-09-949-016-13516	Sequence 13516, A	c 180	19.8	48.3	3178	3	US-10-104-047-989	Sequence 989, App
c 108	20.4	49.8	12768	3	US-09-949-016-16111	Sequence 16111, A	c 181	19.8	48.3	3245	3	US-09-759-143-929	Sequence 929, App
c 109	20.4	49.8	18011	3	US-09-949-016-17055	Sequence 17055, A	c 182	19.8	48.3	3245	3	US-10-012-896-929	Sequence 929, App
c 110	20.4	49.8	28172	3	US-09-902-540-1221	Sequence 1221, Ap	c 183	19.8	48.3	4223	3	US-09-949-016-3720	Sequence 3720, Ap
c 111	20.4	49.8	105733	3	US-09-949-016-13080	Sequence 13080, A	c 184	19.8	48.3	4223	3	US-09-949-016-3721	Sequence 3721, Ap
c 112	20.4	49.8	178883	3	US-09-949-016-12733	Sequence 12733, A	c 185	19.8	48.3	4926	2	US-08-853-310-1	Sequence 1, Appli
c 113	20.4	49.8	178883	3	US-09-949-016-13039	Sequence 13039, A	c 186	19.8	48.3	6433	3	US-08-927-219-128	Sequence 128, App
c 114	20.4	49.8	197336	3	US-09-949-016-12881	Sequence 12881, A	c 187	19.8	48.3	7546	3	US-09-902-540-801	Sequence 801, App
c 115	20.4	49.8	197337	3	US-09-949-016-14376	Sequence 14376, A	c 188	19.8	48.3	7846	3	US-09-902-540-830	Sequence 830, App
c 116	20.4	49.8	197337	3	US-09-949-002-738	Sequence 738, App	c 189	19.8	48.3	9369	3	US-10-237-551-190	Sequence 190, App
c 117	20.4	49.8	234287	3	US-09-949-002-687	Sequence 687, App	c 190	19.8	48.3	9369	3	US-10-237-551-247	Sequence 247, App
c 118	20.4	49.8	234288	3	US-09-949-016-17272	Sequence 17272, A	c 191	19.8	48.3	9440	3	US-09-949-016-15352	Sequence 15352, A
c 119	20.4	49.8	234288	3	US-09-949-002-841	Sequence 841, App	c 192	19.8	48.3	10054	3	US-09-902-540-971	Sequence 971, App
c 120	20.4	49.8	254964	3	US-09-949-016-12583	Sequence 12583, A	c 193	19.8	48.3	13489	3	US-09-949-016-15911	Sequence 15911, A
c 121	20.4	49.8	254964	3	US-09-949-016-17392	Sequence 17392, A	c 194	19.8	48.3	15125	3	US-09-949-016-14647	Sequence 14647, A
c 122	20.4	49.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli	c 195	19.8	48.3	15312	3	US-09-902-540-1115	Sequence 1115, Ap
c 123	20.4	49.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli	c 196	19.8	48.3	15312	3	US-09-902-540-1175	Sequence 1175, Ap
c 124	20.2	49.3	601	3	US-09-949-016-71198	Sequence 71198, A	c 197	19.8	48.3	20468	3	US-09-949-016-15462	Sequence 15462, A
c 125	20.2	49.3	738	3	US-09-252-991A-15795	Sequence 15795, A	c 198	19.8	48.3	20468	3	US-09-949-016-15463	Sequence 15463, A
c 126	20.2	49.3	783	3	US-09-252-991A-9421	Sequence 9421, Ap	c 199	19.8	48.3	36302	3	US-09-949-016-11998	Sequence 11998, A
c 127	20.2	49.3	873	3	US-09-252-991A-15930	Sequence 15930, A	c 200	19.8	48.3	36302	3	US-09-949-016-13891	Sequence 13891, A
c 128	20.2	49.3	927	3	US-09-252-991A-15894	Sequence 15894, A	c 201	19.8	48.3	42250	3	US-09-949-016-17171	Sequence 17171, A
c 129	20.2	49.3	1296	3	US-09-252-991A-9478	Sequence 9478, Ap	c 202	19.8	48.3	62636	3	US-09-949-016-15464	Sequence 15464, A
c 130	20.2	49.3	1650	3	US-09-252-991A-9352	Sequence 9352, Ap	c 203	19.8	48.3	62636	3	US-09-949-016-15465	Sequence 15465, A
c 131	20.2	49.3	1800	3	US-09-266-965-16	Sequence 16, Appl	c 204	19.8	48.3	100468	3	US-09-949-016-12511	Sequence 12511, A
c 132	20.2	49.3	2229	3	US-09-902-540-3307	Sequence 3307, Ap	c 205	19.8	48.3	100468	3	US-09-949-016-13725	Sequence 13725, A
c 133	20.2	49.3	3996	3	US-09-620-312D-195	Sequence 195, App	c 206	19.8	48.3	154749	3	US-09-827-688-8	Sequence 8, Appli
c 134	20.2	49.3	4749	3	US-09-614-034-189	Sequence 189, App	c 207	19.8	48.3	422592	3	US-09-949-016-14182	Sequence 14182, A
c 135	20.2	49.3	17050	3	US-09-949-016-12784	Sequence 12784, A	c 208	19.6	47.8	325	3	US-09-621-976-13184	Sequence 13184, A
c 136	20.2	49.3	17050	3	US-09-949-016-13680	Sequence 13680, A	c 209	19.6	47.8	363	3	US-09-252-991A-8215	Sequence 8215, Ap
c 137	20.2	49.3	17639	3	US-09-902-540-1153	Sequence 1153, Ap	c 210	19.6	47.8	462	3	US-09-252-991A-10080	Sequence 10080, A
c 138	20.2	49.3	31300	3	US-09-949-016-16967	Sequence 16967, A	c 211	19.6	47.8	471	3	US-09-252-991A-4718	Sequence 4718, Ap
c 139	20.2	49.3	35471	3	US-09-949-016-12957	Sequence 12957, A	c 212	19.6	47.8	601	3	US-09-949-016-23197	Sequence 23197, A
c 140	20.2	49.3	53500	3	US-09-266-965-76	Sequence 76, Appl	c 213	19.6	47.8	601	3	US-09-949-016-169586	Sequence 169586,
c 141	20.2	49.3	58443	3	US-09-949-016-13565	Sequence 13565, A	c 214	19.6	47.8	601	3	US-09-949-016-194351	Sequence 194351,
c 142	20.2	49.3	134008	3	US-09-949-016-13841	Sequence 13841, A	c 215	19.6	47.8	612	3	US-09-252-991A-4793	Sequence 4793, Ap
c 143	20	48.8	31	3	US-08-485-355B-6	Sequence 6, Appli	c 216	19.6	47.8	620	3	US-09-533-559-2114	Sequence 2114, Ap
c 144	20	48.8	259	3	US-09-008-892-3	Sequence 3, Appli	c 217	19.6	47.8	757	3	US-09-232-160-15	Sequence 15, Appl
c 145	20	48.8	386	3	US-09-513-999C-11047	Sequence 11047, A	c 218	19.6	47.8	813	3	US-09-266-965-29	Sequence 29, Appl
c 146	20	48.8	394	3	US-09-621-976-3601	Sequence 3601, Ap	c 219	19.6	47.8	954	3	US-09-252-991A-4820	Sequence 4820, Ap
c 147	20	48.8	747	3	US-09-252-991A-2924	Sequence 2924, Ap	c 220	19.6	47.8	1623	3	US-09-252-991A-9839	Sequence 9839, Ap
c 148	20	48.8	762	3	US-09-252-991A-3481	Sequence 3481, Ap	c 221	19.6	47.8	1967	3	US-09-902-540-2665	Sequence 2665, Ap
c 149	20	48.8	822	3	US-09-008-892-1	Sequence 1, Appli	c 222	19.6	47.8	2004	3	US-09-902-540-8007	Sequence 8007, Ap
c 150	20	48.8	854	3	US-09-270-767-29967	Sequence 29967, A	c 223	19.6	47.8	2093	3	US-09-620-312D-999	Sequence 999, App
c 151	20	48.8	1362	3	US-09-252-991A-2945	Sequence 2945, Ap	c 224	19.6	47.8	2124	3	US-09-902-540-7586	Sequence 7586, Ap
c 152	20	48.8	1551	3	US-09-252-991A-3034	Sequence 3034, Ap	c 225	19.6	47.8	2384	2	US-07-688-352C-27	Sequence 27, Appl
c 153	20	48.8	1597	3	US-09-270-767-13899	Sequence 13899, Ap	c 226	19.6	47.8	2384	2	US-08-474-379C-27	Sequence 27, Appl
c 154	20	48.8	1654	3	US-09-023-653-574	Sequence 574, App	c 227	19.6	47.8	2384	3	US-09-146-249A-27	Sequence 27, Appl
c 155	20	48.8	18034	3	US-09-266-965-75	Sequence 75, Appl	c 228	19.6	47.8	2384	3	US-08-206-188B-27	Sequence 27, Appl
c 156	20	48.8	34414	3	US-09-949-016-12330	Sequence 12330, A	c 229	19.6	47.8	2384	6	PCT-US91-02714-25	Sequence 25, Appl
c 157	20	48.8	34414	3	US-09-949-016-16157	Sequence 16157, A	c 230	19.6	47.8	2504	2	US-08-121-713D-63	Sequence 63, Appl
c 158	20	48.8	35256	3	US-09-949-016-11991	Sequence 11991, A	c 231	19.6	47.8	2504	2	US-08-835-268-63	Sequence 63, Appl
c 159	20	48.8	53806	3	US-09-949-016-12572	Sequence 12572, A	c 232	19.6	47.8	2504	2	US-09-060-692-63	Sequence 63, Appl
c 160	20	48.8	254405	3	US-09-949-016-14381	Sequence 14381, A	c 233	19.6	47.8	2504	3	US-08-833-391-63	Sequence 63, Appl
c 161	19.8	48.3	871	3	US-10-105-729-5	Sequence 5, Appli	c 234	19.6	47.8	2504	3	US-09-060-610-63	Sequence 63, Appl
c 162	19.8	48.3	1050	3	US-09-902-540-2539	Sequence 2539, Ap	c 235	19.6	47.8	2504	6	PCT-US94-10151A-63	Sequence 63, Appl
c 163	19.8	48.3	1093	3	US-09-270-767-13464	Sequence 13464, A	c 236	19.6	47.8	2751	3	US-09-252-991A-14671	Sequence 14671, A
c 164	19.8	48.3	1578	3	US-09-902-540-9086	Sequence 9086, Ap	c 237	19.6	47.8	2865	3	US-09-252-991A-4675	Sequence 4675, Ap
c 165	19.8	48.3	1595	3	US-09-774-528-228	Sequence 228, App	c 238	19.6	47.8	3201	3	US-09-252-991A-14959	Sequence 14959, A
c 166	19.8	48.3	1595	3	US-10-120-988-228	Sequence 228, App	c 239	19.6	47.8	3402	3	US-09-252-991A-14791	Sequence 14791, A
c 167	19.8	48.3	1638	3	US-09-484-970B-20	Sequence 20, Appl	c 240	19.6	47.8	3509	3	US-09-949-016-4254	Sequence 4254, Ap
c 168	19.8	48.3	1638	3	US-09-976-594-65	Sequence 65, Appl	c 241	19.6	47.8	3509	3	US-09-949-016-4255	Sequence 4255, Ap
c 169	19.8	48.3	1719	3	US-10-104-047-1668	Sequence 1668, Ap	c 242	19.6	47.8	3722	3	US-09-016-434-1129	Sequence 1129, Ap
c 170	19.8	48.3	2058	2	US-08-358-117-1	Sequence 1, Appli	c 243	19.6	47.8	4026	3	US-09-252-991A-10214	Sequence 10214, A

C 244	19.6	47.8	4563	3	US-09-252-991A-4765	Sequence 4765, Ap	C 317	19.4	47.3	3225	3	US-09-252-991A-4622	Sequence 4622, Ap
C 245	19.6	47.8	7704	3	US-09-902-540-743	Sequence 743, App	318	19.4	47.3	3235	3	US-09-949-016-234	Sequence 234, App
C 246	19.6	47.8	10300	3	US-09-949-016-13663	Sequence 13663, A	319	19.4	47.3	3235	3	US-09-949-016-4621	Sequence 4621, App
C 247	19.6	47.8	11922	3	US-09-902-540-1063	Sequence 1063, Ap	C 320	19.4	47.3	3639	3	US-09-435-945-2	Sequence 2, Appli
C 248	19.6	47.8	13706	3	US-09-902-540-1124	Sequence 1124, Ap	C 321	19.4	47.3	4079	3	US-09-016-434-1208	Sequence 1208, Ap
C 249	19.6	47.8	18008	3	US-09-949-016-13291	Sequence 13291, A	C 322	19.4	47.3	4098	3	US-09-949-016-3092	Sequence 3092, Ap
C 250	19.6	47.8	18331	3	US-09-866-965-96	Sequence 96, Appl	C 323	19.4	47.3	4098	3	US-09-268-866-1	Sequence 1, Appli
C 251	19.6	47.8	19167	3	US-09-949-016-16982	Sequence 16982, A	C 324	19.4	47.3	4098	3	US-09-435-945-1	Sequence 10, Appl
C 252	19.6	47.8	53500	3	US-09-266-965-76	Sequence 76, Appl	C 325	19.4	47.3	4132	3	US-09-300-958A-10	Sequence 1292, Ap
C 253	19.6	47.8	73295	3	US-09-949-016-15151	Sequence 15151, A	C 326	19.4	47.3	4204	3	US-09-023-655-1292	Sequence 8878, Ap
C 254	19.6	47.8	112239	3	US-09-949-016-13144	Sequence 13144, A	C 327	19.4	47.3	4204	3	US-10-131-827-8878	Sequence 745, App
C 255	19.6	47.8	118382	3	US-09-949-016-15996	Sequence 15996, A	C 328	19.4	47.3	5597	3	US-09-902-540-745	Sequence 784, App
C 256	19.6	47.8	118382	3	US-09-949-016-15997	Sequence 15997, A	C 329	19.4	47.3	5589	3	US-09-902-540-784	Sequence 827, App
C 257	19.6	47.8	160759	3	US-09-949-016-16514	Sequence 16514, A	C 330	19.4	47.3	7280	3	US-09-902-540-827	Sequence 14641, A
C 258	19.4	47.3	157	2	US-08-279-058B-14	Sequence 14, Appl	C 331	19.4	47.3	7585	3	US-09-949-016-14641	Sequence 1028, Ap
C 259	19.4	47.3	157	3	US-08-828-323-14	Sequence 14, Appl	C 332	19.4	47.3	10644	3	US-09-902-540-1028	Sequence 967, App
C 260	19.4	47.3	351	3	US-09-489-039A-5341	Sequence 5341, Ap	C 333	19.4	47.3	11295	3	US-09-902-540-967	Sequence 16135, A
C 261	19.4	47.3	456	3	US-09-252-991A-11642	Sequence 11642, A	C 334	19.4	47.3	17657	3	US-09-949-016-16135	Sequence 3, Appli
C 262	19.4	47.3	505	3	US-09-902-540-2	Sequence 2, Appli	C 335	19.4	47.3	18853	3	US-10-109-856-3	Sequence 3, Appli
C 263	19.4	47.3	508	3	US-09-640-211A-1730	Sequence 1730, Ap	C 336	19.4	47.3	18853	3	US-10-767-341-3	Sequence 3, Appli
C 264	19.4	47.3	601	3	US-09-949-016-39156	Sequence 39156, A	C 337	19.4	47.3	18931	3	US-09-949-016-15805	Sequence 15805, A
C 265	19.4	47.3	601	3	US-09-949-016-104752	Sequence 104752, A	C 338	19.4	47.3	19379	3	US-09-949-016-12309	Sequence 12309, A
C 266	19.4	47.3	601	3	US-09-949-016-112208	Sequence 112208, A	C 339	19.4	47.3	19379	3	US-09-949-016-13533	Sequence 13533, A
C 267	19.4	47.3	601	3	US-09-949-016-112249	Sequence 112249, A	C 340	19.4	47.3	22874	3	US-09-949-016-11976	Sequence 11976, A
C 268	19.4	47.3	601	3	US-09-949-016-136504	Sequence 136504, A	C 341	19.4	47.3	22874	3	US-09-949-016-13763	Sequence 13763, A
C 269	19.4	47.3	601	3	US-09-949-016-136505	Sequence 136505, A	C 342	19.4	47.3	23292	3	US-09-949-016-12100	Sequence 12100, A
C 270	19.4	47.3	601	3	US-09-949-016-157320	Sequence 157320, A	C 343	19.4	47.3	23292	3	US-09-949-016-12100	Sequence 12100, A
C 271	19.4	47.3	601	3	US-09-949-016-187320	Sequence 187320, A	C 344	19.4	47.3	23292	3	US-09-949-016-12025	Sequence 12025, A
C 272	19.4	47.3	601	3	US-09-949-016-187754	Sequence 187754, A	C 345	19.4	47.3	23738	3	US-09-902-540-1203	Sequence 1203, Ap
C 273	19.4	47.3	601	3	US-09-949-016-187795	Sequence 187795, A	C 346	19.4	47.3	24665	3	US-09-949-016-17134	Sequence 17134, A
C 274	19.4	47.3	644	3	US-09-621-976-2896	Sequence 2896, Ap	C 347	19.4	47.3	25165	3	US-09-453-702B-39	Sequence 39, Appl
C 275	19.4	47.3	708	3	US-09-489-039A-401	Sequence 401, Ap	C 348	19.4	47.3	25165	3	US-10-114-170-39	Sequence 39, Appl
C 276	19.4	47.3	725	3	US-09-197-801-12	Sequence 12, Appl	C 349	19.4	47.3	25733	3	US-09-902-540-1215	Sequence 1215, Ap
C 277	19.4	47.3	725	3	US-09-551-028-12	Sequence 12, Appl	C 350	19.4	47.3	25733	3	US-09-949-016-11267	Sequence 1267, A
C 278	19.4	47.3	725	3	US-09-564-595A-12	Sequence 12, Appl	C 351	19.4	47.3	25733	3	US-09-949-016-15005	Sequence 15005, A
C 279	19.4	47.3	771	3	US-09-252-991A-4804	Sequence 4804, Ap	C 352	19.4	47.3	27579	3	US-09-902-540-1232	Sequence 1232, Ap
C 280	19.4	47.3	802	3	US-09-949-016-2899	Sequence 2899, Ap	C 353	19.4	47.3	34049	3	US-09-949-016-17276	Sequence 17276, A
C 281	19.4	47.3	810	3	US-09-489-039A-46	Sequence 46, Appl	C 354	19.4	47.3	34266	3	US-09-949-016-13250	Sequence 13250, A
C 282	19.4	47.3	815	3	US-09-674-741-1	Sequence 1, Appli	C 355	19.4	47.3	35614	3	US-09-902-540-1259	Sequence 1259, Ap
C 283	19.4	47.3	815	3	US-10-379-010-1	Sequence 1, Appli	C 356	19.4	47.3	38705	3	US-09-949-016-13883	Sequence 13883, A
C 284	19.4	47.3	843	3	US-09-252-991A-5079	Sequence 5079, Ap	C 357	19.4	47.3	38705	3	US-09-949-016-13884	Sequence 13884, A
C 285	19.4	47.3	849	3	US-09-252-991A-11860	Sequence 11860, A	C 358	19.4	47.3	38954	3	US-09-949-016-12292	Sequence 12292, A
C 286	19.4	47.3	894	3	US-09-252-991A-10907	Sequence 10907, A	C 359	19.4	47.3	44998	3	US-09-949-016-12824	Sequence 12824, A
C 287	19.4	47.3	1044	3	US-09-489-039A-2314	Sequence 2314, Ap	C 360	19.4	47.3	44998	3	US-09-949-016-14832	Sequence 14832, A
C 288	19.4	47.3	1050	3	US-09-252-991A-8232	Sequence 8232, Ap	C 361	19.4	47.3	44999	3	US-09-949-016-14833	Sequence 14833, A
C 289	19.4	47.3	1185	3	US-09-894-844-71	Sequence 71, Appl	C 362	19.4	47.3	44999	3	US-09-949-016-17108	Sequence 17108, A
C 290	19.4	47.3	1206	3	US-09-602-787A-157	Sequence 157, App	C 363	19.4	47.3	44999	3	US-09-949-016-11278	Sequence 12278, A
C 291	19.4	47.3	1218	3	US-09-248-796A-1915	Sequence 1915, Ap	C 364	19.4	47.3	47122	3	US-09-949-016-15278	Sequence 16520, A
C 292	19.4	47.3	1341	3	US-09-902-540-7598	Sequence 7598, Ap	C 365	19.4	47.3	47122	3	US-09-949-016-15278	Sequence 12742, A
C 293	19.4	47.3	1410	3	US-09-252-991A-11715	Sequence 11715, Ap	C 366	19.4	47.3	97423	3	US-09-949-016-15576	Sequence 15576, A
C 294	19.4	47.3	1446	3	US-09-902-540-4331	Sequence 4331, Ap	C 367	19.4	47.3	97423	3	US-09-949-016-15762	Sequence 15762, A
C 295	19.4	47.3	1542	3	US-09-252-991A-4521	Sequence 4521, Ap	C 368	19.4	47.3	107140	3	US-09-949-016-14834	Sequence 14834, A
C 296	19.4	47.3	1581	3	US-09-252-991A-5015	Sequence 5015, Ap	C 369	19.4	47.3	168971	3	US-09-949-016-13807	Sequence 13807, A
C 297	19.4	47.3	1602	3	US-09-489-039A-340	Sequence 340, App	C 370	19.4	47.3	169998	3	US-09-676-610B-34	Sequence 24, Appl
C 298	19.4	47.3	1618	3	US-10-104-047-1463	Sequence 1463, Ap	C 371	19.4	47.3	197496	3	US-09-877-177A-10	Sequence 10, Appl
C 299	19.4	47.3	1754	3	US-09-604-978-1	Sequence 1, Appli	C 372	19.2	46.8	294	3	US-09-902-540-3915	Sequence 3915, Ap
C 300	19.4	47.3	1754	3	US-09-604-728-1	Sequence 1, Appli	C 373	19.2	46.8	300	3	US-09-252-991A-5776	Sequence 5776, Ap
C 301	19.4	47.3	1754	3	US-10-325-878-1	Sequence 1, Appli	C 374	19.2	46.8	474	4	US-09-605-703B-2343	Sequence 2343, Ap
C 302	19.4	47.3	1848	3	US-09-252-991A-10829	Sequence 10829, A	C 375	19.2	46.8	474	4	US-09-252-991A-14265	Sequence 14265, A
C 303	19.4	47.3	2169	3	US-10-237-551-150	Sequence 150, App	C 376	19.2	46.8	539	3	US-09-533-559-7664	Sequence 7664, Ap
C 304	19.4	47.3	2169	3	US-10-237-551-224	Sequence 224, App	C 377	19.2	46.8	565	3	US-08-861-774E-15	Sequence 15, Appl
C 305	19.4	47.3	2310	3	US-09-950-510-11	Sequence 11, Appl	C 378	19.2	46.8	601	3	US-09-949-016-18232	Sequence 18232, A
C 306	19.4	47.3	2407	3	US-09-023-655-812	Sequence 812, App	C 379	19.2	46.8	601	3	US-09-949-016-68820	Sequence 68820, A
C 307	19.4	47.3	2527	3	US-09-950-510-1	Sequence 1, Appli	C 380	19.2	46.8	601	3	US-09-949-016-68820	Sequence 68822, A
C 308	19.4	47.3	2537	3	US-10-104-047-1255	Sequence 1255, Ap	C 381	19.2	46.8	601	3	US-09-949-016-126462	Sequence 126462, A
C 309	19.4	47.3	2592	3	US-09-252-991A-4250	Sequence 4250, Ap	C 382	19.2	46.8	639	3	US-09-252-991A-321	Sequence 321, App
C 310	19.4	47.3	2725	3	US-09-902-540-527	Sequence 527, App	C 383	19.2	46.8	672	3	US-09-252-991A-299	Sequence 299, App
C 311	19.4	47.3	2853	3	US-09-620-312D-463	Sequence 463, App	C 384	19.2	46.8	675	3	US-09-902-540-5378	Sequence 5378, Ap
C 312	19.4	47.3	2854	3	US-09-949-016-1508	Sequence 1508, Ap	C 385	19.2	46.8	750	3	US-09-252-991A-13005	Sequence 13005, A
C 313	19.4	47.3	3050	3	US-09-902-540-5319	Sequence 5319, Ap	C 386	19.2	46.8	759	3	US-09-252-991A-309	Sequence 309, App
C 314	19.4	47.3	3116	3	US-09-976-594-283	Sequence 283, App	C 387	19.2	46.8	903	3	US-09-252-991A-12465	Sequence 12465, A
C 315	19.4	47.3	3137	3	US-09-620-312D-714	Sequence 714, App	C 388	19.2	46.8	936	3	US-09-252-991A-5835	Sequence 5835, Ap
C 316	19.4	47.3	3153	3	US-10-104-047-1302	Sequence 1302, Ap	C 389	19.2	46.8	953	3	US-09-533-559-7602	Sequence 7602, Ap

C 390	19.2	46.8	984	3	US-09-252-991A-14377	Sequence 14377, A
C 391	19.2	46.8	1125	3	US-09-489-039A-1067	Sequence 1067, Ap
C 392	19.2	46.8	1194	3	US-09-252-991A-14406	Sequence 14406, A
C 393	19.2	46.8	1251	3	US-09-252-991A-14352	Sequence 14352, A
C 394	19.2	46.8	1308	3	US-09-949-016-1374	Sequence 1374, Ap
C 395	19.2	46.8	1338	3	US-09-336-536-1	Sequence 1, Appli
C 396	19.2	46.8	1389	3	US-10-029-180-79	Sequence 79, Appl
C 397	19.2	46.8	1404	3	US-09-902-540-3398	Sequence 3398, Ap
C 398	19.2	46.8	1428	3	US-09-489-039A-3514	Sequence 3514, Ap
C 399	19.2	46.8	1470	3	US-09-252-991A-338	Sequence 338, Ap
C 400	19.2	46.8	1548	3	US-09-252-991A-5880	Sequence 5880, Ap
C 401	19.2	46.8	1554	3	US-09-252-991A-3751	Sequence 3751, Ap
C 402	19.2	46.8	1602	3	US-09-902-540-3749	Sequence 3749, Ap
C 403	19.2	46.8	1626	3	US-09-252-991A-14296	Sequence 14296, A
C 404	19.2	46.8	1689	3	US-09-252-991A-355	Sequence 355, Ap
C 405	19.2	46.8	1857	3	US-09-252-991A-5847	Sequence 5847, Ap
C 406	19.2	46.8	2031	3	US-09-252-991A-3214	Sequence 3214, Ap
C 407	19.2	46.8	2454	3	US-09-489-039A-3236	Sequence 3236, Ap
C 408	19.2	46.8	2691	3	US-09-020-743-1	Sequence 1, Appli
C 409	19.2	46.8	2765	3	US-09-949-016-3992	Sequence 3992, Ap
C 410	19.2	46.8	2843	3	US-09-949-016-207	Sequence 207, Ap
C 411	19.2	46.8	3000	3	US-08-460-269C-1	Sequence 1, Appli
C 412	19.2	46.8	3846	3	US-09-489-039A-3225	Sequence 3225, Ap
C 413	19.2	46.8	3967	3	US-09-949-016-3596	Sequence 3596, Ap
C 414	19.2	46.8	3997	3	US-09-409-648-1	Sequence 1, Appli
C 415	19.2	46.8	3997	3	US-09-409-648-2	Sequence 2, Appli
C 416	19.2	46.8	3997	3	US-09-054-272-43	Sequence 43, Appli
C 417	19.2	46.8	3997	3	US-09-949-016-30	Sequence 30, Appli
C 418	19.2	46.8	5309	3	US-09-949-016-13116	Sequence 28, Appli
C 419	19.2	46.8	5561	3	US-09-418-710-28	Sequence 28, Appli
C 420	19.2	46.8	5561	3	US-09-839-479-28	Sequence 30, Appli
C 421	19.2	46.8	5573	3	US-09-418-710-30	Sequence 30, Appli
C 422	19.2	46.8	5573	3	US-09-839-479-30	Sequence 30, Appli
C 423	19.2	46.8	5854	3	US-09-774-528-191	Sequence 191, Appl
C 424	19.2	46.8	5854	3	US-10-120-988-191	Sequence 191, Appl
C 425	19.2	46.8	6063	3	US-09-949-016-1166	Sequence 1166, Ap
C 426	19.2	46.8	7548	3	US-09-949-016-14024	Sequence 14024, A
C 427	19.2	46.8	9497	3	US-09-902-540-1054	Sequence 1054, Ap
C 428	19.2	46.8	9944	3	US-09-949-016-16552	Sequence 16552, A
C 429	19.2	46.8	10717	3	US-09-902-540-991	Sequence 991, App
C 430	19.2	46.8	14464	3	US-09-902-540-1135	Sequence 1135, Ap
C 431	19.2	46.8	14581	3	US-08-520-373D-4	Sequence 4, Appli
C 432	19.2	46.8	15297	3	US-09-817-180-3	Sequence 3, Appli
C 433	19.2	46.8	15297	3	US-10-003-295-3	Sequence 3, Appli
C 434	19.2	46.8	17593	3	US-09-949-016-12145	Sequence 12145, A
C 435	19.2	46.8	17593	3	US-09-949-016-15734	Sequence 15734, A
C 436	19.2	46.8	17897	3	US-09-902-540-1182	Sequence 1182, Ap
C 437	19.2	46.8	19152	3	US-09-949-016-12110	Sequence 12110, A
C 438	19.2	46.8	19153	3	US-09-949-016-15795	Sequence 15795, A
C 439	19.2	46.8	19862	3	US-09-902-540-1198	Sequence 1198, Ap
C 440	19.2	46.8	21375	3	US-09-902-540-1193	Sequence 1193, Ap
C 441	19.2	46.8	22481	6	US-08-367-841A-43	Sequence 43, Appli
C 442	19.2	46.8	22481	6	US-08-367-841A-43	Sequence 43, Appli
C 443	19.2	46.8	22484	3	US-09-875-223-2	Sequence 2, Appli
C 444	19.2	46.8	22484	3	US-09-875-114-2	Sequence 2, Appli
C 445	19.2	46.8	23673	3	US-09-773-816-1	Sequence 1, Appli
C 446	19.2	46.8	27463	3	US-09-949-016-11876	Sequence 11876, A
C 447	19.2	46.8	30783	3	US-09-902-540-1258	Sequence 1258, Ap
C 448	19.2	46.8	44377	2	US-08-804-227C-7	Sequence 7, Appli
C 449	19.2	46.8	44377	2	US-08-804-198-1	Sequence 1, Appli
C 450	19.2	46.8	60788	3	US-09-949-016-16789	Sequence 16789, A
C 451	19.2	46.8	61913	3	US-09-949-016-15338	Sequence 15338, A
C 452	19.2	46.8	61922	3	US-09-949-016-11772	Sequence 11772, A
C 453	19.2	46.8	80161	3	US-09-036-987A-1	Sequence 1, Appli
C 454	19.2	46.8	80161	3	US-09-370-700-1	Sequence 1, Appli
C 455	19.2	46.8	80161	3	US-09-603-207-1	Sequence 1, Appli
C 456	19.2	46.8	85854	3	US-09-949-016-12908	Sequence 12908, A
C 457	19.2	46.8	154746	3	US-09-827-688-8	Sequence 8, Appli
C 458	19.2	46.8	177869	3	US-09-949-016-13713	Sequence 13713, A
C 459	19.2	46.8	636591	3	US-09-949-016-11808	Sequence 11808, A
C 460	19.2	46.8	636591	3	US-09-949-016-13388	Sequence 13388, A
C 461	19	46.3	216	3	US-09-252-991A-35	Sequence 35, Appli
C 462	19	46.3	322	3	US-09-513-999C-12600	Sequence 12600, A
C 463	19	46.3	322	3	US-09-471-276-735	Sequence 735, App
C 464	19	46.3	435	3	US-09-252-991A-5474	Sequence 5474, Ap
C 465	19	46.3	489	3	US-09-252-991A-452	Sequence 452, App
C 466	19	46.3	513	3	US-09-252-991A-411	Sequence 411, App
C 467	19	46.3	579	3	US-09-252-991A-2876	Sequence 2876, Ap
C 468	19	46.3	582	2	US-08-722-001-23	Sequence 23, Appli
C 469	19	46.3	601	3	US-09-949-016-76658	Sequence 76658, A
C 470	19	46.3	601	3	US-09-949-016-76659	Sequence 76659, A
C 471	19	46.3	601	3	US-09-949-016-153265	Sequence 153265, A
C 472	19	46.3	601	3	US-09-949-016-178366	Sequence 178366, A
C 473	19	46.3	882	3	US-09-252-991A-16022	Sequence 16022, A
C 474	19	46.3	939	3	US-09-252-991A-16069	Sequence 16069, A
C 475	19	46.3	966	3	US-09-252-991A-15974	Sequence 15974, A
C 476	19	46.3	981	3	US-09-252-991A-431	Sequence 431, App
C 477	19	46.3	984	3	US-09-489-039A-1470	Sequence 1470, Ap
C 478	19	46.3	1017	3	US-09-902-540-6819	Sequence 6819, Ap
C 479	19	46.3	1059	3	US-09-252-991A-884	Sequence 884, App
C 480	19	46.3	1179	3	US-09-489-039A-1542	Sequence 1542, App
C 481	19	46.3	1197	3	US-09-902-540-5399	Sequence 5399, Ap
C 482	19	46.3	1206	3	US-09-252-991A-801	Sequence 801, App
C 483	19	46.3	1257	3	US-09-252-991A-5429	Sequence 5429, Ap
C 484	19	46.3	1266	3	US-09-902-540-2957	Sequence 2957, Ap
C 485	19	46.3	1302	3	US-09-252-991A-5460	Sequence 5460, Ap
C 486	19	46.3	1470	3	US-09-252-991A-369	Sequence 369, App
C 487	19	46.3	1536	3	US-09-252-991A-3182	Sequence 3182, Ap
C 488	19	46.3	1567	2	US-08-722-001-24	Sequence 24, Appli
C 489	19	46.3	1578	3	US-09-489-039A-3846	Sequence 3846, Ap
C 490	19	46.3	1617	3	US-09-252-991A-16528	Sequence 16528, A
C 491	19	46.3	1632	3	US-09-902-540-3845	Sequence 3845, Ap
C 492	19	46.3	1743	3	US-08-482-677-9	Sequence 9, Appli
C 493	19	46.3	1743	3	US-10-033-174-9	Sequence 9, Appli
C 494	19	46.3	1866	3	US-09-537-120-1	Sequence 1, Appli
C 495	19	46.3	1894	3	US-09-270-767-31098	Sequence 31098, A
C 496	19	46.3	1944	3	US-09-252-991A-16245	Sequence 16245, A
C 497	19	46.3	2070	3	US-09-252-991A-2687	Sequence 2687, Ap
C 498	19	46.3	2108	3	US-09-032-742-6	Sequence 6, Appli
C 499	19	46.3	2131	3	US-09-270-767-14846	Sequence 14846, A
C 500	19	46.3	2160	3	US-09-489-039A-6468	Sequence 6468, Ap

ALIGNMENTS

RESULT 1
US-08-323-443B-1/c
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDER, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: OLAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323.443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0372/0A462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match 100.0%; Score 41; DB 2; Length 31571;
Best Local Similarity 97.6%; Pred. No. 6.7e-05;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGG 41
|||||
DB 3633 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGTCGG 3593
|||||

RESULT 2
US-08-658-136-2
Sequence 2, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5326 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match 100.0%; Score 41; DB 3; Length 53526;
Best Local Similarity 97.6%; Pred. No. 6.9e-05;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGG 41
|||||
DB 3300 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGTCGG 3340
|||||

RESULT 3
US-08-658-136-1
Sequence 1, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match 100.0%; Score 41; DB 3; Length 53577;
Best Local Similarity 97.6%; Pred. No. 6.9e-05;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGG 41
|||||
DB 3300 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGTCGG 3340
|||||

RESULT 4
US-08-460-215A-1
Sequence 1, Application US/08460215A
Patent No. 6867288
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W

/ APPLICANT: LANDES, GREGORY M
/ APPLICANT: BURN, TIMOTHY C
/ APPLICANT: CONNORS, TIMOTHY D
/ APPLICANT: DACKOWSKI, WILLIAM
/ APPLICANT: GERMINO, GREGORY
/ APPLICANT: QIAN, FENG
/ TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: GENZYME CORPORATION
/ STREET: ONE MOUNTAIN ROAD
/ CITY: FRAMINGHAM
/ STATE: MASSACHUSETTS
/ COUNTRY: USA
/ ZIP: 01701
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA: US/08/460,215A
/ APPLICATION NUMBER: US/08/460,215A
/ FILING DATE: 02-JUN-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DUGAN, DEBORAH
/ REGISTRATION NUMBER: 37,315
/ REFERENCE/DOCKET NUMBER: GEN4-17.5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 508-872-8400
/ TELEFAX: 508-872-5415
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 53577 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-460-215A-1

Query Match 100.0%; Score 41; DB 3; Length 53577;
Best Local Similarity 97.6%; Pred. No. 6.9e-05;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
|||||
DB 3300 AACCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 3340

RESULT 5
US-09-902-540-3125/C
; Sequence 3125, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3125
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3125

Query Match 60.0%; Score 24.6; DB 3; Length 1424;
Best Local Similarity 74.4%; Pred. No. 22;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 29; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
|||||
DB 606 GCGCCCGGGGCCAGGCCCTCGATGCTGCGCGGTAGCG 568
|||||

RESULT 6
US-09-902-540-1142/C
; Sequence 1142, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1142
; LENGTH: 15268
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1142

Query Match 60.0%; Score 24.6; DB 3; Length 15268;
Best Local Similarity 74.4%; Pred. No. 25;
Matches 29; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
|||||
DB 14450 GCGCCCGGGGCCAGGCCCTCGATGCTGCGCGGTAGCG 14412
|||||

RESULT 7
US-09-270-767-7807
; Sequence 7807, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7807
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-7807

Query Match 55.1%; Score 22.6; DB 3; Length 369;
Best Local Similarity 73.0%; Pred. No. 97;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 39
|||||
DB 105 GTCTCGGATGCCACCCACAGCGCTGGAGTGGCG 141
|||||

RESULT 8
US-09-270-767-23089
; Sequence 23089, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23089
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23089

Query Match 55.1%; Score 22.6; DB 3; Length 369;
Best Local Similarity 73.0%; Pred. No. 97;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCTCCGGATGCCAGTCCCTCATCTGCTGGCCCGGCG 39
||| ||||| ||| || ||||| ||: ||
Db 105 GTCTGGGATGCCACACCCACGCGTGGAGTGGCG 141

RESULT 9

US-09-252-991A-3470/c
; Sequence 3470, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3470
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3470

Query Match 54.6%; Score 22.4; DB 3; Length 1269;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCCTCATCTGCTGGCCCGGCG 41
||| ||||| ||||| ||| ||| ||||| : |||
Db 998 AGGCTATGATGCCAGCCCCCGATGCCAGACCGCTCGCG 959

RESULT 10

US-09-949-016-12201/c
; Sequence 12201, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12201
; LENGTH: 227390
; TYPE: DNA
; ORGANISM: Human

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(227390)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12201

Query Match 54.6%; Score 22.4; DB 3; Length 227390;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCTGCTGGCCCGGCG 40
||| ||||| ||||| ||| ||| ||||| ||: ||
Db 80961 ATGCCACCTGATGCTGTCTCCCTCCCTGCTGGAGGC 80922

RESULT 11

US-09-949-016-13365/c
; Sequence 13365, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13365
; LENGTH: 227391
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(227391)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13365

Query Match 54.6%; Score 22.4; DB 3; Length 227391;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCTGCTGGCCCGGCG 40
||| ||||| ||||| ||| ||| ||||| ||: ||
Db 80961 ATGCCACCTGATGCTGTCTCCCTCCCTGCTGGAGGC 80922

RESULT 12

US-09-902-540-7196
; Sequence 7196, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7196
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Myxococcus xanthus


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RESULT 17
US-09-313-294A-4625/c
; Sequence 4625, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalugudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4625
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700348748H1
US-09-313-294A-4625

Query Match      53.2%; Score 21.8; DB 3; Length 289;
Best Local Similarity 68.3%; Pred. No. 1.8e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCGCG 41
Db 258 ACGCCTCTGGATGATTGCCCTTACCTCTGGACCTGATGG 218

RESULT 18
US-09-902-540-8880
; Sequence 8880, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8880
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8880

Query Match      53.2%; Score 21.8; DB 3; Length 687;
Best Local Similarity 68.3%; Pred. No. 1.9e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCGCG 41
Db 110 ACGCCTCCGGCGCCAGGCTTCATCGAGCGCCGCGCGTG 150

RESULT 19
US-09-902-540-945/c
; Sequence 945, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
```

```
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 945
; LENGTH: 10528
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-945

Query Match      53.2%; Score 21.8; DB 3; Length 10528;
Best Local Similarity 68.3%; Pred. No. 2.2e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCGCG 41
Db 8588 ACGCCTCCGGCGCCAGGCTTCATCGAGCGCCGCGCGTG 8548

RESULT 20
US-09-060-756-422
; Sequence 422, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 422
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-422

Query Match      52.7%; Score 21.6; DB 3; Length 230;
Best Local Similarity 72.2%; Pred. No. 2.1e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 6 TCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCGCG 41
Db 33 TCCGGATTCTGGGCTTCATCGCTCGCGCGCGTGCG 68

RESULT 21
US-09-670-314-422
; Sequence 422, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
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; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 422
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-422

Query Match 52.7%; Score 21.6; DB 3; Length 230;
Best Local Similarity 72.2%; Pred. No. 2.1e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 6 TCCGATGCCAGTCCCTCATCGTGGCCGCGG 41
Db 33 TCCGATTTCTGGCTTCATCGTCCGCGCGG 68

RESULT 22
US-09-902-540-3347
; Sequence 3347, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3347
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3347

Query Match 52.7%; Score 21.6; DB 3; Length 1689;
Best Local Similarity 72.2%; Pred. No. 2.3e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCGCGNC 38
Db 765 GCCCGCGTGGCCGCTCCCTCCGCGCGCGCGCC 800

RESULT 23
US-09-902-540-1157
; Sequence 1157, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1157
; LENGTH: 18537

; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1157

Query Match 52.7%; Score 21.6; DB 3; Length 18537;
Best Local Similarity 72.2%; Pred. No. 2.6e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCGCGNC 38
Db 1169 GCCCGCGTGGCCGCTCCCTCCGCGCGCGCGCC 1204

RESULT 24
US-09-252-991A-4962
; Sequence 4962, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4962
; LENGTH: 234
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4962

Query Match 52.2%; Score 21.4; DB 3; Length 234;
Best Local Similarity 69.2%; Pred. No. 2.4e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCGCGCG 41
Db 93 GCCGCGAATTCACCTCGCTCTTCACCGCTTGGCGCG 131

RESULT 25
US-09-540-5238/c
; Sequence 5238, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5238
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5238

Query Match 52.2%; Score 21.4; DB 3; Length 409;
Best Local Similarity 69.2%; Pred. No. 2.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCCGATGCCAGTCCCTCATCGTGGCCGCGNC 39
Db 47 ATGCTCGCGCGCCATCCACTCGTCGATGTCCCGTCG 9

```
RESULT 26
US-09-252-991A-11328/c
; Sequence 11328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11328
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11328

Query Match      52.2%; Score 21.4; DB 3; Length 444;
Best Local Similarity 77.4%; Pred. No. 2.5e+02;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      8 CGGATGCCAGTCCCTCATCGCTGCGCCGGNC 38
Db      278 CGAATGCCAGTCCGCGCGCTGCGCCAGGC 248

RESULT 27
US-09-252-991A-11294/c
; Sequence 11294, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11294
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11294

Query Match      52.2%; Score 21.4; DB 3; Length 501;
Best Local Similarity 77.4%; Pred. No. 2.5e+02;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      8 CGGATGCCAGTCCCTCATCGCTGCGCCGGNC 38
Db      337 CGAATGCCAGTCCGCGCGCTGCGCCAGGC 307

RESULT 28
US-09-252-991A-13109/c
; Sequence 13109, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
```

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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13109
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13109

Query Match      52.2%; Score 21.4; DB 3; Length 654;
Best Local Similarity 69.2%; Pred. No. 2.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGATGCCAGTCCCTCATCGCTGCGCCGGNCGCG 41
Db      390 GCAACCGCAGGCCAGTTCCTCGTCGCGCCAGCCAGCG 352

RESULT 29
US-09-252-991A-12833
; Sequence 12833, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12833
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12833

Query Match      52.2%; Score 21.4; DB 3; Length 738;
Best Local Similarity 69.2%; Pred. No. 2.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGATGCCAGTCCCTCATCGCTGCGCCGGNCGCG 41
Db      310 GCAACCGCAGGCCAGTTCCTCGTCGCGCCAGCCAGCG 348

RESULT 30
US-09-252-991A-10112/c
; Sequence 10112, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10112
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
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Query Match      52.2%; Score 21.4; DB 3; Length 909;
Best Local Similarity 69.2; Pred. No. 2.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy      3  GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
          |||
Db      275  GCCACCTGATGCCAGGACAGCTTGACCGGCTGGGGCGCG 313

```

RESULT 35
US-09-270-767-12050
; Sequence 12050, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and
; FILE REFERENCE: File Reference: 7326-0
; CURRENT APPLICATION NUMBER: US/09/270,
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12050
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12050

Query Match          52.2%; Score 21.4; DB 3; Length 1532;
Best Local Similarity 69.2%; Pred. No. 2.7e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      1 AAGCTCCGGATGCCAGTCCCTCATCGTCGTGCCCGGCG 39
Db      604 AACCCAGGATGCCAGTTCCTCAAGGATGCCCGCAATTG 642

RESULT 36
US-09-252-991A-4982/c
; Sequence 4982, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4982
; LENGTH: 2046
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4982

Query Match          52.2%; Score 21.4; DB 3; Length 2046;
Best Local Similarity 69.2%; Pred. No. 2.7e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGTCGTGCCCGGCG 41
Db      1661 GCGCGCGAATTCACCTCGCTCTTCACCCGCTTGGCGCG 1623

RESULT 37
US-09-902-540-5367/c
; Sequence 5367, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5367
; LENGTH: 4236
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5367

Query Match          52.2%; Score 21.4; DB 3; Length 4236;
Best Local Similarity 69.2%; Pred. No. 2.9e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

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Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGCCCGGNCG 39
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 341 AAGTCTCGGGCGGCACCGCCACACCGCTGTCCAGGCCG 303

RESULT 38
US-09-902-540-1037/c
; Sequence 1037, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1037
; LENGTH: 11854
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1037

Query Match 52.2%; Score 21.4; DB 3; Length 11854;
Best Local Similarity 69.2%; Pred. No. 3e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGCCCGGNCG 39
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11492 ATGCTCGCGGCCCATCCACTGTCGATGTCGCGTCG 11454

RESULT 39
US-09-902-540-1261
; Sequence 1261, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1261
; LENGTH: 34662
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1261

Query Match 52.2%; Score 21.4; DB 3; Length 34662;
Best Local Similarity 69.2%; Pred. No. 3.2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGCCCGGNCG 39
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 19290 AAGTCTCGGGCGGCACCGCCACACCGCTGTCCAGGCCG 19328

RESULT 40
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.

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; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          51.7%; Score 21.2; DB 3; Length 4403765;
Best Local Similarity 73.5%; Pred. No. 2.8e+02;
Matches 25; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      8 CGGATGCCAGTCCCTCATCGCTGGCCCGGCGG 41
Db      2011537 CGGACGCGCTCCGTAAACGCGCCGCGCCGCG 2011570

RESULT 41
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          51.7%; Score 21.2; DB 3; Length 4411529;
Best Local Similarity 73.5%; Pred. No. 2.8e+02;
Matches 25; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      8 CGGATGCCAGTCCCTCATCGCTGGCCCGGCGG 41
Db      2014147 CGGACGCGCTCCGTAAACGCGCCGCGCCGCG 2014180

RESULT 42
US-09-252-991A-13290/c
; Sequence 13290, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13290
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13290

Query Match          51.2%; Score 21; DB 3; Length 420;
Best Local Similarity 70.3%; Pred. No. 3.4e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCG 39
Db      110 GCCTTCGGTCGCTGGCGATCATCGCCGACCGCG 74

RESULT 43
US-09-252-991A-12674
; Sequence 12674, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12674
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12674

Query Match          51.2%; Score 21; DB 3; Length 624;
Best Local Similarity 70.3%; Pred. No. 3.5e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCG 39
Db      401 GCCTTCGGTCGCTGGCGATCATCGCCGACCGCG 437

RESULT 44
US-09-758-759-112
; Sequence 112, Application US/09758759
; Patent No. 6861513
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Tim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Everminomicin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(747)
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RESULT 49
US-09-902-540-8360/c
; Sequence 8360, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8360
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8360

Query Match          51.2%; Score 21; DB 3; Length 1362;
Best Local Similarity 70.3%; Pred. No. 3.7e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CTCCTCGGATGCCAGTCCCTCATCGTCGCGCCGCGNCG 40
||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 943 CTCCTCGGAGCCCGCTCCCTCAGCGCACGCGTGTGGC 907

RESULT 50
US-09-902-540-5562
; Sequence 5562, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5562
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5562

Query Match          51.2%; Score 21; DB 3; Length 1737;
Best Local Similarity 70.3%; Pred. No. 3.7e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGTCGCGCCGCGNCG 39
||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1147 GCCTCCGACGGCGAATCTCATCGCGCGCCGCGCG 1183

RESULT 51
US-09-252-991A-13124/c
; Sequence 13124, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
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; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13124
; LENGTH: 1845
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13124

Query Match          51.2%; Score 21; DB 3; Length 1845;
Best Local Similarity 70.3%; Pred. No. 3.7e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGTCGCGCCGCGNCG 39
||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 51 GCCTTCGGTCCGCTGGCGATCATCGCGCACCGCGCG 15

RESULT 52
US-10-104-047-556/c
; Sequence 556, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 556
; LENGTH: 2185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-556

Query Match          51.2%; Score 21; DB 3; Length 2185;
Best Local Similarity 82.8%; Pred. No. 3.8e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTG 30
||||| ||| ||| ||| ||| ||| ||| |||
DB 665 AGCCTCTCAATGCTGCTCCCTCATTTGCTG 637

RESULT 53
US-09-902-540-5156/c
; Sequence 5156, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5156
; LENGTH: 2421
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5156

Query Match          51.2%; Score 21; DB 3; Length 2421;
Best Local Similarity 70.3%; Pred. No. 3.8e+02;
```

Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 5 CTCGGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 795 CTCGTCAGCCACTGCCGACCGTGGCCCGGCGCG 759

RESULT 54

US-09-902-540-875
; Sequence 875, Application US/09902540
; Patent No. 6833447

; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 875

; LENGTH: 7628

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-875

Query Match 51.2%; Score 21; DB 3; Length 7628;

Best Local Similarity 70.3%; Pred. No. 4e+02;

Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCTCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 40
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 CCTCGGAGCCCGTCCCTCAGCGACGCGTGTGGC 458

RESULT 55

US-09-773-816-1/c
; Sequence 1, Application US/09773816
; Patent No. 6340774

; GENERAL INFORMATION:

; APPLICANT: Stanford University

; APPLICANT: Khosla, Chaitan

; TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR

; TITLE OF INVENTION: ANTAGONISTS

; FILE REFERENCE: 28600-20210.00

; CURRENT APPLICATION NUMBER: US/09/773,816

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/243,458

; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER: US 60/179,305

; PRIOR FILING DATE: 2000-01-31

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 23673

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(23623)

; OTHER INFORMATION: n = A,T,C or G

US-09-773-816-1

Query Match 51.2%; Score 21; DB 3; Length 23673;

Best Local Similarity 70.3%; Pred. No. 4.3e+02;

Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AGCCTCGGATGCCAGTCCCTCATCGTGGCCCGGCG 37
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1484 ACGCGTCGGATTCCCGTCCCGACTCGCGGCCAGAT 1448

RESULT 56

US-09-902-540-1254/c
; Sequence 1254, Application US/09902540
; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 1254

; LENGTH: 29559

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-1254

Query Match 51.2%; Score 21; DB 3; Length 29559;

Best Local Similarity 70.3%; Pred. No. 4.4e+02;

Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 5 CTCGGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 14752 CTCGTCAGCCACTGCCGACCGTGGCCCGGCGCG 14716

RESULT 57

US-09-902-540-1267/c
; Sequence 1267, Application US/09902540
; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 1267

; LENGTH: 41170

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)-(41170)

; OTHER INFORMATION: unsure at all n locations

US-09-902-540-1267

Query Match 51.2%; Score 21; DB 3; Length 41170;

Best Local Similarity 70.3%; Pred. No. 4.4e+02;

Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 38840 GCCTCGGACGGGAAATCCTCATCGGCGCGCGCGCG 38804

RESULT 58

US-09-949-016-16519/c

; Sequence 16519, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16519
; LENGTH: 67386
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(67386)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16519
```

```
Query Match 51.2%; Score 21; DB 3; Length 67386;
Best Local Similarity 70.3%; Pred. No. 4.5e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 2 AGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGNC 38
||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66734 AGCCTCCTGAAGCCCTCACTCATCCCTTTCCAGCC 66698
```

RESULT 59

```
US-09-758-759-1/c
; Sequence 1, Application US/09/58759
; Patent No. 6861513
```

```
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Jim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Everninomicin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 109519
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
US-09-758-759-1
```

```
Query Match 51.2%; Score 21; DB 3; Length 109519;
Best Local Similarity 70.3%; Pred. No. 4.6e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 5 CTCGGCTGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70252 CTCGGCTGGCTTCCACATCGCCGCGGCGCGG 70216
```

RESULT 60

```
US-09-949-016-12872/c
; Sequence 12872, Application US/09949016
; Patent No. 6812339
```

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12872
; LENGTH: 146095
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-12872
```

```
Query Match 51.2%; Score 21; DB 3; Length 146095;
Best Local Similarity 82.8%; Pred. No. 4.7e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 2 AGCCTCCGATGCCAGTCCCTCATCGCTG 30
||||| ||| ||| ||| ||| ||| ||| |||
Db 94296 AGCCTCTCAATGCTGTCCTCATTTGCTG 94268
```

RESULT 61

```
US-09-949-016-13239/c
; Sequence 13239, Application US/09949016
; Patent No. 6812339
```

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13239
; LENGTH: 146104
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13239
```

```
Query Match 51.2%; Score 21; DB 3; Length 146104;
Best Local Similarity 82.8%; Pred. No. 4.7e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 2 AGCCTCCGATGCCAGTCCCTCATCGCTG 30
||||| ||| ||| ||| ||| ||| ||| |||
Db 94296 AGCCTCTCAATGCTGTCCTCATTTGCTG 94268
```

RESULT 62

```
US-09-902-540-5941
; Sequence 5941, Application US/09902540
; Patent No. 6833447
```

```
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
```

; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5941
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5941

Query Match 50.7%; Score 20.8; DB 3; Length 570;
Best Local Similarity 67.5%; Pred. No. 4.1e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCGC 40
Db 446 AGGCCACCGTGGACCTGTCCCGCTCGATGGCTGTCCGC 485

RESULT 63

US-08-796-792-1/c
; Sequence 1, Application US/08796792
; Patent No. 6087163
; GENERAL INFORMATION:

; APPLICANT: Gennaro, Maria L.
; APPLICANT: Lyashchenko, Konstantin P.
; APPLICANT: Manca, Claudia M.A.
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS
; TITLE OF INVENTION: SPECIFIC PROTEINS AND GENES, MIXTURES OF ANTIGENS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 45 Rockefeller Plaza, Suite 2800
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,792
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,364
; FILING DATE: 09-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hone, William J.
; REGISTRATION NUMBER: 26,739
; REFERENCE/DOCKET NUMBER: 07763/03301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-765-5070
; TELEFAX: 212-258-2291
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 682 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 109...585

US-08-796-792-1

Query Match 50.7%; Score 20.8; DB 3; Length 682;
Best Local Similarity 67.5%; Pred. No. 4.1e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCGC 41
Db 641 AGCCTCGCGGCCAATACCTCAGCGGTGCGCTGGGCGTG 602

RESULT 64

US-09-491-795-1/c
; Sequence 1, Application US/09491795
; Patent No. 6596281
; GENERAL INFORMATION:
; APPLICANT: Gennaro, Maria L.
; APPLICANT: Lyashchenko, Konstantin P.
; APPLICANT: Manca, Claudia M.A.
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC PROTEINS AND GENES,
; TITLE OF INVENTION: MIXTURES OF ANTIGENS AND USES THEREOF
; FILE REFERENCE: 07763/028002
; CURRENT APPLICATION NUMBER: US/09/491,795
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: US 08/796,792
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: US 60/011,364
; PRIOR FILING DATE: 1996-02-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 682
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)...(585)
US-09-491-795-1

Query Match 50.7%; Score 20.8; DB 3; Length 682;
Best Local Similarity 67.5%; Pred. No. 4.1e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCGC 41
Db 641 AGCCTCGCGGCCAATACCTCAGCGGTGCGCTGGGCGTG 602

RESULT 65

US-09-902-540-194/c
; Sequence 194, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: MYXOCOCCUS XANTHUS Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 194
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-194

Query Match 50.7%; Score 20.8; DB 3; Length 958;
Best Local Similarity 67.5%; Pred. No. 4.2e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCGC 40
Db 127 AGGCCACCGTGGACCTGTCCCGCTCGATGGCTGTCCGC 88

RESULT 66

US-09-342-681C-15
; Sequence 15, Application US/09342681C


```
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16971
; LENGTH: 97196
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(97196)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16971

Query Match          50.7%; Score 20.8; DB 3; Length 97196;
Best Local Similarity 67.5%; Pred. No. 5.4e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      2 AGCCTCGGATGCCAGTCCCTCATCGTGCCTCCGCGCG 41
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      79549 AGCCACGGATGACCTCCCTAAACACCGCGCTTGC 79510

RESULT 71
US-09-949-016-16480
; Sequence 16480, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16480
; LENGTH: 225127
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(225127)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16480

Query Match          50.7%; Score 20.8; DB 3; Length 225127;
Best Local Similarity 67.5%; Pred. No. 5.5e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      2 AGCCTCGGATGCCAGTCCCTCATCGTGCCTCCGCGCG 41
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1121 AGCCCGGCGAGCCAGATCTCAGGCGCGTCCGCGCG 1160

RESULT 72
US-09-902-540-6444/c
; Sequence 6444, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
```

```
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6444
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6444

Query Match          50.2%; Score 20.6; DB 3; Length 744;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      3 GCCTCGGATGCCAGTCCCTCATCGTGCCTCCGCGGN 37
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      635 GCCTCGGCGCGAGCCCTTCATCGCTCTCGGT 601

RESULT 73
US-09-902-540-3367/c
; Sequence 3367, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3367
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3367

Query Match          50.2%; Score 20.6; DB 3; Length 777;
Best Local Similarity 81.5%; Pred. No. 4.9e+02;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      13 GCCAGTCCCTCATCGTGCCTCCGCGCG 39
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      236 GCCAGTCCCTCATCGTGCCTCCGCGCG 210

RESULT 74
US-09-758-759-201/c
; Sequence 201, Application US/09758759
; Patent No. 6861513
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Tim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Evernimycin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 201
```

```
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(927)
; OTHER INFORMATION: ORF10
US-09-758-759-201

Query Match          50.2%; Score 20.6; DB 3; Length 927;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
Db 920 CCGGGTGGCGGGCGCGCTCGCGCGCGGTAGAG 886

RESULT 75
US-09-724-797-43/c
; Sequence 43, Application US/09724797
; Patent No. 6733998
; GENERAL INFORMATION:
; APPLICANT: JON S. THORSON
; TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GENES
; TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF
; TITLE OF INVENTION: CALICHEAMICIN AND SELF-RESISTANCE THERETO
; FILE REFERENCE: 2653-40
; CURRENT APPLICATION NUMBER: US/09/724,797
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/111,325
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1347
; TYPE: DNA
; ORGANISM:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1347)
US-09-724-797-43

Query Match          50.2%; Score 20.6; DB 3; Length 1347;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
Db 94 CCGGGCGCGGGCGGTGACCGTGGCCCGGCGTG 60

RESULT 76
US-09-758-759-182/c
; Sequence 182, Application US/09758759
; Patent No. 6861513
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Tim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Everninomycin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 182
; LENGTH: 12152
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
US-09-758-759-182

Query Match          50.2%; Score 20.6; DB 3; Length 12152;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
Db 10494 CCGGGTGGCGGGCGCGCTCGCGCGCGGTAGAG 10460

RESULT 77
US-09-902-540-1048
; Sequence 1048, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1048
; LENGTH: 12865
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1048

Query Match          50.2%; Score 20.6; DB 3; Length 12865;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGTGGCCCGG 37
Db 5531 GCCTCGGGCGCGAGGCGCTTCATCGCTGCTCGGT 5565

RESULT 78
US-09-902-540-1158/c
; Sequence 1158, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1158
; LENGTH: 17125
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1158

Query Match          50.2%; Score 20.6; DB 3; Length 17125;
Best Local Similarity 81.5%; Pred. No. 5.8e+02;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 13 GCCAGTCCCTCATCGTGGCCCGGCGG 39
Db 13817 GCCAGTCCCTCATCGTGGCCCGGCGG 13791

RESULT 79
```

US-09-847-960-7/c
; Sequence 7, Application US/09847960
; Patent No. 6946247

; GENERAL INFORMATION:

; APPLICANT: Swift, Susan E.

; APPLICANT: Bogenberger, Jakob M.

; TITLE OF INVENTION: RNase PROBE PROTECTION ASSAYS IN SCREENING FOR MODULATORS OF
; FILE REFERENCE: A-69332-1/RMS/JJD

; CURRENT APPLICATION NUMBER: US/09/847,960

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/201,333

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 399

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Germline Ig Alpha-1 probe

US-09-847-960-7

Query Match 49.8%; Score 20.4; DB 3; Length 399;

Best Local Similarity 68.4%; Pred. No. 5.5e+02;

Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCGCAGTCCCTCATCGCTGCGCCGCGCGC 40

DB 102 GCCTCCGCGTGCAGCCCTCATGCGCAGGTCCACCCCTC 65

RESULT 80

US-09-266-965-27

; Sequence 27, Application US/09266965

; Patent No. 6495348

; GENERAL INFORMATION:

; APPLICANT: Sherman, D

; APPLICANT: Maco, Y

; APPLICANT: Varoglu, M

; APPLICANT: He, M

; APPLICANT: Sheldon, P

; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster

; FILE REFERENCE: 600.456US1

; CURRENT APPLICATION NUMBER: US/09/266,965

; CURRENT FILING DATE: 1999-03-12

; EARLIER APPLICATION NUMBER: US 08/624,447

; EARLIER FILING DATE: 1996-08-19

; EARLIER APPLICATION NUMBER: PCT/US94/11279

; EARLIER FILING DATE: 1994-10-06

; EARLIER APPLICATION NUMBER: US 08/133,963

; EARLIER FILING DATE: 1993-10-07

; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 27

; LENGTH: 420

; TYPE: DNA

; ORGANISM: Streptomyces lavendulae

US-09-266-965-27

Query Match 49.8%; Score 20.4; DB 3; Length 420;

Best Local Similarity 76.7%; Pred. No. 5.5e+02;

Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 12 TGCAGTCCCTCATCGCTGCGCCGCGCGG 41

DB 178 TCCAGGACCTCGTCGCGGTCCGCGCGG 207

RESULT 81

US-09-847-960-8/c

; Sequence 8, Application US/09847960

; Patent No. 6946247

; GENERAL INFORMATION:

; APPLICANT: Swift, Susan E.

; APPLICANT: Bogenberger, Jakob M.

; TITLE OF INVENTION: RNase PROBE PROTECTION ASSAYS IN SCREENING FOR MODULATORS OF
; FILE REFERENCE: A-69332-1/RMS/JJD

; CURRENT APPLICATION NUMBER: US/09/847,960

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/201,333

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 430

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Germline Ig Alpha-2 probe

US-09-847-960-8

Query Match 49.8%; Score 20.4; DB 3; Length 430;

Best Local Similarity 68.4%; Pred. No. 5.5e+02;

Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCGCAGTCCCTCATCGCTGCGCCGCGCGC 40

DB 133 GCCTCCGCGTGCAGCCCTCATGCGCAGGTCCACCCCTC 96

RESULT 82

US-09-847-960-1/c

; Sequence 1, Application US/09847960

; Patent No. 6946247

; GENERAL INFORMATION:

; APPLICANT: Swift, Susan E.

; APPLICANT: Bogenberger, Jakob M.

; TITLE OF INVENTION: RNase PROBE PROTECTION ASSAYS IN SCREENING FOR MODULATORS OF
; FILE REFERENCE: A-69332-1/RMS/JJD

; CURRENT APPLICATION NUMBER: US/09/847,960

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/201,333

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 533

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Germline Ig Alpha-2 probe

US-09-847-960-1

Query Match 49.8%; Score 20.4; DB 3; Length 533;

Best Local Similarity 68.4%; Pred. No. 5.6e+02;

Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCGCAGTCCCTCATCGCTGCGCCGCGCGC 40

DB 133 GCCTCCGCGTGCAGCCCTCATGCGCAGGTCCACCCCTC 96

RESULT 83

US-09-252-991A-1469

; Sequence 1469, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

```
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1469
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1469

Query Match          49.8%; Score 20.4; DB 3; Length 549;
Best Local Similarity 68.4%; Pred. No. 5.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGCGC 41
DB 59 CCGCAGGGTGCCAGTACGCGCGCGCGCGCGGCGGAGCG 96

RESULT 84
US-09-949-016-46393/c
; Sequence 46393, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46393
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-46393

Query Match          49.8%; Score 20.4; DB 3; Length 601;
Best Local Similarity 68.4%; Pred. No. 5.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGCGC 40
DB 488 GCGCGGGATGCCCTTCTCGCTGCGCGGCTCC 451

RESULT 85
US-09-902-540-8798
; Sequence 8798, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8798
; LENGTH: 672
; TYPE: DNA
```

```
; ORGANISM: Myxococcus xanthus
US-09-902-540-8798

Query Match          49.8%; Score 20.4; DB 3; Length 672;
Best Local Similarity 68.4%; Pred. No. 5.7e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGCGC 41
DB 184 COTCCGAGGCCACGCCGCCCGCGTGTGACCTGACGCG 221

RESULT 86
US-09-902-540-1910
; Sequence 1910, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1910
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1910

Query Match          49.8%; Score 20.4; DB 3; Length 708;
Best Local Similarity 68.4%; Pred. No. 5.7e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGCGC 40
DB 432 GCTCCGAAGAGCCGACCTCATCTCATGCGCATGACGC 469

RESULT 87
US-09-252-991A-1419
; Sequence 1419, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1419
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1419

Query Match          49.8%; Score 20.4; DB 3; Length 1056;
Best Local Similarity 68.4%; Pred. No. 5.8e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGCGC 41
DB 993 CCGCAGGGTGCCAGTACGCGCGCGCGCGCGGAGCG 1030
```

```
RESULT 88
US-09-902-540-9099/c
; Sequence 9099, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9099
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-9099

Query Match          49.8%; Score 20.4; DB 3; Length 1143;
Best Local Similarity 68.4%; Pred. No. 5.8e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3  GCCTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
      ||||| | | | | | | | | | | | | | | | | | |
Db      282 GCCTCGGAGAGCGGCACCTCATCCATGCCATGACGC 245

RESULT 89
US-09-252-991A-1239
; Sequence 1239, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1239
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1239

Query Match          49.8%; Score 20.4; DB 3; Length 1410;
Best Local Similarity 68.4%; Pred. No. 5.9e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3  GCCTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
      ||||| | | | | | | | | | | | | | | | | | |
Db      584 GCCTCGGAGAGCGGCAGCGCTGCGCCGCGGCGGC 621

RESULT 90
US-09-199-737-3/c
; Sequence 3, Application US/09199737A
; Patent No. 6287788
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Kelli E.
; APPLICANT: Branchek, Theresa A.
; APPLICANT: Gerald, Christophe P.G.
```

```
; APPLICANT: Jones, Kenneth A.
; TITLE OF INVENTION: DNA Encoding Galanin GALR3 Receptors And Uses Thereof
; FILE REFERENCE: 52241-D-PCT-US
; CURRENT APPLICATION NUMBER: US/09/199,737A
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 3
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-199-737-3

Query Match          49.8%; Score 20.4; DB 3; Length 1417;
Best Local Similarity 76.7%; Pred. No. 5.9e+02;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      12  TGCCAGTCCCTCATCGCTGGCCCGGCGC 41
      ||||| | | | | | | | | | | | | | | | | | |
Db      1375 TGGCATTGCCCATCCCTGCGCGGTGGCG 1346

RESULT 91
US-09-058-333A-3/c
; Sequence 3, Application US/09058333A
; Patent No. 6368812
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Kelli E.
; TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,333A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1281
US-09-058-333A-3

Query Match          49.8%; Score 20.4; DB 3; Length 1417;
Best Local Similarity 76.7%; Pred. No. 5.9e+02;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      12  TGCCAGTCCCTCATCGCTGGCCCGGCGC 41
```

```
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5942
; LENGTH: 1881
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5942

Query Match          49.8%; Score 20.4; DB 3; Length 1881;
Best Local Similarity 68.4%; Pred. No. 6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCGC 41
DB 1183 CCACCGGTTGTAGTCGCATCGCCAGCCGCGCGC 1146

RESULT 95
US-09-127-219B-2/c
; Sequence 2, Application US/09127219B
; Patent No. 6372772
; GENERAL INFORMATION:
; APPLICANT: KIRKPATRICK, D. LYNN
; APPLICANT: POWIS, GARTH
; TITLE OF INVENTION: INHIBITORS OF REDOX SIGNALING AND METHODS OF USING SAME
; FILE REFERENCE: 98-571-us
; CURRENT APPLICATION NUMBER: US/09/127,219B
; CURRENT FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/054,566
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2187
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-127-219B-2

Query Match          49.8%; Score 20.4; DB 3; Length 2187;
Best Local Similarity 68.4%; Pred. No. 6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGC 38
DB 903 AAGCCAGCACACTCCAGGCCACATAGCTGCCCGGAC 866

RESULT 96
US-09-595-549-1/c
; Sequence 1, Application US/09595549
; Patent No. 6511827
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Cascieri, Margaret A.
; APPLICANT: Smith, Roy G.
; APPLICANT: Sullivan, Kathleen A.
; APPLICANT: Tan, Carina
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Lynch, Kevin R.
; TITLE OF INVENTION: GALANIN RECEPTOR GALR3 AND NUCLEOTIDES
; FILE REFERENCE: 20148PCA
; CURRENT APPLICATION NUMBER: US/09/595,549
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US98/26812
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/069,725
; PRIOR FILING DATE: 1997-12-17
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1316
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1316

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Best Local Similarity 68.4%; Pred. No. 5.9e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

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RESULT 93
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; Sequence 1519, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1519
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1519

Query Match          49.8%; Score 20.4; DB 3; Length 1593;
Best Local Similarity 68.4%; Pred. No. 5.9e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCGC 41
DB 1525 CCGCAGGTGCCAGTACGCGCGCGCGCGCGCGGAGCG 1562

RESULT 94
US-09-489-039A-5942/c
; Sequence 5942, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Berton et. al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: human
US-09-595-549-1

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Best Local Similarity 76.7%; Pred. No. 6e+02;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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RESULT 97

US-09-252-991A-1366/c
; Sequence 1366, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1366
; LENGTH: 2712
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1366

Query Match 49.8%; Score 20.4; DB 3; Length 2712;
Best Local Similarity 58.4%; Pred. No. 6.1e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

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RESULT 98

US-09-799-451-480
; Sequence 480, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunging
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; POLYPEPTIDES

; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 480
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)..(2730)
US-09-799-451-480

Query Match 49.8%; Score 20.4; DB 3; Length 2733;
Best Local Similarity 58.4%; Pred. No. 6.1e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 40
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RESULT 99

US-09-016-434-1326
; Sequence 1326, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1326:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4080 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g33950
US-09-016-434-1326

Query Match 49.8%; Score 20.4; DB 3; Length 4080;
Best Local Similarity 68.4%; Pred. No. 6.2e+02;

GenCore version 5.1.8
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Title: US-09-904-968A-1_N3336_COPY_3300_3340

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Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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SUMMARIES

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6	29.8	72.7	6423	6	US-10-240-485-122
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10	24	58.5	378	7	US-10-437-963-12669
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12	23	56.1	413	3	US-09-983-965-1143
13	23	56.1	677	8	US-10-425-115-65882
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15	22.6	55.1	400	4	US-09-925-065A-243583
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17	22.6	55.1	1992	7	US-10-437-963-73709
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Sequence 423083, A					
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c 100	21.4	52.2	3680	5	US-10-128-714-1415	Sequence 1415, Ap	c 173	21	51.2	5	US-10-094-154-1079	Sequence 1079, Ap
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c 106	21.4	52.2	6037	10	US-11-097-143-1039	Sequence 1039, Ap	c 179	20.8	50.7	7	US-10-741-601-18747	Sequence 18747, A
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c 115	21.2	51.7	3288	9	US-10-450-763-21814	Sequence 21814, A	c 188	20.8	50.7	497	US-09-918-995-14415	Sequence 14415, A
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c 127	21	51.2	747	3	US-09-758-759-112	Sequence 112, App	c 200	20.8	50.7	1996	US-10-424-599-94969	Sequence 94969, A
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c 131	21	51.2	929	8	US-10-653-047-7620	Sequence 7620, Ap	c 204	20.8	50.7	27756	US-10-741-601-5682	Sequence 5682, Ap
c 132	21	51.2	956	5	US-10-027-632-171670	Sequence 171670, A	c 205	20.8	50.7	561515	US-10-741-600-17730	Sequence 17730, A
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c 156	21	51.2	2133	7	US-10-424-599-122901	Sequence 122901, A	c 229	20.6	50.2	3233	US-10-140-808-81	Sequence 81, Appl
c 157	21	51.2	2185	6	US-10-104-047-556	Sequence 556, App	c 230	20.6	50.2	3233	US-10-121-049-81	Sequence 81, Appl
c 158	21	51.2	2412	6	US-10-156-761-158	Sequence 158, App	c 231	20.6	50.2	3233	US-10-121-049-81	Sequence 81, Appl
c 159	21	51.2	3174	6	US-10-108-260A-2154	Sequence 2154, Ap	c 232	20.6	50.2	3233	US-10-123-904-81	Sequence 81, Appl
c 160	21	51.2	3672	7	US-10-282-122A-31366	Sequence 31366, A	c 233	20.6	50.2	3233	US-10-140-470-81	Sequence 81, Appl
c 161	21	51.2	3921	7	US-10-282-122A-28221	Sequence 28221, A	c 234	20.6	50.2	3233	US-10-176-918-81	Sequence 81, Appl
c 162	21	51.2	5084	7	US-10-437-963-85625	Sequence 85625, A	c 235	20.6	50.2	3233	US-10-176-918-81	Sequence 81, Appl
c 163	21	51.2	6798	3	US-09-918-740-57	Sequence 57, Appl	c 236	20.6	50.2	3233	US-10-137-865-81	Sequence 81, Appl
c 164	21	51.2	6798	8	US-10-204-434A-13	Sequence 13, Appl	c 237	20.6	50.2	3233	US-10-137-865-81	Sequence 81, Appl
c 165	21	51.2	6798	8	US-10-835-516-57	Sequence 57, Appl	c 238	20.6	50.2	3233	US-10-140-474-81	Sequence 81, Appl
c 166	21	51.2	6798	10	US-11-053-541-57	Sequence 57, Appl	c 239	20.6	50.2	3233	US-10-143-431-81	Sequence 81, Appl
c 167	21	51.2	8077	3	US-09-918-740-63	Sequence 63, Appl	c 240	20.6	50.2	3233	US-10-143-431-81	Sequence 81, Appl
c 168	21	51.2	8077	8	US-10-835-516-63	Sequence 63, Appl	c 241	20.6	50.2	3233	US-10-142-419-81	Sequence 81, Appl
c 169	21	51.2	8077	10	US-11-053-541-63	Sequence 63, Appl	c 242	20.6	50.2	3233	US-10-123-262-81	Sequence 81, Appl

389	20.6	50.2	3233	6	US-10-145-748-81	Sequence 81, Appl
390	20.6	50.2	3233	6	US-10-145-823-81	Sequence 81, Appl
391	20.6	50.2	3233	6	US-10-145-826-81	Sequence 81, Appl
392	20.6	50.2	3233	6	US-10-145-870-81	Sequence 81, Appl
393	20.6	50.2	3233	6	US-10-145-876-81	Sequence 81, Appl
394	20.6	50.2	3233	6	US-10-145-953-81	Sequence 81, Appl
395	20.6	50.2	3233	6	US-10-146-724-81	Sequence 81, Appl
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397	20.6	50.2	3233	6	US-10-146-795-81	Sequence 81, Appl
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401	20.6	50.2	3233	6	US-10-147-506-81	Sequence 81, Appl
402	20.6	50.2	3233	6	US-10-147-509-81	Sequence 81, Appl
403	20.6	50.2	3233	6	US-10-147-510-81	Sequence 81, Appl
404	20.6	50.2	3233	6	US-10-147-511-81	Sequence 81, Appl
405	20.6	50.2	3233	6	US-10-147-529-81	Sequence 81, Appl
406	20.6	50.2	3233	6	US-10-152-397-81	Sequence 81, Appl
407	20.6	50.2	3233	6	US-10-153-586-81	Sequence 81, Appl
408	20.6	50.2	3233	6	US-10-158-786-81	Sequence 81, Appl
409	20.6	50.2	3233	6	US-10-137-870-81	Sequence 81, Appl
410	20.6	50.2	3233	6	US-10-140-018-81	Sequence 81, Appl
411	20.6	50.2	3233	6	US-10-140-021-81	Sequence 81, Appl
412	20.6	50.2	3233	6	US-10-140-471-81	Sequence 81, Appl
413	20.6	50.2	3233	6	US-10-140-922-81	Sequence 81, Appl
414	20.6	50.2	3233	6	US-10-145-631-81	Sequence 81, Appl
415	20.6	50.2	3233	6	US-10-145-633-81	Sequence 81, Appl
416	20.6	50.2	3233	6	US-10-158-783-81	Sequence 81, Appl
417	20.6	50.2	3233	6	US-10-140-274-81	Sequence 81, Appl
418	20.6	50.2	3233	6	US-10-140-019-81	Sequence 81, Appl
419	20.6	50.2	3233	6	US-10-140-022-81	Sequence 81, Appl
420	20.6	50.2	3233	6	US-10-140-861-81	Sequence 81, Appl
421	20.6	50.2	3233	6	US-10-140-862-81	Sequence 81, Appl
422	20.6	50.2	3233	6	US-10-141-697-81	Sequence 81, Appl
423	20.6	50.2	3233	6	US-10-141-700-81	Sequence 81, Appl
424	20.6	50.2	3233	6	US-10-141-705-81	Sequence 81, Appl
425	20.6	50.2	3233	6	US-10-141-753-81	Sequence 81, Appl
426	20.6	50.2	3233	6	US-10-141-758-81	Sequence 81, Appl
427	20.6	50.2	3233	6	US-10-142-418-81	Sequence 81, Appl
428	20.6	50.2	3233	6	US-10-142-420-81	Sequence 81, Appl
429	20.6	50.2	3233	6	US-10-142-422-81	Sequence 81, Appl
430	20.6	50.2	3233	6	US-10-142-427-81	Sequence 81, Appl
431	20.6	50.2	3233	6	US-10-142-760-81	Sequence 81, Appl
432	20.6	50.2	3233	6	US-10-145-821-81	Sequence 81, Appl
433	20.6	50.2	3233	6	US-10-152-531-81	Sequence 81, Appl
434	20.6	50.2	3233	6	US-10-127-840A-81	Sequence 81, Appl
435	20.6	50.2	3233	6	US-10-142-424-81	Sequence 81, Appl
436	20.6	50.2	3233	6	US-10-142-761-81	Sequence 81, Appl
437	20.6	50.2	3233	6	US-10-142-763-81	Sequence 81, Appl
438	20.6	50.2	3233	6	US-10-142-765-81	Sequence 81, Appl
439	20.6	50.2	3233	6	US-10-142-887-81	Sequence 81, Appl
440	20.6	50.2	3233	6	US-10-142-888-81	Sequence 81, Appl
441	20.6	50.2	3233	6	US-10-143-034-81	Sequence 81, Appl
442	20.6	50.2	3233	6	US-10-143-116-81	Sequence 81, Appl
443	20.6	50.2	3233	6	US-10-143-117-81	Sequence 81, Appl
444	20.6	50.2	3233	6	US-10-144-957-81	Sequence 81, Appl
445	20.6	50.2	3233	6	US-10-144-992-81	Sequence 81, Appl
446	20.6	50.2	3233	6	US-10-145-015-81	Sequence 81, Appl
447	20.6	50.2	3233	6	US-10-145-090-81	Sequence 81, Appl
448	20.6	50.2	3233	6	US-10-145-091-81	Sequence 81, Appl
449	20.6	50.2	3233	6	US-10-145-629-81	Sequence 81, Appl
450	20.6	50.2	3233	6	US-10-145-630-81	Sequence 81, Appl
451	20.6	50.2	3233	6	US-10-145-747-81	Sequence 81, Appl
452	20.6	50.2	3233	6	US-10-145-752-81	Sequence 81, Appl
453	20.6	50.2	3233	6	US-10-145-754-81	Sequence 81, Appl
454	20.6	50.2	3233	6	US-10-145-755-81	Sequence 81, Appl
455	20.6	50.2	3233	6	US-10-145-818-81	Sequence 81, Appl
456	20.6	50.2	3233	6	US-10-145-820-81	Sequence 81, Appl
457	20.6	50.2	3233	6	US-10-145-872-81	Sequence 81, Appl
458	20.6	50.2	3233	6	US-10-145-873-81	Sequence 81, Appl
459	20.6	50.2	3233	6	US-10-147-481-81	Sequence 81, Appl
460	20.6	50.2	3233	6	US-10-147-482-81	Sequence 81, Appl
461	20.6	50.2	3233	6	US-10-147-503-81	Sequence 81, Appl
462	20.6	50.2	3233	6	US-10-147-522-81	Sequence 81, Appl
463	20.6	50.2	3233	6	US-10-152-401-81	Sequence 81, Appl
464	20.6	50.2	3233	6	US-10-157-783-81	Sequence 81, Appl
465	20.6	50.2	3233	6	US-10-158-792-81	Sequence 81, Appl
466	20.6	50.2	3233	6	US-10-158-462-81	Sequence 81, Appl
467	20.6	50.2	3233	6	US-10-143-035-81	Sequence 81, Appl
468	20.6	50.2	3233	6	US-10-145-751-81	Sequence 81, Appl
469	20.6	50.2	3233	6	US-10-145-822-81	Sequence 81, Appl
470	20.6	50.2	3233	6	US-10-145-824-81	Sequence 81, Appl
471	20.6	50.2	3233	6	US-10-145-827-81	Sequence 81, Appl
472	20.6	50.2	3233	6	US-10-145-869-81	Sequence 81, Appl
473	20.6	50.2	3233	6	US-10-145-875-81	Sequence 81, Appl
474	20.6	50.2	3233	6	US-10-145-877-81	Sequence 81, Appl
475	20.6	50.2	3233	6	US-10-145-958-81	Sequence 81, Appl
476	20.6	50.2	3233	6	US-10-146-787-81	Sequence 81, Appl
477	20.6	50.2	3233	6	US-10-146-790-81	Sequence 81, Appl
478	20.6	50.2	3233	6	US-10-146-793-81	Sequence 81, Appl
479	20.6	50.2	3233	6	US-10-147-480-81	Sequence 81, Appl
480	20.6	50.2	3233	6	US-10-147-485-81	Sequence 81, Appl
481	20.6	50.2	3233	6	US-10-147-486-81	Sequence 81, Appl
482	20.6	50.2	3233	6	US-10-147-487-81	Sequence 81, Appl
483	20.6	50.2	3233	6	US-10-147-490-81	Sequence 81, Appl
484	20.6	50.2	3233	6	US-10-147-494-81	Sequence 81, Appl
485	20.6	50.2	3233	6	US-10-147-498-81	Sequence 81, Appl
486	20.6	50.2	3233	6	US-10-147-514-81	Sequence 81, Appl
487	20.6	50.2	3233	6	US-10-147-524-81	Sequence 81, Appl
488	20.6	50.2	3233	6	US-10-152-379-81	Sequence 81, Appl
489	20.6	50.2	3233	6	US-10-152-394-81	Sequence 81, Appl
490	20.6	50.2	3233	6	US-10-152-406-81	Sequence 81, Appl
491	20.6	50.2	3233	6	US-10-156-847-81	Sequence 81, Appl
492	20.6	50.2	3233	6	US-10-157-778-81	Sequence 81, Appl
493	20.6	50.2	3233	6	US-10-157-799-81	Sequence 81, Appl
494	20.6	50.2	3233	6	US-10-160-504-81	Sequence 81, Appl
495	20.6	50.2	3233	6	US-10-145-634-81	Sequence 81, Appl
496	20.6	50.2	3233	6	US-10-147-520-81	Sequence 81, Appl
497	20.6	50.2	3233	6	US-10-157-781-81	Sequence 81, Appl
498	20.6	50.2	3233	6	US-10-176-989-81	Sequence 81, Appl
499	20.6	50.2	3233	6	US-10-147-491-81	Sequence 81, Appl
500	20.6	50.2	3233	6	US-10-152-378-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-09-904-968A-1
; Sequence 1, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMING, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHAKDEEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; TYPE: DNA
; LENGTH: 53522
; ORGANISM: Homo sapiens
US-09-904-968A-1
Query Match 100.0%; Score 41; DB 3; Length 53522;
Best Local Similarity 97.6%; Pred. No. 5.4e-06;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
|||||
Db 3300 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGTCGCG 3340

RESULT 2

US-10-363-345A-2651/c
; Sequence 2651, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2651
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2651
US-10-363-345A-2651

Query Match 72.7%; Score 29.8; DB 8; Length 623;
Best Local Similarity 80.5%; Pred. No. 0.14;
Matches 33; Conservative 1; Mismatches 0; Indels 7; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
|||||
Db 462 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 422

RESULT 3

US-10-363-345A-2652
; Sequence 2652, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2652
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2652
US-10-363-345A-2652

Query Match 72.7%; Score 29.8; DB 8; Length 623;
Best Local Similarity 80.5%; Pred. No. 0.14;
Matches 33; Conservative 1; Mismatches 0; Indels 7; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
|||||
Db 162 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 202

RESULT 4

US-10-363-483A-2651/c
; Sequence 2651, Application US/10363483A
; Publication No. US20050064401A1

; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2651
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2651
US-10-363-483A-2651

Query Match 72.7%; Score 29.8; DB 9; Length 623;
Best Local Similarity 80.5%; Pred. No. 0.14;
Matches 33; Conservative 1; Mismatches 0; Indels 7; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
|||||
Db 462 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 422

RESULT 5

US-10-363-483A-2652
; Sequence 2652, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2652
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2652
US-10-363-483A-2652

Query Match 72.7%; Score 29.8; DB 9; Length 623;
Best Local Similarity 80.5%; Pred. No. 0.14;
Matches 33; Conservative 1; Mismatches 0; Indels 7; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
|||||
Db 162 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 202

RESULT 6

US-10-240-485-122/c
; Sequence 122, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02

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; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 122
; LENGTH: 6423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-122

Query Match          72.7%; Score 29.8; DB 6; Length 6423;
Best Local Similarity 80.5%; Pred. No.0.1;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAGCTCGGATGCAGTCCTCATCGTCGTGGCCCCGNGCG 41
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1563 AAACCTCGAATACCAATCCCTCATCGCTAACCCGATCGCG 1523

RESULT 7
US-11-097-143-42776
; Sequence 42776, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42776
; LENGTH: 2202
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-42776

Query Match          59.0%; Score 24.2; DB 10; Length 2202;
Best Local Similarity 75.7%; Pred. No.14;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCTCATCGTCGTGGCCCCGNGCG 39
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 GTCTCCGGATGCCACACCCACAGCGCTGGAGTGGCGG 116

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US-10-425-115-65882

Query Match 56.1%; Score 23; DB 8; Length 677;
Best Local Similarity 71.8%; Pred. No. 48;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGTGGCCGCGCG 41
|||||
Db 396 GCCTTCGGCCACAGTTCCTCTGCGCGGACGACGCG 434

RESULT 14

US-09-925-065A-243582
; Sequence 243582, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 243582
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-243582

Query Match 55.1%; Score 22.6; DB 4; Length 400;
Best Local Similarity 73.0%; Pred. No. 72;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGCGATGCCAGTCCCTCATCGTGGCCGCGCGCG 41
|||||
Db 29 CGCCGGTTGCCTGCTGCTGCTGGTGGCCGCGCGCG 65

RESULT 15

US-09-925-065A-243583
; Sequence 243583, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 243583

; LENGTH: 400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-243583

Query Match 55.1%; Score 22.6; DB 4; Length 400;
Best Local Similarity 73.0%; Pred. No. 72;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 5 CTCGCGATGCCAGTCCCTCATCGTGGCCGCGCGCG 41
|||||
Db 29 CGCCGGTTGCCTGCTGCTGCTGGTGGCCGCGCGCG 65

RESULT 16

US-10-369-493-42308/c
; Sequence 42308, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 42308
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Halobacterium sp. NRC-1
US-10-369-493-42308

Query Match 55.1%; Score 22.6; DB 6; Length 768;
Best Local Similarity 73.0%; Pred. No. 66;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGTGGCCGCGCGCG 39
|||||
Db 96 GCGTCGGCGCCAGTCGCTGCGGCGTGGCCGCGCGCG 60

RESULT 17

US-10-437-963-73709
; Sequence 73709, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 73709
; LENGTH: 1992
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73965C.1
US-10-437-963-73709

Query Match 55.1%; Score 22.6; DB 7; Length 1992;
Best Local Similarity 73.0%; Pred. No. 57;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 4 CCTCCGGATCCAGTCCCTCATCGTGGCCGCGCGC 40
|||||
Db 647 CCGCTGCGGCGAGTCCCTCGGCGCTGCGGCGCGC 683

RESULT 18
US-09-997-722-118
; Sequence 118 Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-722-118

Query Match 55.1%; Score 22.6; DB 3; Length 22715;
Best Local Similarity 73.0%; Pred. No. 41;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCTTCGGATGCCAGTCCCTCATCGTGGCCCGGN 37
|||||
Db 15385 AAGCTTCGGATGCCAGTCCCTCATCGTGTGTGAG 15421

RESULT 19
US-10-487-901-5013/c
; Sequence 5013, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5013
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-5013

Query Match 54.6%; Score 22.4; DB 9; Length 622;

Best Local Similarity 70.0%; Pred. No. 80;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCCTCATCGTGGCCGCGCGC 41
|||||
Db 126 AGCTCCGGATGCCAGTCCCTCATCGTGGCGCGCGC 87

RESULT 20
US-10-425-115-72983
; Sequence 72983, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 72983
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_166559C.1
US-10-425-115-72983

Query Match 54.6%; Score 22.4; DB 8; Length 1758;
Best Local Similarity 70.0%; Pred. No. 69;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCTTCGGATGCCAGTCCCTCATCGTGGCCGCGCGC 41
|||||
Db 187 AGCCACGACAGCCAGTCCACCGCTTCCCGTGCAGCG 226

RESULT 21
US-10-496-905-631
; Sequence 631, Application US/10496905
; Publication No. US20050192215A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Zhao, Qing
; APPLICANT: Xu, Chongjun
; APPLICANT: Mulero, Julio J.
; APPLICANT: Boyle, Bryan J.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUC
; FILE REFERENCE: HYS-BICIP/US
; CURRENT APPLICATION NUMBER: US/10/496,905
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: PCT/US00/34263
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05

; PRIOR APPLICATION NUMBER: US 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/04098
; PRIOR FILING DATE: 2001-02-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 631
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-496-905-631

Query Match 54.6%; Score 22.4; DB 9; Length 2940;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTTCGGATGCCACTCCCTCATCGCTGCGCGCNCGC 40
||| || | ||| ||| ||| ||| ||| ||| |||
Db 1538 AAGACGACGACTGCTCCCTGCTCTCGTACCCTGCGC 1577

RESULT 22
US-10-496-905-629
; Sequence 629, Application US/10496905
; Publication No. US20050192215A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Y. Tom
; APPLICANT: Tang, Y. Rui
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Zhao, Qing
; APPLICANT: Xu, Chongjun
; APPLICANT: Mulero, Julio J
; APPLICANT: Boyle, Bryan J.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: HYS-BICIP/US
; CURRENT APPLICATION NUMBER: US/10/496,905
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: PCT/US00/34263
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/04098
; PRIOR FILING DATE: 2001-02-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 629
; LENGTH: 3568
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2940)
US-10-496-905-629

Query Match 54.6%; Score 22.4; DB 9; Length 3568;
Best Local Similarity 70.0%; Pred. No. 63;

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 243390
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(243390)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-462

Query Match 54.6%; Score 22.4; DB 7; Length 243390;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGNCGC 40
|||||
Db 88961 ATGCCACCTGATGCTCTCCCTCCCTGCTGGAGGC 88922

RESULT 25
US-10-027-632-174961/c
; Sequence 174961, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174961
; LENGTH: 3186778
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(3186778)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961

Query Match 54.6%; Score 22.4; DB 5; Length 3186778;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGNCGC 40
|||||
Db 2154393 AAGCTTCAGGCTGCACTTCCCTCACCCTGGTCCCTGGGC 2154354

RESULT 26
US-10-027-632-174961/c

; Sequence 174961, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174961
; LENGTH: 3186778
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(3186778)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961

Query Match 54.6%; Score 22.4; DB 6; Length 3186778;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGNCGC 40
|||||
Db 2154393 AAGCTTCAGGCTGCACTTCCCTCACCCTGGTCCCTGGGC 2154354

RESULT 27
US-10-211-028-38
; Sequence 38, Application US/10211028
; Publication No. US20050027113A1
; GENERAL INFORMATION:
; APPLICANT: CUBIST PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
; FILE REFERENCE: CUB-12 PCT CIP
; CURRENT APPLICATION NUMBER: US/10/211,028
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: PCT/US02/24310
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US01/32354
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/310,385
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 60/379,866
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Streptomyces roseosporus
US-10-211-028-38

Query Match 53.7%; Score 22; DB 8; Length 279;
Best Local Similarity 71.1%; Pred. No. 1.3e+02;

```
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 234 CCTCCGATGGTGGCCACAGCGGGTCCCGGCCCG 271
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 28
US-10-767-701-23293/c
; Sequence 23293, Application US/10767701
; Publication No. US20040172694A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 23293
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 14689033
US-10-767-701-23293

Query Match 53.7%; Score 22; DB 7; Length 548;
Best Local Similarity 71.1%; Pred. No. 1.1e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 40
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 353 GCCTCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 316

RESULT 29
US-09-770-445-425/c
; Sequence 425, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 918
```

```
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(918)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-425

Query Match 53.7%; Score 22; DB 3; Length 918;
Best Local Similarity 71.1%; Pred. No. 1.1e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGCGC 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 508 AGCTCCGATGCATGCTCTCGATCGTGGCTCGTACG 471
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 30
US-10-437-963-94320
; Sequence 94320, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 94320
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92620C.1
US-10-437-963-94320

Query Match 53.7%; Score 22; DB 7; Length 1497;
Best Local Similarity 71.1%; Pred. No. 1e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1022 CCTCCGGTGGCCCTCTCTCGGCGGCGCGCGAG 1059
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 31
US-10-282-122A-31337/c
; Sequence 31337, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
```

```
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31337
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Pseudomonas putida
US-10-282-122A-31337

Query Match      53.7%; Score 22; DB 7; Length 2145;
Best Local Similarity 71.1%; Pred. No. 95;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY  2 AGCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCG 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  985 AGCATCGGAGGACGCGCTCACGCGCGCGCGCGCG 948

RESULT 32
US-09-938-842A-48
; Sequence 48, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 48
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-48

Query Match      53.7%; Score 22; DB 3; Length 2979;
Best Local Similarity 71.1%; Pred. No. 90;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY  2 AGCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCG 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  985 AGCATCGGAGGACGCGCTCACGCGCGCGCGCGCG 948

RESULT 33
US-09-938-842A-48
; Sequence 48, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 48
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-48

Query Match      53.7%; Score 22; DB 6; Length 4257;
Best Local Similarity 71.1%; Pred. No. 86;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY  3 GCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCG 40
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  126 GCGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCG 163

RESULT 35
US-10-437-963-42040
```

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RESULT 33
US-09-938-842A-48
; Sequence 48, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 48
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-48

Query Match      53.7%; Score 22; DB 3; Length 2979;
Best Local Similarity 71.1%; Pred. No. 90;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY  2 AGCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCG 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  2598 AGCTCCGGATGCCAGTCCCTCATCGCTGCGCTCGTACG 2635

RESULT 34
US-10-369-493-24352
; Sequence 24352, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 24352
; LENGTH: 4257
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans
US-10-369-493-24352

Query Match      53.7%; Score 22; DB 6; Length 4257;
Best Local Similarity 71.1%; Pred. No. 86;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY  3 GCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCG 40
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  126 GCGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCG 163

RESULT 35
US-10-437-963-42040
```

```
; Sequence 42040, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 42040
; LENGTH: 4959
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45328C.1
US-10-437-963-42040

Query Match          53.7%; Score 22; DB 7; Length 4959;
Best Local Similarity 71.1%; Pred. No. 84;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCTCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
DB 463 CATTCGGCTGCCACTCCCTCATCGGCGCTCCGACTCG 500

RESULT 36
US-10-437-963-42038
; Sequence 42038, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 42038
; LENGTH: 5946
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45326C.1
US-10-437-963-42038

Query Match          53.7%; Score 22; DB 7; Length 5946;
Best Local Similarity 71.1%; Pred. No. 82;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCTCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
DB 463 CATTCGGCTGCCACTCCCTCATCGGCGCTCCGACTCG 500

RESULT 37
US-10-087-192-904/c
; Sequence 904, Application US/10087192
```

```
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 904
; LENGTH: 75252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-904

Query Match          53.7%; Score 22; DB 5; Length 75252;
Best Local Similarity 71.1%; Pred. No. 57;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 40
DB 50417 GGCCCTGGATGCCACACCCCTCATTCCTGCGCGGTTTCAC 50380

RESULT 38
US-10-211-028-1
; Sequence 1, Application US/10211028
; Publication No. US20050027113A1
; GENERAL INFORMATION:
; APPLICANT: CUBIST PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: CUB-12 PCT CIP
; CURRENT APPLICATION NUMBER: US/10/211,028
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: PCT/US02/24310
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US01/32354
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/310,385
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 60/379,866
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 90597
; TYPE: DNA
; ORGANISM: Streptomyces roseosporus
US-10-211-028-1

Query Match          53.7%; Score 22; DB 8; Length 90597;
Best Local Similarity 71.1%; Pred. No. 56;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCTCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
DB 14303 CCTCGCATGGTGTCCACCCAGCGGGTCCCGGCCCG 14340

RESULT 39
US-10-156-761-7469
; Sequence 7469, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
```

APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7469
TYPE: DNA
LENGTH: 564
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(564)
US-10-156-761-7469

Query Match 53.2%; Score 21.8; DB 6; Length 564;
Best Local Similarity 68.3%; Pred. No. 1.4e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 41
DB 404 ACGCCCGGATGGGAGGTCTGCTCGCCCGCTGGACGCG 444

RESULT 40

US-10-363-345A-2649
Sequence 2649, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:

APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 2649
LENGTH: 623
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-2649

Query Match 53.2%; Score 21.8; DB 8; Length 623;
Best Local Similarity 68.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 41
DB 162 AAGTTTCGGATGTTAGTTTATCATCGTTGGTTCGTCGCG 202

RESULT 41

US-10-363-345A-2650/c
Sequence 2650, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:

APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined

TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 2650
LENGTH: 623
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 2650
US-10-363-345A-2650

Query Match 53.2%; Score 21.8; DB 8; Length 623;
Best Local Similarity 68.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 41
DB 462 AAGTTTCGGATGTTAGTTTATCATCGTTGGTTCGTCGCG 422

RESULT 42

US-10-363-483A-2649
Sequence 2649, Application US/10363483A
Publication No. US20050064401A1
GENERAL INFORMATION:

APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
TITLE OF INVENTION: illnesses
FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 2649
LENGTH: 623
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-2649

Query Match 53.2%; Score 21.8; DB 9; Length 623;
Best Local Similarity 68.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 41
DB 162 AAGTTTCGGATGTTAGTTTATCATCGTTGGTTCGTCGCG 202

RESULT 43

US-10-363-483A-2650/c
Sequence 2650, Application US/10363483A
Publication No. US20050064401A1
GENERAL INFORMATION:

APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
TITLE OF INVENTION: illnesses
FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 2650
LENGTH: 623
TYPE: DNA
ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 2650
US-10-363-483A-2650

Query Match 53.2%; Score 21.8; DB 9; Length 623;
Best Local Similarity 68.3%; Pred. No. 1.3e+02;

Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41

Db 462 AAGTTTCGGATTAGTATTTTATCGTTGGTTCGGTCGCG 422

RESULT 44

US-10-425-114-36530/c
; Sequence 36530, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36530
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE117E11_FLI
US-10-425-114-36530

Query Match 53.2%; Score 21.8; DB 7; Length 963;

Best Local Similarity 68.3%; Pred. No. 1.3e+02;

Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41

Db 566 AGCGCTCGGATGATGTCCTCACCTCTGGACCTGATGGG 526

RESULT 45

US-10-425-115-87792/c
; Sequence 87792, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 87792
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_180064C.1
US-10-425-115-87792

Query Match 53.2%; Score 21.8; DB 8; Length 995;

Best Local Similarity 68.3%; Pred. No. 1.3e+02;

Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41

Db 566 AGCGCTCGGATGATGTCCTCACCTCTGGACCTGATGGG 526

RESULT 46

US-10-156-761-6527
; Sequence 6527, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-282
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6527
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1383)
US-10-156-761-6527

Query Match 53.2%; Score 21.8; DB 6; Length 1383;

Best Local Similarity 68.3%; Pred. No. 1.2e+02;

Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41

Db 1133 AGCGACCGGACGGCAGTCTCTCGTACGCGGAGCGG 1173

RESULT 47

US-10-437-963-45894
; Sequence 45894, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 45894
; LENGTH: 1891
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48814C.1
US-10-437-963-45894


```
Query Match          53.2%; Score 21.8; DB 7; Length 1891;
Best Local Similarity 68.3%; Pred. No. 1.1e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTCGGCCGCGCGG 41
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1174 ACGCACCACTACTACCTTCGGCGCGCGCGCGGCGG 1214

RESULT 48
US-10-425-115-112928
; Sequence 112928, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 112928
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_34479C.1
US-10-425-115-112928

Query Match          53.2%; Score 21.8; DB 8; Length 2976;
Best Local Similarity 75.8%; Pred. No. 1.1e+02;
Matches 25; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 5 CTCGCGATCCAGTCCCTCATCGTCGGCCGCGG 37
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2802 CGCCGAATCCGAGGCCCTCATCGCTGACCTGGA 2834

RESULT 49
US-10-437-963-50368
; Sequence 50368, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 50368
; LENGTH: 3004
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(3004)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MPT4530_52861C.1
US-10-437-963-50368

Query Match          53.2%; Score 21.8; DB 7; Length 3004;
```

```
Best Local Similarity 68.3%; Pred. No. 1.1e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTCGGCCGCGCGG 41
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 751 AAGCCTCGTTATTTGGAGTCCCTCATCACACGACCGGTGCCG 791

RESULT 50
US-10-425-115-87785/c
; Sequence 87785, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 87785
; LENGTH: 3721
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_180058C.1
US-10-425-115-87785

Query Match          53.2%; Score 21.8; DB 8; Length 3721;
Best Local Similarity 68.3%; Pred. No. 1.1e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTCGGCCGCGCGG 41
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3153 ACGCCTCGGATGATTGCCCTCACCTCTGGACCTGATGGG 3113

RESULT 51
US-10-240-485-121
; Sequence 121, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: Olek, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 121
; LENGTH: 6423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-121

Query Match          53.2%; Score 21.8; DB 6; Length 6423;
```

```
Best Local Similarity 68.3%; Pred. No. 96;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGC 41
    ||| ||||| ||| ||||| ||||| ||||| |||||
Db 4861 AAGTTTCGGATGTTAGTTTTTTTATCGTTGGTTCGGTCGC 4901

RESULT 52
US-11-097-143-1121
; Sequence 1121, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1121
; LENGTH: 6492
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-1121

Query Match 53.2%; Score 21.8; DB 10; Length 6492;
Best Local Similarity 68.3%; Pred. No. 96;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGC 41
    ||| ||||| ||| ||||| ||||| ||||| |||||
Db 238 AAGTCGGGATGCCCTCACCCTCCTGTGGTGGCCGGAAG 278

RESULT 53
US-10-915-740A-9
; Sequence 9, Application US/10915740A
; Publication No. US20050191316A1
; GENERAL INFORMATION:
; APPLICANT: Frazer, Claire M.
; APPLICANT: Hickey, Erin
; APPLICANT: Peterson, Jeremy
; APPLICANT: Tettelin, Herve
; APPLICANT: Venter, J. Craig
; APPLICANT: Massignani, Vega
; APPLICANT: Galeotti, Cesira
; APPLICANT: Mora, Manroza
; APPLICANT: Ratti, Giulio
; APPLICANT: Scarselli, Maria
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
```

```
; TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
; FILE REFERENCE: 002441.00090
; CURRENT APPLICATION NUMBER: US/10/915,740A
; CURRENT FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 09/806,866
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: USN 60/103,794
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: USN 60/132,068
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/US99/25373
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 1068
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 9941
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-915-740A-9

Query Match 53.2%; Score 21.8; DB 9; Length 9941;
Best Local Similarity 68.3%; Pred. No. 90;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGC 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1752 AAGCGCGCCTCGAGTACGGTATGGCGCGCGGATCG 1792

RESULT 54
US-11-097-143-1120
; Sequence 1120, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1120
; LENGTH: 16105
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-1120

Query Match 53.2%; Score 21.8; DB 10; Length 16105;
Best Local Similarity 68.3%; Pred. No. 85;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGC 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1238 AAGTCGGGATGCCCTCACCCTCCTGTGGTGGCCGGAAG 1278
```



```
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127507
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-127507
```

```
Query Match 52.7%; Score 21.6; DB 6; Length 633;
Best Local Similarity 72.2%; Pred. No. 1.6e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 3 GCTCCGGATGCCAGTCCCTCATCGCTGCCCGGNC 38
|||||
Db 394 GCCCTGGATCCAGTCCCTCATCGCTGGTCTGGTC 429
|||||
```

```
RESULT 59
US-10-027-632-166051/c
; Sequence 166051, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166051
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-166051
```

```
Query Match 52.7%; Score 21.6; DB 5; Length 831;
Best Local Similarity 72.2%; Pred. No. 1.5e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 4 CTTCCGGATGCCAGTCCCTCATCGCTGCCCGGNC 39
|||||
Db 454 CCTCTGCACTCCAGACCCCATCTCTGGCTCTGGCG 419
|||||
```

```
RESULT 60
US-10-027-632-166051/c
; Sequence 166051, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166051
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-166051
```

```
Query Match 52.7%; Score 21.6; DB 6; Length 831;
Best Local Similarity 72.2%; Pred. No. 1.5e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 4 CTTCCGGATGCCAGTCCCTCATCGCTGCCCGGNC 39
|||||
Db 454 CCTCTGCACTCCAGACCCCATCTCTGGCTCTGGCG 419
|||||
```

```
RESULT 61
US-10-425-115-113559
; Sequence 113559, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
```

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 113559
; LENGTH: 835
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_35046C.1
US-10-425-115-113559
```

```
Query Match 52.7%; Score 21.6; DB 8; Length 835;
Best Local Similarity 72.2%; Pred. No. 1.5e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 4 CTTCCGGATGCCAGTCCCTCATCGCTGCCCGGNC 39
|||||
Db 188 CCTCTGCTCTGCCAGCGCTCACCGCGGCCACGACG 223
|||||
```

```
RESULT 62
US-10-156-761-774
; Sequence 774, Application US/10156761
; Publication No. US20030119018A1
```

```
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 774
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; NAME/KEY: CDS
; LOCATION: (1)..(2772)
US-10-156-761-774

Query Match      52.7%; Score 21.6; DB 6; Length 2772;
Best Local Similarity 72.2%; Pred. No. 1.3e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      3 GCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
      |||||
DB      1387 GACTACGGATCCATTCCTCATCGCGCCCGGATC 1422

RESULT 63
US-10-322-281-1
; Sequence 1, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 24883
; TYPE: DNA
; ORGANISM: Mus musculus
; NAME/KEY: misc_feature
; LOCATION: (1)..(24883)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-1

Query Match      52.7%; Score 21.6; DB 7; Length 24883;
Best Local Similarity 72.2%; Pred. No. 94;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 39
      |||||
DB      6088 CTCAGGATGATGTCATCATTAGGCTGCCCGGATCG 6123

RESULT 64
US-10-470-565-1/c
; Sequence 1, Application US/10470565
; Publication No. US20040126870A1
; GENERAL INFORMATION:
; APPLICANT: Societe des Produits Nestle S.A.
```

```
; TITLE OF INVENTION: NCC2705 - the genome of a Bifidobacterium
; FILE REFERENCE: 80290/WO
; CURRENT APPLICATION NUMBER: US/10/470,565
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: EP 01102050.0
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2256646
; TYPE: DNA
; ORGANISM: Bifidobacterium longum
US-10-470-565-1

Query Match      52.7%; Score 21.6; DB 7; Length 2256646;
Best Local Similarity 72.2%; Pred. No. 49;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 39
      |||||
DB      1095460 CCTCGAAGCCACAGCCTGATCGCGGCGCTGTCCG 1095425

RESULT 65
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      52.7%; Score 21.6; DB 6; Length 9025608;
Best Local Similarity 72.2%; Pred. No. 40;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      3 GCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
      |||||
DB      937341 GACTACGGATCCATTCCTCATCGCGCCCGGATC 937306

RESULT 66
US-10-156-761-6408/c
; Sequence 6408, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
```

; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 719
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 17-LIB188-005-Q1-E1-E1
US-09-983-965-719

Query Match 52.2%; Score 21.4; DB 3; Length 381;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AGCTCCGGATGCCAGTCCCTCATCGCTGCGCCGNCGC 40
||| ||| ||| ||| ||| ||| ||| ||| ||| : ||
Db 121 AACACGGGAGACAGTCCCGCTTGGCAGGCCCTGAAGC 159

RESULT 69
US-09-983-965-1061/C
; Sequence 1061, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalegan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 1061
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 55-LIB188-019-Q1-E1-F12
US-09-983-965-1061

Query Match 52.2%; Score 21.4; DB 3; Length 381;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AGCTCCGGATGCCAGTCCCTCATCGCTGCGCCGNCGC 40
||| ||| ||| ||| ||| ||| ||| ||| ||| : ||
Db 261 AACACGGGAGACAGTCCCGCTTGGCAGGCCCTGAAGC 223

RESULT 70
US-09-983-965-1105
; Sequence 1105, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalegan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 1105
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 55-LIB188-019-Q1-E1-F12
US-09-983-965-1105

Query Match 52.2%; Score 21.4; DB 3; Length 381;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AGCTCCGGATGCCAGTCCCTCATCGCTGCGCCGNCGC 40
||| ||| ||| ||| ||| ||| ||| ||| ||| : ||
Db 261 AACACGGGAGACAGTCCCGCTTGGCAGGCCCTGAAGC 223

US-10156-761-2289/c
; Sequence 2289, Application US/10156761
; Publication NO. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI

```
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2289
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(429)
US-10-156-761-2289

Query Match          52.2%; Score 21.4; DB 6; Length 429;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCAGTCCCTCATCGTGGCCGCGCGG 41
   ||||| ||||| ||||| ||||| ||||| |||||
DB 56 GCCCGCGACGTCCGGCGTCTGTCGGCCGCGCGGAG 18
   ||||| ||||| ||||| ||||| ||||| |||||

RESULT 75
US-10-425-115-3328/c
; Sequence 3328, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 3328
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_103036C.1
US-10-425-115-3328

Query Match          52.2%; Score 21.4; DB 8; Length 477;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCAGTCCCTCATCGTGGCCGCGCGG 41
   ||||| ||||| ||||| ||||| ||||| |||||
DB 98 GCCCGCGCGCGGTCCCTCGTCTGCGTCCGATGGG 60
   ||||| ||||| ||||| ||||| ||||| |||||

RESULT 76
US-10-027-632-184352/c
; Sequence 184352, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184352
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-184352

Query Match          52.2%; Score 21.4; DB 5; Length 484;
Best Local Similarity 77.4%; Pred. No. 2e+02;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 GGATGCCAGTCCCTCATCGTGGCCGCGGCG 39
   ||||| ||||| ||||| ||||| ||||| |||||
DB 316 GGAGGCGGTCCCTCACCCTGGCCCGCAGAGG 286
   ||||| ||||| ||||| ||||| ||||| |||||

RESULT 77
US-10-027-632-184353/c
; Sequence 184353, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US/10/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/10/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US/10/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US/10/167,363
; PRIOR APPLICATION NUMBER: US/10/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US/10/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184353
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-184353

Query Match          52.2%; Score 21.4; DB 5; Length 484;
Best Local Similarity 77.4%; Pred. No. 2e+02;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 GGATGCCAGTCCCTCATCGTGGCCGCGGCG 39
   ||||| ||||| ||||| ||||| ||||| |||||
DB 316 GGAGGCGGTCCCTCACCCTGGCCCGCAGAGG 286
   ||||| ||||| ||||| ||||| ||||| |||||

RESULT 78
```



```

US-10-027-632-184352/c
; Sequence 184352, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184352
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-184352

Query Match          52.2%; Score 21.4; DB 6; Length 484;
Best Local Similarity 77.4%; Pred. No. 2e+02;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 9 GGATGCGAGTCCTCATGCTGGCCCGGCG 39
   ||| || ||||| ||||| ||||| |||
Db 316 GGAGGCGGTCCTCACCGCTGGCCAGG 286

RESULT 79
US-10-027-632-184353/c
; Sequence 184353, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184353
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-184353

```

..

; APPLICANT: OMURA, SATOSH

; APPLICANT: OMURA, SATOSH

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGNCG 39

; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7131
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1071)
US-10-156-761-7131

Query Match 52.2%; Score 21.4; DB 6; Length 1071;
Best Local Similarity 69.2%; Pred. No. 1.7e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AGCCCTCCGATGCCAGTCCCTCATCGCTGCCCGGCG 39
Db 13 ACGGACCGGACGAGTCCCTCGTCGGCGCTCGCGG 51

RESULT 86

US-10-369-493-45519/c
; Sequence 45519, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 45519

; LENGTH: 1236

; TYPE: DNA

; ORGANISM: Rhodobacter capsulatus

US-10-369-493-45519

Query Match 52.2%; Score 21.4; DB 6; Length 1236;
Best Local Similarity 69.2%; Pred. No. 1.7e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCG 41
Db 476 GCTCCGGATGCCAGGCTCATCGCGCTCCAGGTGCG 438

RESULT 87

US-10-128-558-37/c
; Sequence 37, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Wang, Zhiwei

; APPLICANT: Weng, Gezhi

; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 812A
; CURRENT APPLICATION NUMBER: US/10/128,558
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 37
; LENGTH: 1329
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (587)..(1285)
US-10-128-558-37

Query Match 52.2%; Score 21.4; DB 8; Length 1329;
Best Local Similarity 69.2%; Pred. No. 1.7e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGATGCCAGTCCCTCATCGCTGCCCGGCG 40
Db 380 AGCCTCCGATGCCCTCCCTCCCTCCCTCCCTCC 342

RESULT 88

US-10-425-115-84915/c
; Sequence 84915, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 84915

; LENGTH: 1500

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_177450C.1

US-10-425-115-84915

Query Match 52.2%; Score 21.4; DB 8; Length 1500;
Best Local Similarity 69.2%; Pred. No. 1.7e+02;


```

: FILE REFERENCE: 38-21(53222)B
: CURRENT APPLICATION NUMBER: US/10/425,115
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 369326
: SEQ ID NO 119462
: LENGTH: 2435
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: MRT4577_404
US-10-425-115-119462

```

Query Match	52.2%	Score 21.4;	DB 8;	Length 2435;
Best Local Similarity	69.2%;	Pred. No. 1.6e+02;		
Matches 27; Conservative	1;	Mismatches 11;	Indels 0	

Oy

3 GCCTCGGATGCAGTCCCTCATCGCTGGCCCCGCCGCG 41
||| ||| ||| ||| ||| ||| | | | : |||
D6

2287 GCGTTCCGATCCAAGACCTCACCTGGGTTCGGGACGCG 2249

```

RESULT 93
US-10-369-493-34212/c
; Sequence 34212, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICR
; TITLE OF INVENTION: PLANTS WITH IMPRO
; FILE REFERENCE: 38-10(52052) B
; CURRENT APPLICATION NUMBER: US/10/369,
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,03
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 34212
; LENGTH: 2751
; TYPE: DNA
; ORGANISM: Sphingomonas aromaticivoran
US-10-369-493-34212

```

Query Match 52.2%; Score 21.4; DB 6; Length 2751;
Best Local Similarity 69.2%; Pred. No. 1.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCAGTCCCTCATCGTGGCCCGGNCG 39
||| ||| ||| ||| ||| ||| ||| ||| ||| :||
Db 1763 AGGTCGCCAAGCGCAGTGCCCTCGCCGTGCCCCAGTCG 1725

```

RESULT 94
US-10-156-761-923
/ Sequence 923, Application US/10156761
/ Publication No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: IKEDA, HARUO
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HATTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDE
/ FILE REFERENCE: 249-262
/ CURRENT APPLICATION NUMBER: US/10/15
/ PRIOR FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: JP 2001-20
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-27

```

```

; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 923
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2847)
US-10-156-761-923

```

Query Match	52.2%;	Score 21.4;	DB 6;	Length 2847;
Best Local Similarity	69.2%;	Pred. No. 1.5e+02;		
Matches 27; Conservative	1;	Mismatches 11;	Indels 0	

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGNCGC 41
 ||| ||| ||| ||| ||| ||| ||| ||| : |||
Db 2173 GCCGCCGTCCGCGACTTCCTCACCGCCGCCGGGTGGCG 2211

```

RESULT 95
US-10-739-930-1807
; Sequence 1807, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 1807
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-CLUSTER13300_1
US-10-739-930-1807

```

Query Match	52.2%	Score 21.4;	DB 8;	Length 2886;
Best Local Similarity	69.2%	Pred. No. 1.5e+02;		
Matches 27; Conservative	1;	Mismatches 11;	Indels 0;	Gaps 0;

Qy

3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGCGC 41
||| ||| ||| ||| ||| ||| ||| ||| : |||
Db

600 GCGTTCCGGATCCAAGACCTCACCTGGGTGCGGAACGCG 638

```

RESULT 96
US-10-027-632-114768
; Sequence 114768, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002

```

```

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114768
; LENGTH: 3110
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114768

Query Match          52.2%   Score 21.4; DB 5; Length 3110;
Best Local Similarity 69.2%; Pred.No. 1.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy      2  AGCCTCGGATGCCAGTCCCTCATCGCTGCCCGGCGC 40
      |||||  ||  |||||  |||||  |||||  |||||  ||
Db      2786  AGCCTCCGCGCTCCCTCCCTCCCTCTCTCTGCGCGGCTC 2824

RESULT 97
US-10-027-632-114768
; Sequence 114768, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114768
; LENGTH: 3110
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114768

Query Match          52.2%   Score 21.4; DB 6; Length 3110;
Best Local Similarity 69.2%; Pred.No. 1.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy      2  AGCCTCGGATGCCAGTCCCTCATCGCTGCCCGGCGC 40
      |||||  ||  |||||  |||||  |||||  |||||  ||
Db      2786  AGCCTCCGCGCTCCCTCCCTCCCTCTCTCTGCGCGGCTC 2824

RESULT 98
US-10-128-714-2415/c
; Sequence 2415, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use

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RESULT 100
US-10-128-714-1415/c
; Sequence 1415, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1415
; LENGTH: 3880
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-1415

Query Match 52.2%; Score 21.4; DB 5; Length 3880;
Best Local Similarity 77.4%; Pred. NO. 1.5e+02;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 11 ATGCCAGTCCCTCATCGCTGGCCCGGCGG 41
||||| || ||||| ||||| : |||
Db 878 ATGCCACTCGATCATCTCTGGCCCGGCGG 848

Search completed: May 9, 2006, 22:27:44
Job time : 460 secs

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 22:23:49 ; Search time 334 Seconds
(without alignments)
499.922 Million cell updates/sec

Title: US-09-904-968A-1_N3336_COPY_3300_3340

Perfect score: 41

Sequence: 1 agcctccgagtcagctcc.....tcctcgctgcccgcgncgcg 41

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612855

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications NA New.*

1:	/SIDSS/ptodata/1/pubpna/US08_NEW_PUB.seq.1*
2:	/SIDSS/ptodata/1/pubpna/US06_NEW_PUB.seq.2*
3:	/SIDSS/ptodata/1/pubpna/US07_NEW_PUB.seq.3*
4:	/SIDSS/ptodata/1/pubpna/US08_NEW_PUB.seq.4*
5:	/SIDSS/ptodata/1/pubpna/PCT_NEW_PUB.seq.5*
6:	/SIDSS/ptodata/1/pubpna/US05_NEW_PUB.seq.6*
7:	/SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq.7*
8:	/SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq.8*
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18:	/SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq.18*
19:	/SIDSS/ptodata/1/pubpna/US60_NEW_PUB.seq.19*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 1	22.6	55.1	390	12	US-10-301-480-324267
C 2	22.6	55.1	390	12	US-10-301-480-324268
C 3	22.6	55.1	390	12	US-10-301-480-937676
C 4	22.6	55.1	390	12	US-10-301-480-937677
C 5	22.6	55.1	400	7	US-09-925-065A-243582
C 6	22.6	55.1	400	7	US-09-925-065A-243583
C 7	22.6	55.1	3008	17	US-11-010-239-114
C 8	22.6	55.1	23704	17	US-11-124-367A-2905
C 9	21.6	52.7	230	10	US-10-802-796-422
C 10	21.6	52.7	230	18	US-11-221-284-422
C 11	21.6	52.7	777	10	US-10-750-185-41952
C 12	21.6	52.7	777	10	US-10-750-623-41952
C 13	21.4	52.2	600	17	US-11-136-527-6815
C 14	21.4	52.2	630	18	US-11-285-798-28

15	21.4	52.2	1222	18	US-11-096-568A-21580
C 16	21.4	52.2	6683	17	US-11-136-527-2719
C 17	21.4	52.2	196200	17	US-11-121-086-9
C 18	21.4	52.2	246960	17	US-11-121-086-8
C 19	21.4	51.2	617	7	US-09-925-065A-404740
C 20	21.4	51.2	1025	7	US-09-925-065A-23066
C 21	21.4	51.2	1025	11	US-10-301-480-124303
C 22	21.4	51.2	1025	12	US-10-301-480-737712
C 23	21.4	51.2	1623	7	US-09-925-065A-8417
C 24	21.4	51.2	1623	11	US-10-301-480-109654
C 25	21.4	51.2	1623	12	US-10-301-480-723063
C 26	21.4	51.2	2185	18	US-11-072-512-556
C 27	21.4	51.2	3921	17	US-11-052-554A-523
C 28	20.8	50.7	518	7	US-09-925-065A-748954
C 29	20.8	50.7	891	11	US-10-517-696-5
C 30	20.8	50.7	1253	11	US-10-517-696-6
C 31	20.8	50.7	1440	18	US-11-096-568A-22339
C 32	20.8	50.7	1477	18	US-11-096-568A-19669
C 33	20.8	50.7	54985	17	US-11-124-367A-5047
C 34	20.8	50.7	113193	13	US-10-478-943D-1
C 35	20.8	50.7	163162	17	US-11-121-086-66
C 36	20.6	50.2	1206	17	US-11-052-554A-450
C 37	20.6	50.2	1209	17	US-11-052-554A-567
C 38	20.6	50.2	1297	18	US-11-096-568A-25599
C 39	20.6	50.2	1947	7	US-09-925-065A-70542
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C 42	20.6	50.2	1947	11	US-10-301-480-171782
C 43	20.6	50.2	1947	12	US-10-301-480-785190
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C 46	20.6	50.2	3233	11	US-10-973-115B-81
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C 49	20.6	50.2	3233	18	US-11-290-153-81
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C 52	20.4	49.8	201	10	US-10-995-561-57494
C 53	20.4	49.8	201	10	US-10-995-561-74443
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C 58	20.4	49.8	546	17	US-11-128-061-2397
C 59	20.4	49.8	546	17	US-11-128-061-6039
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C 62	20.4	49.8	546	18	US-11-021-492-611
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C 64	20.4	49.8	558	10	US-10-750-623-35711
C 65	20.4	49.8	626	7	US-09-925-065A-778479
C 66	20.4	49.8	632	7	US-09-925-065A-795922
C 67	20.4	49.8	750	12	US-10-301-480-612927
C 68	20.4	49.8	750	12	US-10-301-480-1226336
C 69	20.4	49.8	1074	10	US-10-467-657-1437
C 70	20.4	49.8	1234	10	US-10-947-249-148
C 71	20.4	49.8	2180	9	US-10-505-928-771
C 72	20.4	49.8	2463	17	US-11-147-047-5
C 73	20.4	49.8	2625	9	US-10-370-959-151
C 74	20.4	49.8	2643	9	US-11-036-136-1453
C 75	20.4	49.8	5994	9	US-10-505-928-701
C 76	20.4	49.8	5994	17	US-11-169-041-71
C 77	20.4	49.8	20945	10	US-10-995-561-13463
C 78	20.4	49.8	23082	10	US-10-995-561-13457
C 79	20.4	49.8	79528	10	US-10-276-233A-6
C 80	20.4	49.8	94510	10	US-10-995-561-13332
C 81	20.4	49.8	212805	17	US-11-112-908-19
C 82	20.2	49.3	553	7	US-09-925-065A-546446
C 83	20.2	49.3	553	12	US-10-301-480-524396
C 84	20.2	49.3	553	12	US-10-301-480-1137805
C 85	20.2	49.3	628	7	US-09-925-065A-717469
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C 87	20.2	49.3	658	7	US-09-925-065A-354975

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c 89	20.2	49.3	659	12	US-10-301-480-426503	Sequence 426503,	c 162	19.8	48.3	1719	18	US-11-072-512-1668	Sequence 1668, Ap
c 90	20.2	49.3	659	12	US-10-301-480-1039911	Sequence 1039911,	c 163	19.8	48.3	1759	17	US-11-096-568A-24520	Sequence 24520, A
c 91	20.2	49.3	659	12	US-10-301-480-1039912	Sequence 1039912,	c 164	19.8	48.3	2067	17	US-11-036-527-1005	Sequence 1005, Ap
c 92	20.2	49.3	1331	10	US-10-301-185-24911	Sequence 24911, A	c 165	19.8	48.3	3178	18	US-11-072-512-989	Sequence 989, App
c 93	20.2	49.3	1331	10	US-10-750-623-24911	Sequence 24911, A	c 166	19.8	48.3	3509	18	US-11-072-512-989	Sequence 7, Appli
c 94	20.2	49.3	1348	10	US-10-750-185-34602	Sequence 34602, A	c 167	19.8	48.3	4805	17	US-11-136-527-667	Sequence 667, App
c 95	20.2	49.3	1348	10	US-10-750-623-34602	Sequence 34602, A	c 168	19.8	48.3	5545	17	US-11-136-527-2815	Sequence 2815, Ap
c 96	20.2	49.3	1306	10	US-10-467-657-7961	Sequence 7961, Ap	c 169	19.8	48.3	6309	13	US-10-204-639-75	Sequence 75, Appl
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c 98	20.2	49.3	1608	10	US-10-750-623-50981	Sequence 50981, A	c 171	19.8	48.3	188682	17	US-11-112-908-23	Sequence 23, Appl
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c 107	20	48.8	620	7	US-09-925-065A-808555	Sequence 808555,	c 180	19.6	47.8	595	12	US-10-301-480-474027	Sequence 474027,
c 108	20	48.8	638	12	Sequence 529550,	Sequence 529550,	c 181	19.6	47.8	595	12	US-10-301-480-474028	Sequence 474028,
c 109	20	48.8	638	12	US-10-301-480-562950	Sequence 562950,	c 182	19.6	47.8	595	12	US-10-301-480-1087436	Sequence 1087436,
c 110	20	48.8	687	11	US-10-714-887-89	Sequence 89, Appl	c 183	19.6	47.8	595	12	US-10-301-480-1087437	Sequence 1087437,
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c 112	20	48.8	716	7	US-09-925-065A-688354	Sequence 688354,	c 185	19.6	47.8	608	7	US-09-925-065A-407422	Sequence 407422,
c 113	20	48.8	716	7	US-09-925-065A-688355	Sequence 688355,	c 186	19.6	47.8	1237	18	US-11-096-568A-16603	Sequence 16603, A
c 114	20	48.8	716	7	Sequence 688356,	Sequence 688356,	c 187	19.6	47.8	2348	7	US-09-925-065A-57360	Sequence 57360, A
c 115	20	48.8	855	18	Sequence 13696,	Sequence 13696, A	c 188	19.6	47.8	2348	11	US-10-301-480-158598	Sequence 158598,
c 116	20	48.8	1071	17	Sequence 13,	Sequence 13, Appl	c 189	19.6	47.8	2348	12	US-10-301-480-772007	Sequence 772007,
c 117	20	48.8	1071	18	Sequence 21279, A	Sequence 21279, A	c 190	19.6	47.8	2590	11	US-10-897-981-3	Sequence 3, Appli
c 118	20	48.8	1300	7	Sequence 78483, A	Sequence 78483, A	c 191	19.6	47.8	3424	10	US-10-775-169-111	Sequence 111, App
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c 120	20	48.8	1300	12	Sequence 793131,	Sequence 793131,	c 193	19.6	47.8	95604	17	US-11-124-367A-5097	Sequence 5097, Ap
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c 122	20	48.8	1729	10	Sequence 63455, A	Sequence 63455, A	c 195	19.6	47.8	348101	11	US-10-330-773-122	Sequence 122, App
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c 124	20	48.8	14603	10	US-10-750-623-63455	Sequence 63455, A	c 201	19.4	47.3	201	10	US-10-995-561-22244	Sequence 22244, A
c 125	20	48.8	128361	9	US-10-995-561-13361	Sequence 13361, A	c 197	19.4	47.3	201	10	US-10-995-561-56901	Sequence 56901, A
c 126	19.8	48.3	201	17	US-10-505-928-151	Sequence 151, App	c 198	19.4	47.3	201	10	US-10-995-561-56901	Sequence 56901, A
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c 130	19.8	48.3	521	7	US-09-925-065A-547413	Sequence 547413,	c 202	19.4	47.3	416	7	US-09-925-065A-508626	Sequence 508626,
c 131	19.8	48.3	521	12	Sequence 525363,	Sequence 525363,	c 203	19.4	47.3	417	7	US-09-925-065A-621663	Sequence 621663,
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c 133	19.8	48.3	553	7	US-09-925-065A-1138772	Sequence 1138772,	c 205	19.4	47.3	429	13	US-10-986-405-187	Sequence 187, App
c 134	19.8	48.3	553	12	Sequence 543445,	Sequence 543445,	c 206	19.4	47.3	494	7	US-09-925-065A-783256	Sequence 783256,
c 135	19.8	48.3	553	12	Sequence 524395,	Sequence 524395,	c 207	19.4	47.3	494	7	US-09-925-065A-783257	Sequence 783257,
c 136	19.8	48.3	605	7	Sequence 621667, A	Sequence 621667, A	c 208	19.4	47.3	494	7	US-09-925-065A-843676	Sequence 843676,
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c 142	19.8	48.3	703	10	US-10-750-185-54839	Sequence 54839, A	c 214	19.4	47.3	569	12	US-10-301-480-241093	Sequence 241093,
c 143	19.8	48.3	703	10	US-10-750-185-54839	Sequence 54839, A	c 215	19.4	47.3	569	12	US-10-301-480-854502	Sequence 854502,
c 144	19.8	48.3	837	10	US-10-750-185-31418	Sequence 31418, A	c 216	19.4	47.3	579	7	US-09-925-065A-527802	Sequence 527802,
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c 149	19.8	48.3	1000	10	US-10-750-185-48873	Sequence 48873, A	c 221	19.4	47.3	627	18	US-11-096-568A-97	Sequence 97, Appl
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c 154	19.8	48.3	1243	10	US-10-750-623-64805	Sequence 64805, A	c 226	19.4	47.3	850	12	US-10-301-480-574808	Sequence 574808,
c 155	19.8	48.3	1243	10	US-10-750-185-47013	Sequence 47013, A	c 227	19.4	47.3	850	12	US-10-301-480-1188217	Sequence 1188217,
c 156	19.8	48.3	1417	10	US-10-750-623-47013	Sequence 47013, A	c 228	19.4	47.3	984	12	US-10-301-480-533465	Sequence 533465,
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c 159	19.8	48.3	1480	10	Sequence 60827, A	Sequence 60827, A	c 231	19.4	47.3	985	12	US-10-301-480-1188218	Sequence 1188218,
c 160	19.8	48.3	1592	18	Sequence 60827, A	Sequence 60827, A	c 232	19.4	47.3	990	12	US-10-301-480-542195	Sequence 542195,
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					Sequence 31722, A	Sequence 31722, A						US-10-301-480-1155604	Sequence 1155604,

C 234	19.4	47.3	1034	18	US-11-096-568A-15838	Sequence 15838, A	C 307	19.4	47.3	1080000	10	US-10-928-446A-193	Sequence 193, App
C 235	19.4	47.3	1110	10	US-10-750-185-29993	Sequence 29993, A	C 308	19.4	47.3	1080000	10	US-10-928-446A-195	Sequence 195, App
C 236	19.4	47.3	1110	10	US-10-750-623-29993	Sequence 29993, A	C 309	19.4	47.3	1080000	10	US-10-928-446A-197	Sequence 197, App
C 237	19.4	47.3	1167	18	US-11-228-659-19	Sequence 19, Appl	C 310	19.4	47.3	1080000	10	US-10-928-446A-199	Sequence 199, App
C 238	19.4	47.3	1185	17	US-11-143-401-71	Sequence 71, Appl	C 311	19.4	47.3	1080000	10	US-10-928-446A-201	Sequence 201, App
C 239	19.4	47.3	1201	18	US-11-096-568A-19966	Sequence 19966, A	C 312	19.2	46.8	86	10	US-10-310-914A-203	Sequence 4203, App
C 240	19.4	47.3	1206	16	US-11-082-389-63	Sequence 63, Appl	C 313	19.2	46.8	201	17	US-11-124-367A-25367	Sequence 25367, A
C 241	19.4	47.3	1251	7	US-09-925-065A-2773	Sequence 2773, App	C 314	19.2	46.8	201	17	US-11-124-367A-25367	Sequence 25367, A
C 242	19.4	47.3	1251	11	US-10-301-480-104010	Sequence 104010, A	C 315	19.2	46.8	385	7	US-09-925-065A-469722	Sequence 469722, A
C 243	19.4	47.3	1251	11	US-10-301-480-104010	Sequence 104010, A	C 316	19.2	46.8	385	7	US-09-925-065A-469722	Sequence 469722, A
C 244	19.4	47.3	1251	11	US-10-301-480-104010	Sequence 104010, A	C 317	19.2	46.8	385	7	US-09-925-065A-469722	Sequence 469722, A
C 245	19.4	47.3	1251	12	US-10-301-480-717419	Sequence 717419, A	C 318	19.2	46.8	385	7	US-09-925-065A-469722	Sequence 469722, A
C 246	19.4	47.3	1251	12	US-10-301-480-717420	Sequence 717420, A	C 319	19.2	46.8	385	7	US-09-925-065A-469722	Sequence 469722, A
C 247	19.4	47.3	1284	11	US-10-297-341-10	Sequence 10, Appl	C 320	19.2	46.8	403	17	US-11-055-822-271	Sequence 271, App
C 248	19.4	47.3	1374	18	US-11-096-568A-2065	Sequence 2065, App	C 321	19.2	46.8	417	7	US-09-925-065A-501351	Sequence 501351, App
C 249	19.4	47.3	1432	7	US-09-925-065A-69293	Sequence 69293, A	C 322	19.2	46.8	452	7	US-09-925-065A-790392	Sequence 790392, App
C 250	19.4	47.3	1432	11	US-10-301-480-170532	Sequence 170532, A	C 323	19.2	46.8	491	7	US-09-925-065A-537194	Sequence 537194, App
C 251	19.4	47.3	1432	12	US-10-301-480-783941	Sequence 783941, A	C 324	19.2	46.8	505	7	US-09-925-065A-531645	Sequence 531645, App
C 252	19.4	47.3	1553	17	US-11-105-864-1	Sequence 1, Appl	C 325	19.2	46.8	521	18	US-11-021-492-104	Sequence 104, App
C 253	19.4	47.3	1618	18	US-11-072-512-1463	Sequence 1463, App	C 326	19.2	46.8	530	7	US-09-925-065A-500354	Sequence 500354, App
C 254	19.4	47.3	1698	18	US-11-096-568A-9856	Sequence 9856, App	C 327	19.2	46.8	543	11	US-10-301-480-117434	Sequence 117434, A
C 255	19.4	47.3	1751	7	US-09-925-065A-69096	Sequence 69096, A	C 328	19.2	46.8	543	11	US-10-301-480-117434	Sequence 117434, A
C 256	19.4	47.3	1751	11	US-10-301-480-170335	Sequence 170335, A	C 329	19.2	46.8	543	12	US-10-301-480-730843	Sequence 730843, A
C 257	19.4	47.3	1751	12	US-10-301-480-783744	Sequence 783744, A	C 330	19.2	46.8	574	11	US-10-301-480-47004	Sequence 47004, A
C 258	19.4	47.3	1934	17	US-11-105-864-7	Sequence 7, Appl	C 331	19.2	46.8	574	12	US-10-301-480-660413	Sequence 660413, A
C 259	19.4	47.3	1934	10	US-10-750-185-50132	Sequence 50132, A	C 332	19.2	46.8	598	7	US-09-925-065A-34031	Sequence 34030, A
C 260	19.4	47.3	1934	10	US-10-750-623-50132	Sequence 50132, A	C 333	19.2	46.8	598	7	US-09-925-065A-34031	Sequence 34031, A
C 261	19.4	47.3	2000	7	US-09-925-065A-679193	Sequence 679193, A	C 334	19.2	46.8	598	11	US-10-301-480-135268	Sequence 135268, App
C 262	19.4	47.3	2000	7	US-09-925-065A-679194	Sequence 679194, A	C 335	19.2	46.8	598	11	US-10-301-480-135269	Sequence 135269, App
C 263	19.4	47.3	2000	7	US-09-925-065A-679195	Sequence 679195, A	C 336	19.2	46.8	598	12	US-10-301-480-748677	Sequence 748677, App
C 264	19.4	47.3	2000	7	US-09-925-065A-679196	Sequence 679196, A	C 337	19.2	46.8	598	12	US-10-301-480-748678	Sequence 748678, App
C 265	19.4	47.3	2067	10	US-10-750-185-33091	Sequence 33091, A	C 338	19.2	46.8	623	11	US-10-301-480-52983	Sequence 52983, A
C 266	19.4	47.3	2067	10	US-10-750-623-33091	Sequence 33091, A	C 339	19.2	46.8	623	12	US-10-301-480-666392	Sequence 666392, A
C 267	19.4	47.3	2346	17	US-11-136-527-1329	Sequence 129, App	C 340	19.2	46.8	631	7	US-09-925-065A-814548	Sequence 814548, App
C 268	19.4	47.3	2537	18	US-11-072-512-1325	Sequence 1255, App	C 341	19.2	46.8	661	7	US-09-925-065A-814548	Sequence 814548, App
C 269	19.4	47.3	3133	18	US-11-072-512-1302	Sequence 1302, App	C 342	19.2	46.8	666	7	US-09-925-065A-910183	Sequence 910183, App
C 270	19.4	47.3	3236	11	US-10-501-035-79	Sequence 79, Appl	C 343	19.2	46.8	739	7	US-09-925-065A-91616	Sequence 91616, App
C 271	19.4	47.3	3419	18	US-11-228-659-17	Sequence 17, Appl	C 344	19.2	46.8	739	7	US-09-925-065A-91616	Sequence 9166, App
C 272	19.4	47.3	3579	10	US-10-858-730-143	Sequence 143, App	C 345	19.2	46.8	739	7	US-09-925-065A-91616	Sequence 9167, App
C 273	19.4	47.3	3624	9	US-10-370-959-79	Sequence 79, Appl	C 346	19.2	46.8	739	7	US-09-925-065A-91616	Sequence 9167, App
C 274	19.4	47.3	3624	9	US-10-510-508-2	Sequence 2, Appl	C 347	19.2	46.8	739	11	US-10-301-480-110401	Sequence 110401, App
C 275	19.4	47.3	4098	17	US-11-000-688-433	Sequence 433, App	C 348	19.2	46.8	739	11	US-10-301-480-110402	Sequence 110402, App
C 276	19.4	47.3	4204	9	US-10-505-928-760	Sequence 760, App	C 349	19.2	46.8	739	11	US-10-301-480-110403	Sequence 110403, App
C 277	19.4	47.3	4392	17	US-11-080-991-73	Sequence 73, Appl	C 350	19.2	46.8	739	11	US-10-301-480-110403	Sequence 110403, App
C 278	19.4	47.3	4510	17	US-11-136-527-1828	Sequence 1828, App	C 351	19.2	46.8	739	12	US-10-301-480-723810	Sequence 723810, App
C 279	19.4	47.3	4873	17	US-11-091-883-479	Sequence 479, App	C 352	19.2	46.8	739	12	US-10-301-480-723811	Sequence 723811, App
C 280	19.4	47.3	6377	10	US-10-995-561-401	Sequence 401, App	C 353	19.2	46.8	739	12	US-10-301-480-723812	Sequence 723812, App
C 281	19.4	47.3	6868	17	US-11-186-284-190	Sequence 190, App	C 354	19.2	46.8	739	12	US-10-301-480-723813	Sequence 723813, App
C 282	19.4	47.3	6891	14	US-11-251-724-2	Sequence 2, Appl	C 355	19.2	46.8	849	18	US-11-096-568A-15643	Sequence 15643, A
C 283	19.4	47.3	6891	17	US-11-101-000-2	Sequence 2, Appl	C 356	19.2	46.8	1143	17	US-11-055-822-269	Sequence 269, App
C 284	19.4	47.3	6891	17	US-11-130-945-2	Sequence 2, Appl	C 357	19.2	46.8	1303	18	US-11-096-568A-22714	Sequence 22714, App
C 285	19.4	47.3	9724	17	US-11-128-049-857	Sequence 857, App	C 358	19.2	46.8	1303	11	US-10-301-480-31025	Sequence 31025, A
C 286	19.4	47.3	9724	17	US-11-128-049-857	Sequence 857, App	C 359	19.2	46.8	1303	11	US-10-301-480-31026	Sequence 31026, A
C 287	19.4	47.3	14172	10	US-10-995-561-13226	Sequence 13226, A	C 360	19.2	46.8	1303	11	US-10-301-480-31027	Sequence 31027, A
C 288	19.4	47.3	14196	10	US-10-995-561-13429	Sequence 13429, A	C 361	19.2	46.8	1303	12	US-10-301-480-644434	Sequence 644434, App
C 289	19.4	47.3	15118	17	US-11-124-367A-5029	Sequence 5029, App	C 362	19.2	46.8	1303	12	US-10-301-480-644435	Sequence 644435, App
C 290	19.4	47.3	15876	17	US-11-052-554A-660	Sequence 660, App	C 363	19.2	46.8	1303	12	US-10-301-480-644436	Sequence 644436, App
C 291	19.4	47.3	19691	17	US-11-124-367A-5034	Sequence 5034, App	C 364	19.2	46.8	1470	10	US-10-750-185-48974	Sequence 48974, A
C 292	19.4	47.3	60729	11	US-10-330-773-841	Sequence 841, App	C 365	19.2	46.8	1470	10	US-10-750-623-48974	Sequence 48974, A
C 293	19.4	47.3	88892	11	US-10-330-773-672	Sequence 672, App	C 366	19.2	46.8	1500	17	US-11-087-100-7	Sequence 7, Appl
C 294	19.4	47.3	100000	17	US-11-124-367A-5004	Sequence 5004, App	C 367	19.2	46.8	1500	17	US-11-087-100-7	Sequence 7, Appl
C 295	19.4	47.3	101046	10	US-10-995-561-13330	Sequence 13330, A	C 368	19.2	46.8	1500	17	US-11-087-085-7	Sequence 7, Appl
C 296	19.4	47.3	159781	17	US-11-121-086-92	Sequence 92, Appl	C 369	19.2	46.8	1500	17	US-11-087-085-7	Sequence 7, Appl
C 297	19.4	47.3	185750	18	US-11-114-798-56	Sequence 56, Appl	C 370	19.2	46.8	1720	10	US-10-750-185-24896	Sequence 24896, A
C 298	19.4	47.3	212716	17	US-11-121-086-95	Sequence 95, Appl	C 371	19.2	46.8	1720	10	US-10-750-623-24896	Sequence 24896, A
C 299	19.4	47.3	220895	10	US-10-775-169-88	Sequence 88, Appl	C 372	19.2	46.8	1802	7	US-09-925-065A-78109	Sequence 78109, A
C 300	19.4	47.3	1080000	10	US-10-928-446A-1	Sequence 1, Appl	C 373	19.2	46.8	1802	7	US-09-925-065A-78110	Sequence 78110, A
C 301	19.4	47.3	1080000	10	US-10-928-446A-181	Sequence 181, App	C 374	19.2	46.8	1802	11	US-10-301-480-179348	Sequence 179348, App
C 302	19.4	47.3	1080000	10	US-10-928-446A-183	Sequence 183, App	C 375	19.2	46.8	1802	11	US-10-301-480-179349	Sequence 179349, App
C 303	19.4	47.3	1080000	10	US-10-928-446A-185	Sequence 185, App	C 376	19.2	46.8	1802	12	US-10-301-480-792757	Sequence 792757, App
C 304	19.4	47.3	1080000	10	US-10-928-446A-187	Sequence 187, App	C 377	19.2	46.8	1814	10	US-10-750-185-51922	Sequence 51922, A
C 305	19.4	47.3	1080000	10	US-10-928-446A-189	Sequence 189, App	C 378	19.2	46.8	1814	10	US-10-750-623-51922	Sequence 51922, A
C 306	19.4	47.3	1080000	10	US-10-928-446A-191	Sequence 191, App	C 379	19.2	46.8	2001	17	US-11-043-752-2129	Sequence 2129, App

380	19.2	46.8	2691	10	US-10-775-169-41	Sequence 41, Appl	453	19	46.3	2788	7	US-09-925-065A-69158	Sequence 69158, A
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383	19.2	46.8	3298	17	US-11-136-527-3261	Sequence 3261, Ap	456	19	46.3	2788	11	US-10-301-480-170395	Sequence 170395,
384	19.2	46.8	3997	17	US-11-000-688-1114	Sequence 1114, Ap	457	19	46.3	2788	11	US-10-301-480-170396	Sequence 170396,
385	19.2	46.8	4973	13	US-10-204-639-80	Sequence 80, Appl	458	19	46.3	2788	11	US-10-301-480-170397	Sequence 170397,
C 386	19.2	46.8	5677	13	US-10-960-414-349	Sequence 349, App	459	19	46.3	2788	12	US-10-301-480-783803	Sequence 783803,
C 387	19.2	46.8	5677	17	US-11-000-688-618	Sequence 618, App	460	19	46.3	2788	12	US-10-301-480-783804	Sequence 783804,
C 388	19.2	46.8	7465	9	US-10-505-928-311	Sequence 311, App	461	19	46.3	2788	12	US-10-301-480-783805	Sequence 783805,
389	19.2	46.8	8730	17	US-11-087-100-1	Sequence 1, Appl	462	19	46.3	2788	12	US-10-301-480-783806	Sequence 783806,
390	19.2	46.8	8730	17	US-11-087-084-1	Sequence 1, Appl	463	19	46.3	3893	17	US-11-136-527-2295	Sequence 2295, Ap
391	19.2	46.8	8730	17	US-11-087-085-1	Sequence 1, Appl	464	19	46.3	8280	17	US-11-000-688-641	Sequence 641, App
C 392	19.2	46.8	15510	10	US-10-995-561-13281	Sequence 13281, A	465	19	46.3	23803	10	US-10-995-561-13406	Sequence 13406, A
C 393	19.2	46.8	22868	10	US-11-201-443-43	Sequence 43, Appl	466	19	46.3	37507	10	US-10-522-037-2	Sequence 2, Appli
C 394	19.2	46.8	25868	10	US-10-995-561-13248	Sequence 13248, A	C 467	19	46.3	138808	11	US-10-330-773-905	Sequence 905, App
C 395	19.2	46.8	28933	10	US-10-995-561-13285	Sequence 13285, A	C 468	19	46.3	142605	17	US-11-121-086-64	Sequence 64, Appl
C 396	19.2	46.8	43103	10	US-10-995-561-13346	Sequence 13346, A	C 469	19	46.3	168516	17	US-11-121-086-61	Sequence 61, Appl
C 397	19.2	46.8	257645	11	US-10-330-773-266	Sequence 266, App	470	19	46.3	169495	17	US-11-121-086-61	Sequence 61, Appl
398	19	46.3	201	10	US-10-995-561-18779	Sequence 18779, A	C 471	18.8	45.9	201	10	US-10-995-561-8624	Sequence 8624, Ap
399	19	46.3	341	7	US-09-925-065A-16934	Sequence 416934,	C 472	18.8	45.9	201	10	US-10-995-561-32707	Sequence 32707, A
400	19	46.3	341	7	US-09-925-065A-416935	Sequence 416935,	C 473	18.8	45.9	201	10	US-10-995-561-45482	Sequence 45482, A
401	19	46.3	341	7	US-09-925-065A-416936	Sequence 416936,	C 474	18.8	45.9	201	10	US-10-995-561-47203	Sequence 47203, A
402	19	46.3	341	7	US-09-925-065A-416937	Sequence 416937,	C 475	18.8	45.9	201	10	US-10-995-561-60927	Sequence 60927, A
403	19	46.3	379	7	US-09-925-065A-248632	Sequence 248632,	C 476	18.8	45.9	201	10	US-10-995-561-77410	Sequence 77410, A
404	19	46.3	388	12	US-10-301-480-328613	Sequence 328613,	C 477	18.8	45.9	472	12	US-10-301-480-350308	Sequence 350308,
405	19	46.3	388	12	US-10-301-480-942022	Sequence 942022,	C 478	18.8	45.9	472	12	US-10-301-480-963717	Sequence 963717,
C 406	19	46.3	507	7	US-09-925-065A-497331	Sequence 497331,	C 479	18.8	45.9	473	7	US-09-925-065A-273050	Sequence 273050,
C 407	19	46.3	527	7	US-09-925-065A-481730	Sequence 481730,	C 480	18.8	45.9	506	17	US-11-128-061-3386	Sequence 3386, Ap
C 408	19	46.3	550	7	US-09-925-065A-575784	Sequence 575784,	C 481	18.8	45.9	506	17	US-11-128-049-3386	Sequence 7028, Ap
C 409	19	46.3	554	7	US-09-925-065A-545616	Sequence 545616,	C 482	18.8	45.9	506	17	US-11-128-049-3386	Sequence 3386, Ap
C 410	19	46.3	585	7	US-09-925-065A-351221	Sequence 351221,	C 483	18.8	45.9	506	17	US-11-128-049-7028	Sequence 7028, Ap
C 411	19	46.3	587	12	US-10-301-480-423125	Sequence 423125,	C 484	18.8	45.9	532	18	US-11-086-568A-10554	Sequence 10554, A
C 412	19	46.3	587	12	US-10-301-480-1036534	Sequence 1036534,	C 485	18.8	45.9	539	7	US-09-925-065A-931955	Sequence 931955,
413	19	46.3	632	7	US-09-925-065A-481730	Sequence 543858	C 486	18.8	45.9	563	11	US-10-301-480-6383	Sequence 6383, Ap
414	19	46.3	647	12	US-10-301-480-268286	Sequence 268286,	C 487	18.8	45.9	563	12	US-10-301-480-619792	Sequence 619792,
415	19	46.3	647	12	US-10-301-480-1871695	Sequence 881695,	C 488	18.8	45.9	587	7	US-09-925-065A-743199	Sequence 743199,
416	19	46.3	648	7	US-09-925-065A-177126	Sequence 177126,	C 489	18.8	45.9	593	7	US-09-925-065A-43611	Sequence 43611, A
417	19	46.3	666	7	US-09-925-065A-72163	Sequence 72163, A	C 490	18.8	45.9	593	7	US-09-925-065A-750466	Sequence 750466,
418	19	46.3	666	11	US-10-301-480-773402	Sequence 773402,	C 491	18.8	45.9	593	11	US-10-301-480-144849	Sequence 144849,
419	19	46.3	666	12	US-10-301-480-786811	Sequence 786811,	C 492	18.8	45.9	593	12	US-10-301-480-758258	Sequence 758258,
420	19	46.3	669	12	US-10-301-480-220272	Sequence 220272,	C 493	18.8	45.9	594	7	US-09-925-065A-367184	Sequence 367184,
421	19	46.3	669	12	US-10-301-480-320273	Sequence 320273,	C 494	18.8	45.9	594	12	US-10-301-480-437532	Sequence 437532,
422	19	46.3	669	12	US-10-301-480-833681	Sequence 833681,	C 495	18.8	45.9	594	12	US-10-301-480-437532	Sequence 437532,
423	19	46.3	669	12	US-10-301-480-833682	Sequence 833682,	C 496	18.8	45.9	594	12	US-10-301-480-1050941	Sequence 1050941,
424	19	46.3	670	7	US-09-925-065A-122101	Sequence 122101,	C 497	18.8	45.9	595	7	US-09-925-065A-546918	Sequence 546918,
425	19	46.3	670	7	US-09-925-065A-122102	Sequence 122102,	C 498	18.8	45.9	595	12	US-10-301-480-524868	Sequence 524868,
426	19	46.3	769	18	US-11-096-568A-4531	Sequence 4531, Ap	C 499	18.8	45.9	595	12	US-10-301-480-524869	Sequence 524869,
427	19	46.3	952	17	US-11-128-061-826	Sequence 826, App	C 500	18.8	45.9	595	12	US-10-301-480-1138277	Sequence 1138277,
428	19	46.3	952	17	US-11-128-049-826	Sequence 826, App							
C 429	19	46.3	957	17	US-11-136-527-1484	Sequence 1484, Ap							
430	19	46.3	957	17	US-11-136-527-5580	Sequence 5580, Ap							
431	19	46.3	977	12	US-10-301-480-570506	Sequence 570506,							
C 432	19	46.3	977	12	US-10-301-480-1183915	Sequence 1183915,							
C 433	19	46.3	977	12	US-10-301-480-320272	Sequence 320272,							
C 434	19	46.3	977	12	US-10-301-480-320273	Sequence 320273,							
C 435	19	46.3	977	12	US-10-301-480-833681	Sequence 833681,							
C 436	19	46.3	1035	10	US-10-750-185-56691	Sequence 56691, A							
C 437	19	46.3	1035	10	US-10-750-623-56691	Sequence 56691, A							
438	19	46.3	1176	10	US-10-392-234A-49	Sequence 49, Appl							
439	19	46.3	1309	10	US-10-750-185-60398	Sequence 60398, A							
C 440	19	46.3	1309	10	US-10-750-623-60398	Sequence 60398, A							
C 441	19	46.3	1336	18	US-11-096-568A-21078	Sequence 21078, A							
442	19	46.3	1400	17	US-11-136-527-5713	Sequence 5713, Ap							
443	19	46.3	1726	7	US-09-925-065A-704759	Sequence 704759,							
444	19	46.3	2003	7	US-09-925-065A-699708	Sequence 699708,							
445	19	46.3	2003	7	US-09-925-065A-699709	Sequence 699709,							
446	19	46.3	2003	7	US-09-925-065A-699710	Sequence 699710,							
447	19	46.3	2003	7	US-09-925-065A-699711	Sequence 699711,							
C 448	19	46.3	2047	7	US-09-925-065A-678586	Sequence 678586,							
449	19	46.3	2475	17	US-11-136-527-1617	Sequence 1617, Ap							
C 450	19	46.3	2717	18	US-11-072-512-47	Sequence 47, Appl							
451	19	46.3	2788	7	US-09-925-065A-69155	Sequence 69155, A							
452	19	46.3	2788	7	US-09-925-065A-69156	Sequence 69156, A							
					Sequence 69157, A								

ALIGNMENTS

RESULT 1
US-10-301-480-324267/c
; Sequence 324267, Application US/10301480
; Publication NO. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1228618
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324267
; LENGTH: 390
; TYPE: DNA

[illegible]

Query Match 53.7%; Score 22; DB 17; Length 23704;
Best Local Similarity 71.1%; Pred. No. 91;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCGCCGCGCGC 40
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6147 GCCTGGGGGTCAGGCTCCCATCCATCGTGGCCCGCGCC 6110

RESULT 9

US-10-802-796-422
; Sequence 422, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIESER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 422
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (145)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (230)
; OTHER INFORMATION: a, t, c or g
US-10-802-796-422

Query Match 52.7%; Score 21.6; DB 10; Length 230;
Best Local Similarity 72.2%; Pred. No. 2.5e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 6 TCCGGATGCCAGTCCCTCATCGCTGGCGCCGCGCGC 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 33 TCCGGATTTCTGGGCTTCATCGCTCGCGCGCGCGC 68

RESULT 10

US-11-221-284-422
; Sequence 422, Application US/11221284
; Publication No. US20060063182A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/11/221,284
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: US/09/060,756

; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 422
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"

US-11-221-284-422

Query Match 52.7%; Score 21.6; DB 18; Length 230;
Best Local Similarity 72.2%; Pred. No. 2.5e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 6 TCCGGATGCCAGTCCCTCATCGCTGGCGCCGCGCGC 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 33 TCCGGATTTCTGGGCTTCATCGCTCGCGCGCGCGC 68

RESULT 11

US-10-750-185-41952
; Sequence 41952, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41952
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Bovine 19866881725438
US-10-750-185-41952

Query Match 52.7%; Score 21.6; DB 10; Length 777;
Best Local Similarity 72.2%; Pred. No. 2.1e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCGCCGCGN 37
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 433 AGGCTCCGATGCCCTGTCCCTCTCGCAGTCTCTGT 468

RESULT 12

US-10-750-623-41952
; Sequence 41952, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31

;
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41952
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Bovine 19866881725438
US-10-750-623-41952

Query Match 52.7%; Score 21.6; DB 10; Length 777;
Best Local Similarity 72.2%; Pred. No. 2.1e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 2 AGCCTCCGATGCCAGTCCCTCATCGCTGCCCGCGN 37
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 433 AGGCTCCGATGCCGTGCTCCCTCGCAGTCTGT 468

RESULT 13
US-11-136-527-6815/c
; Sequence 6815, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6815
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6815

Query Match 52.2%; Score 21.4; DB 17; Length 600;
Best Local Similarity 69.2%; Pred. No. 2.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGCTGCCCGCGCG 41
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 292 GCCTACGGAAGCGGACCTCATCCTCCAGGCCCG 254

RESULT 14
US-11-285-798-28/c
; Sequence 28, Application US/11285798
; Publication No. US20060079451A1
; GENERAL INFORMATION:
; APPLICANT: Inamura, Toru
; APPLICANT: Asada, Masahiro
; APPLICANT: Oka, Syuichi
; APPLICANT: Suzuki, Masashi
; APPLICANT: Yoneda, Atsuko
; APPLICANT: Ota, Keiko
; APPLICANT: Oda, Yuko
; APPLICANT: Miyakawa, Kazuko
; APPLICANT: Orikasa, Noriko
; APPLICANT: Asada, Chie
; APPLICANT: Kojima, Tetsuhito
; TITLE OF INVENTION: HEPARIN-BINDING PROTEINS MODIFIED WITH SUGAR CHAINS,
; METHOD OF PRODUCING THE SAME AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS CONTAINING THE SAME
; FILE REFERENCE: 382.1019
; CURRENT APPLICATION NUMBER: US/11/285,798
; CURRENT FILING DATE: 2005-11-23
; PRIOR APPLICATION NUMBER: US/09/121,017
; PRIOR FILING DATE: 1998-07-22

;
; PRIOR APPLICATION NUMBER: 307721/1997
; PRIOR FILING DATE: 1997-11-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion of
; OTHER INFORMATION: sequence for a part of mouse fibroblast growth factor 6 and
; OTHER INFORMATION: a part of human fibroblast growth 1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(630)
US-11-285-798-28

Query Match 52.2%; Score 21.4; DB 18; Length 630;
Best Local Similarity 69.2%; Pred. No. 2.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGATGCCAGTCCCTCATCGCTGCCCGCGCGC 40
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 130 AGCCTCGAGTCCAGTAGCGTGGCGGCGCGCGC 92

RESULT 15
US-11-096-568A-21580
; Sequence 21580, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: therapy
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 21580
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1222)
; OTHER INFORMATION: Ceres Seq. ID no. 12405362
US-11-096-568A-21580

Query Match 52.2%; Score 21.4; DB 18; Length 1222;
Best Local Similarity 69.2%; Pred. No. 2.3e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGCTGCCCGCGCGCG 41
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 600 GCGTTCGATCCAGACCTCATCCTGCGGCGGCGCG 638

RESULT 16
US-11-136-527-2719/c
; Sequence 2719, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2719


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; LENGTH: 6683
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2719

Query Match      52.2%; Score 21.4; DB 17; Length 6683;
Best Local Similarity 69.2%; Pred. No. 1.1e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6375 GCCTACGAGGCGGACCTCATCTCCCTTCCAGGCCCG 6337

RESULT 17
US-11-121-086-9
; Sequence 9, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 196200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-9

Query Match      52.2%; Score 21.4; DB 17; Length 196200;
Best Local Similarity 69.2%; Pred. No. 1.1e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCCCGATGCCAGTCCCTCATCGCTGGCCCGCGCG 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 142580 AGGCTTCCCGCCGAGAGTCCCCAGAGCGCGCCCGGGG 142618

RESULT 18
US-11-121-086-8
; Sequence 8, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 246960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-8

Query Match      52.2%; Score 21.4; DB 17; Length 246960;
Best Local Similarity 69.2%; Pred. No. 1e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCCCGATGCCAGTCCCTCATCGCTGGCCCGCGCG 39
Db 17716 AGGCTTCCCGCCGAGAGTCCCCAGAGCGCGCCCGGGG 17754
```

```
RESULT 19
US-09-925-065A-404740/c
; Sequence 404740, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 404740
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-404740

Query Match      51.2%; Score 21; DB 7; Length 617;
Best Local Similarity 70.3%; Pred. No. 3.5e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCTCCCGATGCCAGTCCCTCATCGCTGGCCCGCGN 37
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 547 AAGCTTCTGTATGCCACACCCCTCATCGCTGCCCTGA 511

RESULT 20
US-09-925-065A-23066/c
; Sequence 23066, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23066
; LENGTH: 1025
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-23066

Query Match      51.2%; Score 21; DB 7; Length 1025;
Best Local Similarity 70.3%; Pred. No. 3.2e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCTCCCGATGCCAGTCCCTCATCGCTGGCCCGCGNC 38
```

Db 37 AGCCCCGGGATCGCGGCCCGAGCGCTGGGGGGCC 1
||||| ||||| ||||| ||||| ||||| |||||

RESULT 21

US-10-301-480-124303/c
; Sequence 124303, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124303
; LENGTH: 1025
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-124303

Query Match 51.2%; Score 21; DB 11; Length 1025;

Best Local Similarity 70.3%; Pred. No. 3.2e+02;

Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATCGCGTCCCTCATCGCTGGCCCGGNC 38
||||| ||||| ||||| ||||| ||||| |||||

Db 37 AGCCCCGGGATCGCGGCCCGAGCGCTGGGGGGCC 1
||||| ||||| ||||| ||||| ||||| |||||

RESULT 22

US-10-301-480-737712/c
; Sequence 737712, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 737712
; LENGTH: 1025
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-737712

Query Match 51.2%; Score 21; DB 12; Length 1025;

Best Local Similarity 70.3%; Pred. No. 3.2e+02;

Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATCGCGTCCCTCATCGCTGGCCCGGNC 38
||||| ||||| ||||| ||||| ||||| |||||

Db 37 AGCCCCGGGATCGCGGCCCGAGCGCTGGGGGGCC 1
||||| ||||| ||||| ||||| ||||| |||||

RESULT 23

US-09-925-065A-8417/c
; Sequence 8417, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8417
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-8417

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8417
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-8417

Query Match 51.2%; Score 21; DB 7; Length 1623;

Best Local Similarity 82.8%; Pred. No. 3e+02;

Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATCGCGTCCCTCATCGCTG 30
||||| ||||| ||||| ||||| |||||

Db 235 AGCCTCTCAATGCTGTCCTCATTTGCTG 207
||||| ||||| ||||| ||||| |||||

RESULT 24

US-10-301-480-109654/c
; Sequence 109654, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109654
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-109654

Query Match 51.2%; Score 21; DB 11; Length 1623;

Best Local Similarity 82.8%; Pred. No. 3e+02;

Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATCGCGTCCCTCATCGCTG 30
||||| ||||| ||||| ||||| |||||

Db 235 AGCCTCTCAATGCTGTCCTCATTTGCTG 207
||||| ||||| ||||| ||||| |||||

RESULT 25

US-10-301-480-723063/c
; Sequence 723063, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8417
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-8417

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8417
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-8417

; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 723063
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-723063

Query Match 51.2%; Score 21; DB 12; Length 1623;
Best Local Similarity 82.8%; Pred. No. 3e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGCCTCGGATGCCAGTCCCTCATCGCTG 30
||||| ||||| ||||| ||||| |||||
Db 235 AGCCTCTCAATGCTGTCCCTCATTTGCTG 207

RESULT 26

US-11-072-512-556/c
; Sequence 556, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 556
; LENGTH: 2185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-556

Query Match 51.2%; Score 21; DB 18; Length 2185;
Best Local Similarity 82.8%; Pred. No. 2.9e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGCCTCGGATGCCAGTCCCTCATCGCTG 30
||||| ||||| ||||| ||||| |||||
Db 665 AGCCTCTCAATGCTGTCCCTCATTTGCTG 637

RESULT 27

US-11-052-554A-523/c
; Sequence 523, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 523
; LENGTH: 3921
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-523

Query Match 51.2%; Score 21; DB 17; Length 3921;
Best Local Similarity 70.3%; Pred. No. 2.7e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGCTGCCCGCGCGCG 41
||||| ||||| ||||| ||||| ||||| |||||
Db 1375 CTCGGATCCAAATCCGAGACCGCGCGCGCGCG 1339

RESULT 28

US-09-925-065A-748954
; Sequence 748954, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 748954
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-748954

Query Match 50.7%; Score 20.8; DB 7; Length 518;
Best Local Similarity 67.5%; Pred. No. 4.2e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCCGCGCGCG 40
||||| ||||| ||||| ||||| ||||| |||||
Db 204 AAGTCTACAGCTTCCAGTCCCTCATGCGATGAGCAGTGGC 243

RESULT 29

US-10-517-696-5
; Sequence 5, Application US/10517696
; Publication No. US20060051759A1


```
; SEQ ID NO 5047
; LENGTH: 54985
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 48521, 48522, 48523, 48524, 48525, 48526, 48527, 48528, 48529,
; LOCATION: 48530, 48531, 48532, 48533, 48534, 48535, 48536, 48537,
; LOCATION: 48538, 48539, 48540, 48541, 48542, 48543, 48544, 48545,
; LOCATION: 48546, 48547, 48548, 48549, 48550, 48551, 48552, 48553
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 48554, 48555, 48556, 48557, 48558, 48559, 48560, 48561, 48562,
; LOCATION: 48563, 48564, 48565, 48566, 48567, 48568, 48569, 48570,
; LOCATION: 48571, 48572, 48573, 48574, 48575, 48576, 48577, 48578,
; LOCATION: 48579, 48580, 48581, 48582, 48583, 48584, 48585, 48586
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 48587, 48588, 48589, 48590, 48591, 48592, 48593, 48594, 48595,
; LOCATION: 48596, 48597, 48598, 48599, 48600, 48601, 48602, 48603,
; LOCATION: 48604, 48605, 48606, 48607, 48608, 48609, 48610, 48611,
; LOCATION: 48612, 48613, 48614, 48615, 48616, 48617, 48618, 48619
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 48620, 48621, 48622, 48623, 48624, 48625, 48626, 48627, 48628,
; LOCATION: 48629, 48630, 48631, 48632, 48633, 48634, 48635, 48636,
; LOCATION: 48637, 48638, 48639, 48640, 48641, 48642, 48643, 48644,
; LOCATION: 48645, 48646, 48647, 48648, 48649, 48650, 48651, 48652
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 48653, 48654, 48655, 48656, 48657, 48658, 48659, 48660, 48661,
; LOCATION: 48662, 48663, 48664, 48665, 48666, 48667, 48668, 48669,
; LOCATION: 48670, 48671, 48672, 48673, 48674, 48675, 48676, 48677,
; LOCATION: 48678, 48679, 48680, 48681, 48682, 48683, 48684, 48685
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 48686, 48687, 48688, 48689, 48690, 48691, 48692, 48693, 48694,
; LOCATION: 48695, 48696, 48697, 48698, 48699, 48700, 48701, 48702,
; LOCATION: 48703, 48704, 48705, 48706, 48707, 48708, 48709, 48710,
; LOCATION: 48711, 48712, 48713, 48714, 48715, 48716, 48717, 48718
; OTHER INFORMATION: n = A,T,C or G
US-11-124-367A-5047

Query Match 50.7%; Score 20.8; DB 17; Length 54985;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 24; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGCTGCGCCGCGNC 38
Db 17389 CTGGAACAGCCCTCATCGGAGCGCC 17420

RESULT 34
US-10-478-943D-1
; Sequence 1, Application US/10478943D
; Publication No. US20060073574A1
; GENERAL INFORMATION:
; APPLICANT: University College Dublin, National University of Ireland
; TITLE OF INVENTION: Engineered biosynthesis of novel polyenes
; FILE REFERENCE: PC-1638US
; CURRENT APPLICATION NUMBER: US/10/478,943D
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: S2001/0527
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 113193
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; TYPE: DNA
; ORGANISM: Streptomyces nodosus
US-10-478-943D-1

Query Match 50.7%; Score 20.8; DB 13; Length 113193;
Best Local Similarity 67.5%; Pred. No. 1.9e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNC 40
Db 70159 ACGACCCCGAGCCAGCGCGCTGCGGACCGCTGGAGCG 70198

RESULT 35
US-11-121-086-66
; Sequence 66, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 163162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-66

Query Match 50.7%; Score 20.8; DB 17; Length 163162;
Best Local Similarity 67.5%; Pred. No. 1.8e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNC 40
Db 61548 AATCCTCCAGATCCAGCCCTCAAAATCTAGACCCACCC 61587

RESULT 36
US-11-052-554A-450/c
; Sequence 450, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 450
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-450

Query Match 50.2%; Score 20.6; DB 17; Length 1206;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGCTGCGCCGNC 37
Db 984 GCCTCCGATGCCAGACCTTCGTTGTCGCAAGT 950
```



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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 171781
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-171781

Query Match          50.2%; Score 20.6; DB 11; Length 1947;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGCG 41
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12 CCGGGGGCCAGGGCCTCATCGCAGGACGGGAAGAG 46

RESULT 42
US-10-301-480-171782
; Sequence 171782, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 171782
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-171782

Query Match          50.2%; Score 20.6; DB 11; Length 1947;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGCG 41
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12 CCGGGGGCCAGGGCCTCATCGCAGGACGGGAAGAG 46

RESULT 43
US-10-301-480-171782
; Sequence 171782, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 785190
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-785190

Query Match          50.2%; Score 20.6; DB 12; Length 1947;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGCG 41
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12 CCGGGGGCCAGGGCCTCATCGCAGGACGGGAAGAG 46

RESULT 44
US-10-301-480-785191
; Sequence 785191, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 785191
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-785191

Query Match          50.2%; Score 20.6; DB 12; Length 1947;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGCG 41
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12 CCGGGGGCCAGGGCCTCATCGCAGGACGGGAAGAG 46

RESULT 45
US-10-131-826A-81
; Sequence 81, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 81
; LENGTH: 3233
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-131-826A-81

Query Match 50.2%; Score 20.6; DB 10; Length 3233;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 4 CCTCCGATGCCAGTCCCTCATCGTGGCCCGGNC 38
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 823 CCCCGTATGCCAGGCCCTCTCTGGCAGCCCGGCC 857

RESULT 46
US-10-973-1158-81
; Sequence 81, Application US/109731158
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT APPLICATION NUMBER: US/10/973,1158
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
```

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; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 81
; LENGTH: 3233
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-973-1158-81

Query Match 50.2%; Score 20.6; DB 11; Length 3233;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 4 CCTCCGATGCCAGTCCCTCATCGTGGCCCGGNC 38
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 823 CCCCGTATGCCAGGCCCTCTCTGGCAGCCCGGCC 857

RESULT 47
US-10-137-873A-81
; Sequence 81, Application US/10137873A
; Publication No. US20060084138A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C149
; CURRENT APPLICATION NUMBER: US/10/137,873A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
```



```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-5108

Query Match      50.2%; Score 20.6; DB 17; Length 13310;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      3  GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGCGN 37
Db      5399  GGCCTCTTAGGCATTCCTCCTGTCTGCTGGCCGGG 5365

RESULT 51
US-11-114-798-54/c
; Sequence 54, Application US/11114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 0618.011.0004
; CURRENT APPLICATION NUMBER: US/11/114,798
; PRIOR FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 198977
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-54

Query Match      50.2%; Score 20.6; DB 18; Length 198977;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      4  CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
Db      25857  CCCCAGTATGCCAGGCCCTCTCTGGCAGCCCGGCC 25823

RESULT 52
US-10-995-561-57494/c
; Sequence 57494, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57494
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-57494

Query Match      49.8%; Score 20.4; DB 10; Length 201;
Best Local Similarity 65.0%; Pred. No. 6.7e+02;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY      2  AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 41
Db      137  AGGCTCCGGCGGCAAGTCCCGCAGGTGGCAGCGCGG 98

RESULT 53
US-10-995-561-74443
; Sequence 74443, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74443
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-74443

Query Match      49.8%; Score 20.4; DB 10; Length 201;
Best Local Similarity 65.0%; Pred. No. 6.7e+02;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY      2  AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 41
Db      65  AGGCTCCGGCGGCAAGTCCCGCAGGTGGCAGCGCGG 104

RESULT 54
US-10-995-561-75232
; Sequence 75232, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75232
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-75232

Query Match      49.8%; Score 20.4; DB 10; Length 201;
Best Local Similarity 65.0%; Pred. No. 6.7e+02;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY      2  AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 41
Db      65  AGGCTCCGGCGGCAAGTCCCGCAGGTGGCAGCGCGG 104

RESULT 55
US-09-925-065A-777593
; Sequence 777593, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
```

```
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 777593
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-777593
```

```
Query Match 49.8%; Score 20.4; DB 7; Length 506;
Best Local Similarity 68.4%; Pred. No. 5.8e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGG 41
DB 233 CCTCCGGTCTCCGACCGGCGCGGTGGTG 270
```

```
RESULT 56
US-10-301-480-67259/c
; Sequence 67259, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67259
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-67259
```

```
Query Match 49.8%; Score 20.4; DB 11; Length 532;
Best Local Similarity 68.4%; Pred. No. 5.8e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGG 40
DB 262 GCCTCCGGTCTCCGACCGGCGGCGGTGGTG 225
```

```
RESULT 57
US-10-301-480-680668/c
; Sequence 680668, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
```

```
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 680668
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-680668
```

```
Query Match 49.8%; Score 20.4; DB 12; Length 532;
Best Local Similarity 68.4%; Pred. No. 5.8e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGG 40
DB 262 GCCTCCGGTCTCCGACCGGCGGCGGTGGTG 225
```

```
RESULT 58
US-11-128-061-2397
; Sequence 2397, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2397
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (219)..(233)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-2397
```

```
Query Match 49.8%; Score 20.4; DB 17; Length 546;
Best Local Similarity 68.4%; Pred. No. 5.8e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 2 AGCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGG 39
DB 53 ACCCTCCGAGAGGACTTCCCGGCGGCGGTGGTG 90
```

```
RESULT 59
US-11-128-061-6039
; Sequence 6039, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
```

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION

; FILE REFERENCE: 01997.027701

; CURRENT APPLICATION NUMBER: US/11/128,061

; CURRENT FILING DATE: 2005-05-11

; PRIOR APPLICATION NUMBER: US 60/570,425

; PRIOR FILING DATE: 2004-05-11

; NUMBER OF SEQ ID NOS: 7285

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 6039

; LENGTH: 546

; TYPE: DNA

; ORGANISM: Cricetulus griseus

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (219)..(233)

; OTHER INFORMATION: n is a, c, g, or t

US-11-128-061-6039

Query Match 49.8%; Score 20.4; DB 17; Length 546;

Best Local Similarity 68.4%; Pred. No. 5.8e+02;

Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39

Db 53 ACCCTCCGGAAGCGACTTCCCAACGCGCTGCCCGGAG 90

RESULT 60

US-11-128-049-2397

; Sequence 2397, Application US/11/128049

; Publication No. US20060010513A1

; GENERAL INFORMATION:

; APPLICANT: Melville, Mark W.

; APPLICANT: Charlebois, Timothy S.

; APPLICANT: Mounts, William M.

; APPLICANT: Hann, Louane E.

; APPLICANT: Sinacore, Martin S.

; APPLICANT: Leonard, Mark W.

; APPLICANT: Brown, Eugene L.

; APPLICANT: Miller, Christopher P.

; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

; FILE REFERENCE: 01997.027700

; CURRENT APPLICATION NUMBER: US/11/128,049

; CURRENT FILING DATE: 2005-05-11

; PRIOR APPLICATION NUMBER: US 60/570,425

; PRIOR FILING DATE: 2004-05-11

; NUMBER OF SEQ ID NOS: 7285

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2397

; LENGTH: 546

; TYPE: DNA

; ORGANISM: Cricetulus griseus

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (219)..(233)

; OTHER INFORMATION: n is a, c, g, or t

US-11-128-049-2397

Query Match 49.8%; Score 20.4; DB 17; Length 546;

Best Local Similarity 68.4%; Pred. No. 5.8e+02;

Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39

Db 53 ACCCTCCGGAAGCGACTTCCCAACGCGCTGCCCGGAG 90

RESULT 61

US-11-128-049-6039

; Sequence 6039, Application US/11/128049

; Publication No. US20060010513A1

; GENERAL INFORMATION:

; APPLICANT: Melville, Mark W.

; APPLICANT: Charlebois, Timothy S.

; APPLICANT: Mounts, William M.

; APPLICANT: Hann, Louane E.

; APPLICANT: Sinacore, Martin S.

; APPLICANT: Leonard, Mark W.

; APPLICANT: Brown, Eugene L.

; APPLICANT: Miller, Christopher P.

; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

; FILE REFERENCE: 01997.027700

; CURRENT APPLICATION NUMBER: US/11/128,049

; CURRENT FILING DATE: 2005-05-11

; PRIOR APPLICATION NUMBER: US 60/570,425

; PRIOR FILING DATE: 2004-05-11

; NUMBER OF SEQ ID NOS: 7285

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 6039

; LENGTH: 546

; TYPE: DNA

; ORGANISM: Cricetulus griseus

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (219)..(233)

; OTHER INFORMATION: n is a, c, g, or t

US-11-128-049-6039

Query Match

Best Local Similarity 49.8%; Score 20.4; DB 17; Length 546;

Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39

Db 53 ACCCTCCGGAAGCGACTTCCCAACGCGCTGCCCGGAG 90

RESULT 62

US-11-021-492-611

; Sequence 611, Application US/11/021492

; Publication No. US20060031947A1

; GENERAL INFORMATION:

; APPLICANT: Abuin, Alejandro

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: Novel Mutated Mammalian Cells and

; FILE REFERENCE: LEX-0368-USA

; CURRENT APPLICATION NUMBER: US/11/021,492

; CURRENT FILING DATE: 2004-12-23

; PRIOR APPLICATION NUMBER: US 60/307,670

; PRIOR FILING DATE: 2001-07-25

; NUMBER OF SEQ ID NOS: 698

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 611

; LENGTH: 546

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 25

; OTHER INFORMATION: n = A,T,C or G

US-11-021-492-611

Query Match

Best Local Similarity 49.8%; Score 20.4; DB 18; Length 546;

Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39

Db 144 ACCCTTCGGAAGCGACTTCCCAACGCGCTTGCCCGGAG 181


```
RESULT 67
US-10-301-480-612927/c
; Sequence 612927, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108927.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 612927
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-612927

Query Match          49.8%; Score 20.4; DB 12; Length 750;
Best Local Similarity 68.4%; Pred. No. 5.5e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
Db 200 AACCTTCAAAATCCCGTCCCGCAAAAGCTGTGCAGTC 163

RESULT 68
US-10-301-480-1226336/c
; Sequence 1226336, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108927.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1226336
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1226336

Query Match          49.8%; Score 20.4; DB 12; Length 750;
Best Local Similarity 68.4%; Pred. No. 5.5e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
Db 200 AACCTTCAAAATCCCGTCCCGCAAAAGCTGTGCAGTC 163

RESULT 69
US-10-467-657-1437
; Sequence 1437, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
```

```
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1437
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1437

Query Match          49.8%; Score 20.4; DB 10; Length 1074;
Best Local Similarity 68.4%; Pred. No. 5.2e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
Db 869 AAGCCGCCGAAGCAATCCCTCATCGGACGCGCGAC 906

RESULT 70
US-10-947-249-148/c
; Sequence 148, Application US/10947249
; Publication No. US20050287541A1
; GENERAL INFORMATION:
; APPLICANT: Akira NAKAGAWARA
; APPLICANT: Miki OHIRA
; APPLICANT: Shin ISHII
; APPLICANT: Takeshi GOTO
; APPLICANT: Hiroyuki KUBO
; APPLICANT: Takahiro HIRATA
; APPLICANT: Yasuko YOSHIDA
; APPLICANT: Saichi YAMADA
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma
; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 148
; LENGTH: 1234
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-947-249-148

Query Match          49.8%; Score 20.4; DB 10; Length 1234;
Best Local Similarity 68.4%; Pred. No. 5.1e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 CTTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 41
Db 474 CTTGCGGTTGGCGGTGCTCGGCTTCACCGGCGCG 437

RESULT 71
US-10-503-928-771/c
; Sequence 771, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
```

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; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 771
; LENGTH: 2180
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-771

Query Match          49.8%; Score 20.4; DB 9; Length 2180;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCGGATGCCAGTCCCTCATCGTGGCCGCGNC 38
||||| | | | | | | | | | | | | | | | | |
Db 896 AAGCCAGCACACTCCAGGGCCACATAGCTGGCCCCGAC 859

RESULT 72
US-11-147-047-5
; Sequence 5, Application US/11147047
; Publication No. US20050260668A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2463
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-147-047-5

Query Match          49.8%; Score 20.4; DB 17; Length 2463;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGTGGCCGCGNC 40
||||| | | | | | | | | | | | | | | | | |
Db 1723 GCCTCGGATGCCAGTCCCTCATCGTGGCTGTCGCGC 1760

RESULT 73
US-10-370-959-151
; Sequence 151, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar

; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND
; TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0170NMIM
; CURRENT APPLICATION NUMBER: US/10/370,959
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)...(2151)
US-10-370-959-151

Query Match          49.8%; Score 20.4; DB 9; Length 2625;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCGGATGCCAGTCCCTCATCGTGGCCGCGNC 40
||||| | | | | | | | | | | | | | | | | |
Db 87 GGCCCTGTGTCCAGACCTCTGTCGAGCCCCGCGC 124

RESULT 74
US-11-036-196-1453/c
; Sequence 1453, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castie, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
```

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; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1453
; LENGTH: 2643
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. L25387
US-11-036-196-1453

Query Match          49.8%; Score 20.4; DB 18; Length 2643;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3  GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGC 40
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1794 GCGTCCCGGTGCAAGTCCCTCATCGCTGCGCCGCGTAGC 1757

RESULT 75
US-10-505-928-701
; Sequence 701, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 701
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-701

Query Match          49.8%; Score 20.4; DB 9; Length 5994;
Best Local Similarity 68.4%; Pred. No. 4.1e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3  GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGC 40
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2936 GCCCCCGGTACTACACCTCATCGTGCAGACGAGGACGC 2973

RESULT 76
US-11-169-041-71
; Sequence 71, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
```

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; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-169-041-71

Query Match          49.8%; Score 20.4; DB 17; Length 5994;
Best Local Similarity 68.4%; Pred. No. 4.1e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3  GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGC 40
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2936 GCCCCCGGTACTACACCTCATCGTGCAGACGAGGACGC 2973

RESULT 77
US-10-995-561-13463
; Sequence 13463, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13463
; LENGTH: 20945
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(20945)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13463

Query Match          49.8%; Score 20.4; DB 10; Length 20945;
Best Local Similarity 65.0%; Pred. No. 3.4e+02;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY      2  AGCTCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNCGCG 41
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4557 AGGCTCCGGCGGCAAGTCCCGCGCAGGTGGCAGCGCGCG 4596

RESULT 78
US-10-995-561-13457
; Sequence 13457, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13457
; LENGTH: 23082
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(23082)
```



```
Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 41
Db ||||| ||||| ||||| ||||| ||||| ||||| :||
462 AAGACCCCGCGCGCCACTCCCTCCGCGGCCACTCCCTCG 502

RESULT 83
US-10-301-480-524396
; Sequence 524396, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US 10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 524396
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-524396

Query Match 49.3%; Score 20.2; DB 12; Length 553;
Best Local Similarity 65.9%; Pred. No. 6.8e+02;
Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 41
Db ||||| ||||| ||||| ||||| ||||| ||||| :||
462 AAGACCCCGCGCGCCACTCCCTCCGCGGCCACTCCCTCG 502

RESULT 84
US-10-301-480-1137805
; Sequence 1137805, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1137805
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1137805

Query Match 49.3%; Score 20.2; DB 12; Length 553;
Best Local Similarity 65.9%; Pred. No. 6.8e+02;
Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGC 41
Db ||||| ||||| ||||| ||||| ||||| ||||| :||
462 AAGACCCCGCGCGCCACTCCCTCCGCGGCCACTCCCTCG 502

RESULT 85
US-09-925-065A-717469
```

```
; Sequence 717469, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 717469
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-717469

Query Match 49.3%; Score 20.2; DB 7; Length 628;
Best Local Similarity 75.8%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGTGGCC 34
Db ||||| ||||| ||||| ||||| ||||| |||||
318 AGCCTACTGATTCACCTCCTCATCATCTGCC 350

RESULT 86
US-09-925-065A-354974/c
; Sequence 354974, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 354974
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-354974

Query Match 49.3%; Score 20.2; DB 7; Length 658;
Best Local Similarity 72.7%; Pred. No. 6.6e+02;
Matches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTGGCCCGG 37
Db ||||| ||||| ||||| ||||| ||||| |||||
269 CTGTAGTTTCCAGTCCATCAGCAGTGGCCGGA 237
```


; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1039912
; LENGTH: 659
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1039912

Query Match 49.3%; Score 20.2; DB 12; Length 659;
Best Local Similarity 72.7%; Pred. No. 6e+02;
Matches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTGGCCCGGN 37
DB 269 CTTGAGTTCCAGTCCATCAGCACTGGCCCGGA 237

RESULT 92

US-10-750-185-24911/c
; Sequence 24911, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 24911
; LENGTH: 1331
; TYPE: DNA
; ORGANISM: Bovine 19866880925243
US-10-750-185-24911

Query Match 49.3%; Score 20.2; DB 10; Length 1331;
Best Local Similarity 84.0%; Pred. No. 6e+02;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 AGTCCCTCATCGTGGCCCGGCGC 40
DB 1308 AGTCCCTCTCTCCCTGGCCCGGCGCC 1284

RESULT 93

US-10-750-623-24911/c
; Sequence 24911, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1

; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 24911
; LENGTH: 1331
; TYPE: DNA
; ORGANISM: Bovine 19866880925243
US-10-750-623-24911

Query Match 49.3%; Score 20.2; DB 10; Length 1331;
Best Local Similarity 84.0%; Pred. No. 6e+02;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 AGTCCCTCATCGTGGCCCGGCGC 40
DB 1308 AGTCCCTCTCTCCCTGGCCCGGCGCC 1284

RESULT 94

US-10-750-185-34602
; Sequence 34602, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 34602
; LENGTH: 1348
; TYPE: DNA
; ORGANISM: Bovine 19866880447689
US-10-750-185-34602

Query Match 49.3%; Score 20.2; DB 10; Length 1348;
Best Local Similarity 65.9%; Pred. No. 6e+02;
Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGCGC 41
DB 194 AACCTTCGTATGCCAGTACTATAGCTCCCGGGAGGG 234

RESULT 95

US-10-750-623-34602
; Sequence 34602, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1

; SEQ ID NO 34602

; LENGTH: 1348

; TYPE: DNA

; ORGANISM: Bovine 19866880447689

US-10-750-623-34602

Query Match

Best Local Similarity 49.3%; Score 20.2; DB 10; Length 1348;

Mismatches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGCGG 41

DB 194 AACCTTCGTATGCCAGTCACTCATAGCTCCCGGGGGGG 234

RESULT 96

US-10-467-657-7961/c

; Sequence 7961, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; PRIOR FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 7961

; LENGTH: 1506

; TYPE: DNA

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-7961

Query Match

Best Local Similarity 49.3%; Score 20.2; DB 10; Length 1506;

Mismatches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGCGG 41

DB 572 AGCGCCGCCCTCGGATGAGTATGCGGCGGACCGATGCG 532

RESULT 97

US-10-750-185-50981/c

; Sequence 50981, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; PRIOR FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 50981

; LENGTH: 1608

; TYPE: DNA

; ORGANISM: Bovine 19866880622200

US-10-750-185-50981

Query Match

Best Local Similarity 49.3%; Score 20.2; DB 10; Length 1608;

Mismatches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Matches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTGGCCCGG 37

DB 575 CCCCTGACCCAGGCCCTCTCGTCCCGCTGG 543

RESULT 98

US-10-750-623-50981/c

; Sequence 50981, Application US/10750623

; Publication No. US20050287531A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-1

; CURRENT APPLICATION NUMBER: US/10/750,623

; PRIOR FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 50981

; LENGTH: 1608

; TYPE: DNA

; ORGANISM: Bovine 19866880622200

US-10-750-623-50981

Query Match

Best Local Similarity 49.3%; Score 20.2; DB 10; Length 1608;

Mismatches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Matches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTGGCCCGG 37

DB 575 CCCCTGACCCAGGCCCTCTCGTCCCGCTGG 543

RESULT 99

US-11-124-368A-2902

; Sequence 2902, Application US/11124368A

; Publication No. US20050287559A1

; GENERAL INFORMATION:

; APPLICANT: Michele Cargill

; APPLICANT: James J. Devlin

; APPLICANT: May Luke

; TITLE OF INVENTION: Genetic Polymorphisms Associated with

; FILE REFERENCE: CL001524

; CURRENT APPLICATION NUMBER: US/11/124,368A

; PRIOR FILING DATE: 2005-05-09

; PRIOR APPLICATION NUMBER: US 60/568,845

; PRIOR FILING DATE: 2004-05-07

; PRIOR APPLICATION NUMBER: US 60/625,936

; PRIOR FILING DATE: 2004-11-09

; NUMBER OF SEQ ID NOS: 21112

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2902

; LENGTH: 94035

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-124-368A-2902

Query Match

Best Local Similarity 49.3%; Score 20.2; DB 17; Length 94035;

Mismatches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:42:48 ; Search time 0.001 Seconds
(without alignments)
3.570 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336

Perfect score: 21

Sequence: 1 gctggccggcgctgtggc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 85 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 8 summaries

Database : estdb1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	38.1	11	1	DN756222
2	7.8	37.1	11	1	AJ679435
3	7.8	37.1	11	1	AJ681247
4	7.8	37.1	11	1	AJ683713
5	7.8	37.1	11	1	AJ686459
6	7.4	35.2	10	1	BM396011
7	7.4	35.2	10	1	BM398849
8	7	33.3	10	1	AJ599908

ALIGNMENTS

RESULT 1
DN756222/c
LOCUS DN756222 11 bp mRNA linear EST 01-APR-2005
DEFINITION GL-Cf-13018 GLGC-LIB0001-cf Canis familiaris Normalized Mixed
Tissue cDNA Library Canis familiaris cDNA, mRNA sequence.
ACCESSION DN756222 GI:62145335
VERSION DN756222.1
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 11)
AUTHORS Liu, Q.
TITLE Direct Submission Gene Logic Inc
JOURNAL Unpublished (2005)
COMMENT Contact: Qing Liu
Gene Logic Inc.
610 Professional Drive, Gaithersburg, MD 20879, USA

Tel: 301 987 1700
Email: qliu@genelogic.com.
Location/Qualifiers
1. .11
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/lab_host="EMDH10B"
/clone_lib="GLGC-LIB0001-cf Canis familiaris Normalized Mixed Tissue cDNA Library"
/note="Organ: heart, liver, kidney, testis, and brain;
Vector: PCWVSPORT6.0; Site_1: NotI; Site_2: SalI"

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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTGGCCCG 9
|||||
DB 9 CTGGCCCG 2

RESULT 2
AJ679435
LOCUS AJ679435 11 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ679435 CSEQRAN04 Sus scrofa cDNA clone C0001779_B18, mRNA
sequence.
ACCESSION AJ679435
VERSION AJ679435.1 GI:49412022
KEYWORDS Sus scrofa (pig)
SOURCE EST.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1 (bases 1 to 11)
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII (KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.

FEATURES
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001779_B18"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pBlueScriptII (KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 CGCGCTGTGGC 21
|||||
DB 1 CCCGCGTGGC 11

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RESULT 3
AJ681247
LOCUS
DEFINITION
AJ681247 11 bp mRNA linear EST 29-JUN-2004
sequence.
ACCESSION
AJ681247
VERSION
AJ681247.1 GI:49413837
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL
Unpublished (2004)
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES
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/organism="Sus scrofa"
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/clone="C0001795_I24"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 CGCGCTGTGGC 21
| ||| |||||
Db 1 CCCGCGGTGGC 11

RESULT 4
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LOCUS
DEFINITION
AJ683713 11 bp mRNA linear EST 29-JUN-2004
sequence.
ACCESSION
AJ683713
VERSION
AJ683713.1 GI:49416303
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL
Unpublished (2004)
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred

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v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001802_O06"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 CGCGCTGTGGC 21
| ||| |||||
Db 1 CCCGCGGTGGC 11

RESULT 5
AJ686459
LOCUS
DEFINITION
AJ686459 CSEQRAN04 Sus scrofa cDNA clone C0001811_K23, mRNA
sequence.
ACCESSION
AJ686459
VERSION
AJ686459.1 GI:49419049
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL
Unpublished (2004)
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES
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1..11
/organism="Sus scrofa"
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/tissue_type="uterus"
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/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 CGCGCTGTGGC 21
| ||| |||||
Db 1 CCCGCGGTGGC 11

RESULT 6
AJ686459
LOCUS
DEFINITION
AJ686459 CSEQRAN04 Sus scrofa cDNA clone C0001811_K23, mRNA
sequence.
ACCESSION
AJ686459
VERSION
AJ686459.1 GI:49419049
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL
Unpublished (2004)
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES
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1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001811_K23"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 CGCGCTGTGGC 21
| ||| |||||
Db 1 CCCGCGGTGGC 11

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Db      1  ||| |||||
          CCGCGGTGGC 11

RESULT 6
LOCUS   BM396011
DEFINITION 10 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA (large fraction)
ACCESSION BM396011
VERSION   1
KEYWORDS EST.
SOURCE   Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 10)
AUTHORS  Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE    EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL  Unpublished (2002)
COMMENT  Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
          Location/Qualifiers
            1..10
              /organism="Tetrahymena thermophila"
              /mol_type="mRNA"
              /strain="CU428.1"
              /db_xref="taxon:5911"
              /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
              /note="Vector: Bluescript2 SK+; Details on library
              preparation can be found in Chilcoat and Turkewitz (2001)
              Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 CCGTGTGGC 21
Db 2 CCGCGTGGC 10

RESULT 8
LOCUS   AJ599908
DEFINITION 10 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
496D12, genomic survey sequence.
ACCESSION AJ599908
VERSION   1 GI:37949536
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE   Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS  Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE    T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL  EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED   12446565
REFERENCE 2 (bases 1 to 10)
AUTHORS  Balzerque,S.
TITLE    Direct Submision
JOURNAL  Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT  PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobio.gen.fr).
          Location/Qualifiers
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              /db_xref="taxon:3702"
              /clone_lib="496D12"
              /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
              /ecotype="Wassilewskija"
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              left border"

misc_feature
1..10
/note="T-DNA flanking sequence
left border"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2;
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FEATURES
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/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 CGCTGTGGC 21
Db 2 CCGCGTGGC 10

RESULT 7
LOCUS   BM398849
DEFINITION 10 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398849
VERSION   1
KEYWORDS EST.
SOURCE   Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 10)
AUTHORS  Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE    EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL  Unpublished (2002)
COMMENT  Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu

```

Qy 4 GGCCCG 10
|||
Db 4 GGCCCG 10
|||

Search completed: May 10, 2006, 10:42:48
Job time : 0.001 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:45:14 ; Search time 0.001 Seconds
(without alignments)
44.394 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336
Perfect score: 21
Sequence: 1 gctggccgcgcgcgtgtggc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 100 seqs, 1057 residues

Total number of hits satisfying chosen parameters: 200

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 110 summaries

Database : issdb1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	14.4	68.6	20	1	US-09-364-416-40
C 3	11	52.4	15	1	US-07-626-923A-11
C 4	10.8	51.4	15	1	US-08-861-096A-42
C 5	9.8	46.7	14	1	US-08-964-877-7
C 6	9.4	44.8	12	1	US-09-724-028A-20
C 7	9.4	44.8	13	1	US-09-474-432B-161
C 8	9.4	44.8	13	1	US-09-476-387-161
C 9	9.2	43.8	15	1	US-07-626-923A-11
C 10	9	42.9	10	1	US-09-875-453B-199
C 11	9	42.9	12	1	US-09-875-453B-145
C 12	8.8	41.9	12	1	US-10-053-526B-9
C 13	8.8	41.9	12	1	US-10-053-526B-15
C 14	8.4	40.0	10	1	US-08-441-887A-183
C 15	8.4	40.0	10	1	US-09-875-453B-195
C 16	8.4	40.0	12	1	US-09-949-041A-50
C 17	8	38.1	10	1	US-08-857-534-4
C 18	8	38.1	10	1	US-09-720-201A-24
C 19	8	38.1	10	1	US-09-613-298-4
C 20	8	38.1	10	1	US-09-875-453B-200
C 21	8	38.1	10	1	PCT-US95-04971-4
C 22	8	38.1	11	1	US-09-249-155A-6
C 23	8	38.1	11	1	US-09-249-155A-170
C 24	8	38.1	11	1	US-09-249-155A-305
C 25	8	38.1	11	1	US-09-984-292-42
C 26	7.8	37.1	11	1	US-09-040-025-51
C 27	7.8	37.1	11	1	US-09-040-025-51
C 28	7.8	37.1	11	1	US-09-291-129-16
C 29	7.4	35.2	10	1	US-08-857-534-4
C 30	7.4	35.2	10	1	US-09-613-298-4
C 31	7.4	35.2	10	1	PCT-US95-04971-4
C 32	7.4	35.2	10	1	US-08-753-829A-4
C 33	7.4	35.2	10	1	US-08-734-973-10

Sequence 15, Appl	10	35.2	7.4	34	US-08-734-973-15	Sequence 15, Appl
Sequence 16, Appl	10	35.2	7.4	35	US-08-734-973-16	Sequence 16, Appl
Sequence 386, App	10	35.2	7.4	36	US-08-388-353-386	Sequence 386, App
Sequence 397, App	10	35.2	7.4	37	US-08-388-353-387	Sequence 397, App
Sequence 386, App	10	35.2	7.4	38	US-08-488-551B-386	Sequence 386, App
Sequence 387, App	10	35.2	7.4	39	US-08-488-551B-387	Sequence 387, App
Sequence 43, Appl	10	35.2	7.4	40	US-08-651-472-43	Sequence 43, Appl
Sequence 42, Appl	10	35.2	7.4	41	US-08-522-384-42	Sequence 42, Appl
Sequence 43, Appl	10	35.2	7.4	42	US-08-358-928-43	Sequence 43, Appl
Sequence 240, App	10	35.2	7.4	43	US-08-899-241-240	Sequence 240, App
Sequence 240, App	10	35.2	7.4	44	US-08-899-241-240	Sequence 240, App
Sequence 12, Appl	10	35.2	7.4	45	US-09-154-750A-12	Sequence 12, Appl
Sequence 36, Appl	10	35.2	7.4	46	US-09-475-947A-36	Sequence 36, Appl
Sequence 159, App	10	35.2	7.4	47	US-09-475-947A-159	Sequence 159, App
Sequence 5, Appli	10	35.2	7.4	48	US-09-537-186-5	Sequence 5, Appli
Sequence 3, Appli	10	35.2	7.4	49	US-09-538-456-3	Sequence 3, Appli
Sequence 63, Appl	10	35.2	7.4	50	US-09-769-482-63	Sequence 63, Appl
Sequence 194, App	10	35.2	7.4	51	US-09-875-453B-194	Sequence 194, App
Sequence 204, App	10	35.2	7.4	52	US-09-875-453B-204	Sequence 204, App
Sequence 207, App	10	35.2	7.4	53	US-09-875-453B-207	Sequence 207, App
Sequence 6, Appli	10	35.2	7.4	54	US-09-263-790-6	Sequence 6, Appli
Sequence 4, Appli	10	35.2	7.4	55	US-09-538-341-4	Sequence 4, Appli
Sequence 6, Appli	10	35.2	7.4	56	US-09-785-716A-6	Sequence 6, Appli
Sequence 6, Appli	10	35.2	7.4	57	US-09-799-880-6	Sequence 6, Appli
Sequence 6, Appli	10	35.2	7.4	58	US-09-482-645A-6	Sequence 6, Appli
Sequence 42, Appl	11	35.2	7.4	59	US-09-984-292-42	Sequence 42, Appl
Sequence 40, Appl	20	34.3	7.2	60	US-08-837-201C-40	Sequence 40, Appl
Sequence 5, Appli	20	34.3	7.2	61	US-09-364-416-40	Sequence 5, Appli
Sequence 5, Appli	20	34.3	7.2	62	US-07-627-53B-5	Sequence 5, Appli
Sequence 20, Appl	10	33.3	7	63	US-08-734-973-20	Sequence 20, Appl
Sequence 21, Appl	10	33.3	7	64	US-08-734-973-21	Sequence 21, Appl
Sequence 6, Appli	10	33.3	7	65	US-08-265-484B-6	Sequence 6, Appli
Sequence 388, App	10	33.3	7	66	US-08-388-353-388	Sequence 388, App
Sequence 389, App	10	33.3	7	67	US-08-388-353-389	Sequence 389, App
Sequence 580, App	10	33.3	7	68	US-08-388-353-580	Sequence 580, App
Sequence 581, App	10	33.3	7	69	US-08-388-353-581	Sequence 581, App
Sequence 582, App	10	33.3	7	70	US-08-388-353-582	Sequence 582, App
Sequence 388, App	10	33.3	7	71	US-08-488-551B-388	Sequence 388, App
Sequence 389, App	10	33.3	7	72	US-08-488-551B-389	Sequence 389, App
Sequence 580, App	10	33.3	7	73	US-08-488-551B-580	Sequence 580, App
Sequence 581, App	10	33.3	7	74	US-08-488-551B-581	Sequence 581, App
Sequence 582, App	10	33.3	7	75	US-08-488-551B-582	Sequence 582, App
Sequence 36, Appl	10	33.3	7	76	US-08-478-087-36	Sequence 36, Appl
Sequence 30, Appl	10	33.3	7	77	US-08-765-257A-30	Sequence 30, Appl
Sequence 26, Appl	10	33.3	7	78	US-08-522-384-26	Sequence 26, Appl
Sequence 48, Appl	10	33.3	7	79	US-08-522-384-48	Sequence 48, Appl
Sequence 71, Appl	10	33.3	7	80	US-08-522-384-71	Sequence 71, Appl
Sequence 10, Appl	10	33.3	7	81	US-09-307-924-10	Sequence 10, Appl
Sequence 6, Appli	10	33.3	7	82	US-09-336-946B-6	Sequence 6, Appli
Sequence 13, Appl	10	33.3	7	83	US-09-535-754-6	Sequence 13, Appl
Sequence 72, Appl	10	33.3	7	84	US-09-508-753B-72	Sequence 72, Appl
Sequence 404, App	10	33.3	7	85	US-09-508-753B-404	Sequence 404, App
Sequence 23, Appl	10	33.3	7	86	US-10-042-111-23	Sequence 23, Appl
Sequence 54, Appl	10	33.3	7	87	US-10-108-077-6	Sequence 54, Appl
Sequence 6, Appli	10	33.3	7	88	US-09-769-482-54	Sequence 6, Appli
Sequence 5, Appli	10	33.3	7	89	US-09-867-263-5	Sequence 5, Appli
Sequence 6, Appli	10	33.3	7	90	US-09-867-263-5	Sequence 6, Appli
Sequence 10, Appl	10	33.3	7	91	US-10-087-426-6	Sequence 10, Appl
Sequence 6, Appli	10	33.3	7	92	US-09-498-557-10	Sequence 6, Appli
Sequence 197, App	10	33.3	7	93	US-09-885-551A-6	Sequence 197, App
Sequence 203, App	10	33.3	7	94	US-09-875-453B-197	Sequence 203, App
Sequence 29, Appl	10	33.3	7	95	US-09-875-453B-203	Sequence 29, Appl

c 107 7 33.3 10 1 US-09-479-608A-30 Sequence 30, Appl
c 108 7 33.3 10 1 US-09-479-608A-31 Sequence 31, Appl
c 109 7 33.3 10 1 US-09-479-608A-32 Sequence 32, Appl
110 7 33.3 10 1 US-10-029-221C-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-08-837-201C-40/c
; Sequence 40, Application US/08837201C
; Patent No. 5985558
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of
; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,201C
FILING DATE: April 14, 1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0209

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 810-1515

TELEFAX: (609) 810-1454

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

US-08-837-201C-40

Query Match 68.6%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 4.7;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCTGTGC 21

DB 16 CCCGGCGCGCTGTGC 1

RESULT 2

US-09-364-416-40/c
; Sequence 40, Application US/09364416
; Patent No. 6312900
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of

; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,416
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/837,201

FILING DATE: April 14, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0209

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 810-1515

TELEFAX: (609) 810-1454

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

US-09-364-416-40

Query Match 68.6%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 4.7;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCTGTGC 21

DB 16 CCCGGCGCGCTGTGC 1

RESULT 3

US-07-626-923A-11/c

; Sequence 11, Application US/07626923A

; GENERAL INFORMATION:

APPLICANT: Yoshimura, Akihiko

APPLICANT: Longmore, Gregory D.

APPLICANT: Lodish, Harvey

TITLE OF INVENTION: MUTANT EPO RECEPTOR AND USES

TITLE OF INVENTION: THEREFOR

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/626,923A

FILING DATE: 13 December 1990

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

```
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: WHI90-08
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 861-6240
;; TELEFAX: (617) 861-5540
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..15
;; OTHER INFORMATION: /product= "Internal portion of
;; OTHER INFORMATION: wild-type murine EPOR"
US-07-626-923A-11
Query Match 52.4%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCCGGCGCGC 15
Db 14 GCCGGCGCGC 4

RESULT 4
US-08-861-096A-42/c
; Sequence 42, Application US/08861096A
; Patent No. 5958689
; GENERAL INFORMATION:
; APPLICANT: Scholin, Christopher A.
; APPLICANT: Cangelosi, Gerard A.
; APPLICANT: Haydock, Paul V.
; TITLE OF INVENTION: Detection of Toxigenic Marine Diatoms of
; TITLE OF INVENTION: the Genus Pseudo-nitzschia
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,096A
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/018,143
; FILING DATE: 22-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 017748-000110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

US-08-861-096A-42
Query Match 51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CCGCGCGCGCTGTGG 20
Db 15 CCTGGGCGCTGTGG 2

RESULT 5
US-08-964-877-7/c
; Sequence 7, Application US/08964877
; Patent No. 6204026
; GENERAL INFORMATION:
; APPLICANT: DesJardins et al.
; TITLE OF INVENTION: Detection of M. tuberculosis Complex via
; TITLE OF INVENTION: Reverse Transcriptase SDA
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,877
; FILING DATE: 05 NOV 97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D6006.B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: (713) 777-6908
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bp
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
US-08-964-877-7
Query Match 46.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CCGCGCGCGCTGTGG 20
Db 14 CCGCTCGCTGTGG 2

RESULT 6
```

US-09-724-028A-20/c
; Sequence 20, Application US/09724028A
; Patent No. 6777180
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; TITLE OF INVENTION: METHOD FOR FULL-LENGTH CDNA CLONING
; TITLE OF INVENTION: USING DEGENERATE STEM LOOP ANNEALING PRIMERS
; FILE REFERENCE: A34701 (070050.1728)
; CURRENT APPLICATION NUMBER: US/09/724,028A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the 5' end of the C-ORF product of
; Patent No. 6777180
; OTHER INFORMATION: mda-5
US-09-724-028A-20

Query Match 44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 15
| | | | | | | | | |
DB 11 GGCGCGCGCGC 1

RESULT 7
US-09-474-432B-161
; Sequence 161, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 161
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-161

Query Match 44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 23;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGCGCGCGC 11
| | | | | | | | | |
DB 3 GCUGGCGCGC 13

RESULT 8
US-09-476-387-161
; Sequence 161, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
; FILE REFERENCE: MBH00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 161
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-161

Query Match 44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 23;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGCGCGCGC 11
| | | | | | | | | |
DB 3 GCUGGCGCGC 13

RESULT 9
US-07-626-923A-11
; Sequence 11, Application US/07626923A
; GENERAL INFORMATION:
; APPLICANT: Yoshimura, Akihiko
; APPLICANT: Longmore, Gregory D.
; APPLICANT: Lodish, Harvey
; TITLE OF INVENTION: MUTANT EPO RECEPTOR AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/626,923A
; FILING DATE: 13 December 1990
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227

```

; REFERENCE/DOCKET NUMBER: WHI90-08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; OTHER INFORMATION: /product= "Internal portion of
; OTHER INFORMATION: wild-type murine EPOR"
US-07-626-923A-11

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Query Match 43.8%; Score 9.2; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 39;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2 CTGGCCGCGCGGC 15
    |||||
Db 1 CTGGCCGCGCGGC 14

```

```

RESULT 10
US-09-875-453B-199
; Sequence 199, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsoh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruce, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135 US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-199

```

```

Query Match 42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 GCGCGCGCTG 17
    |||||
Db 1 GCGCGCGCTG 9

```

```

RESULT 11
US-09-875-453B-145/c
; Sequence 145, Application US/09875453B
; Patent No. 6838556

```

```

; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsoh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruce, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135 US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-145

```

```

Query Match 42.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 10 GCGCGCTGT 18
    |||||
Db 9 GCGCGCTGT 1

```

```

RESULT 12
US-10-053-526B-9/c
; Sequence 9, Application US/10053526B
; Patent No. 6936418
; GENERAL INFORMATION:
; APPLICANT: Dutreix, Marie
; APPLICANT: Sun, Jian-Sheng
; APPLICANT: Biet, Elodie
; APPLICANT: Maurisse, Rosalie
; APPLICANT: Feugeas, Jean-Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EFFECTING HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 03754/000K213-US0
; CURRENT APPLICATION NUMBER: US/10/053,526B
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/IB01/00749
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: EP 0401218.3
; PRIOR FILING DATE: 2000-03-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-053-526B-9

```

```

Query Match 41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 GCTGGCCCGCG 12
    |||||
Db 12 GCTGGCCCGCG 1

```

```
RESULT 13
US-10-053-526B-15/c
; Sequence 15, Application US/10053526B
; Patent No. 6936418
; GENERAL INFORMATION:
; APPLICANT: Dutreix, Marie
; APPLICANT: Sun, Jian-Sheng
; APPLICANT: Biet, Elodie
; APPLICANT: Maurisse, Rosalie
; APPLICANT: Feugeas, Jean-Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EFFECTING HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 03754/000K213-US0
; CURRENT APPLICATION NUMBER: US/10/053,526B
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/IB01/00749
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: EP 00401218.3
; PRIOR FILING DATE: 2000-03-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-053-526B-15

Query Match 41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGCGC 12
Db 12 GCTGGCCACGCG 1

RESULT 14
US-08-441-887A-183
; Sequence 183, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipschutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-183

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCCGCGCGC 13
Db 1 GGCCCGGAGC 10

RESULT 15
US-09-875-453B-195/c
; Sequence 195, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135,US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-195

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCGC 15
Db 10 CCGGGCGCGC 1
```



```
RESULT 16
US-09-949-041A-50/c
; Sequence 50, Application US/09949041A
; Patent No. 6902894
; GENERAL INFORMATION:
; APPLICANT: Yang, Meng
; APPLICANT: Woo, Hok
; TITLE OF INVENTION: Mutation Detection of RNA Polymerase Beta Subunit Gene Having Rf
; FILE OF INVENTION: Resistance
; FILE REFERENCE: fp4637
; CURRENT APPLICATION NUMBER: US/09/949,041A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-949-041A-50

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 32;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCGCTGTGGC 21
      ||||| |||
Db 11 GCGCTGGGC 2

RESULT 17
US-08-857-534-4/c
; Sequence 4, Application US/08857534
; Patent No. 6087170
; GENERAL INFORMATION:
; APPLICANT: George W. Kemble
; TITLE OF INVENTION: A No. 6087170el VZV Gene, Mutant VZV and Immunogenic
; FILE OF INVENTION: Compositions
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/857,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/235,406
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-004/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown

; MOLECULE TYPE: Oligomer DNA
; US-08-857-534-4
Query Match          38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCGCGGC 15
      ||||| |||
Db 10 CGCGCGGC 3

RESULT 18
US-09-720-201A-24/c
; Sequence 24, Application US/09720201A
; Patent No. 6524853
; GENERAL INFORMATION:
; APPLICANT: KOHARA, MICHINORI
; APPLICANT: KOHARA, KYOKO
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: MATSUZAKI, JUNICHI
; APPLICANT: OHMORI, HIROSHI
; TITLE OF INVENTION: A VECTOR EXPRESSING AN RNA VIRAL FULL-LENGTH GENE AND
; FILE OF INVENTION: ITS USE
; FILE REFERENCE: 04853.0051-00000
; CURRENT APPLICATION NUMBER: US/09/720,201A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: JP 98/177,820
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: PCT/JP99/03381
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-720-201A-24

Query Match          38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
      ||||| |||
Db 8 GCTGGCCC 1

RESULT 19
US-09-613-298-4/c
; Sequence 4, Application US/09613298
; Patent No. 6713296
; GENERAL INFORMATION:
; APPLICANT: George W. Kemble
; TITLE OF INVENTION: A No. 6713296el VZV Gene, Mutant VZV and Immunogenic
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/613,298
```

```

; FILING DATE: 10-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-004/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Oligomer DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-613-298-4

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCGCGGC 15
DB 10 CGCGCGGC 3
```

```

RESULT 20
US-09-875-453B-200/c
; Sequence 200, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruce, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-200

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCGCGCTG 17
DB 9 GCGCGCTG 2
```

```

RESULT 21
PCT-US95-04971-4/c
; Sequence 4, Application PC/TUS9504971
; GENERAL INFORMATION:
; APPLICANT: George W. Kemble
; TITLE OF INVENTION: A Novel VZV Gene, Mutant VZV and Immunogenic
; COMPOSITIONS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04971
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,406
; FILING DATE: APRIL 28, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-004/00WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Oligomer DNA
PCT-US95-04971-4

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCGCGGC 15
DB 10 CGCGCGGC 3

RESULT 22
US-09-249-155A-6
; Sequence 6, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; HEALING
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-6

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCCC 8
Db      1 GCTGGCCC 8

RESULT 23
US-09-249-155A-170
; Sequence 170, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-170

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCCC 8
Db      1 GCTGGCCC 8

RESULT 24
US-09-249-155A-305
; Sequence 305, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-305

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCCC 8
Db      1 GCTGGCCC 8

RESULT 25
US-09-984-292-42/c
; Sequence 42, Application US/09984292
; Patent No. 6818747
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: Oligonucleotide
US-09-984-292-42

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGCGCGC 15
Db      9 CGGCGCGC 2

RESULT 26
US-09-040-025-51
; Sequence 51, Application US/09040025
; Patent No. 6117637
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben
; APPLICANT: Kretzschmar, Titus
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: Shuffling of Heterologous DNA Sequences
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117637o No. 6117637disk of No. 6117637th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,025
; FILING DATE: 17-MAR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A

```

```
;
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 5113.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-040-025-51

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGCGCGCT 16
DB 1 CCCGACGCGT 11

RESULT 27
US-09-040-025-51
; Sequence 51, Application US/09040025
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben
; Kretzschmar, Titus
; Cherry, Joel
; TITLE OF INVENTION: Shuffling of Heterologous DNA Sequences
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10017
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/09/040,025
; FILING DATE: 17-Mar-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 5113.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-040-025-51

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGCGCGCT 16
DB 1 CCCGACGCGT 11
```

```
RESULT 28
US-09-291-129-16/c
; Sequence 16, Application US/09291129
; Patent No. 6468742
; GENERAL INFORMATION:
; APPLICANT: Nerenberg, Michael I.
; APPLICANT: Canter, David W.
; APPLICANT: Radtkey, Ray R.
; TITLE OF INVENTION: METHODS FOR DETERMINATION OF SINGLE
; NUCLEIC ACID POLYMORPHISMS USING A
; BIOELECTRIC MICROCHIP
; TITLE OF INVENTION: NUCLEIC ACID POLYMORPHISMS USING A
; BIOELECTRIC MICROCHIP
; FILE REFERENCE: 240/240
; CURRENT APPLICATION NUMBER: US/09/291,129
; CURRENT FILING DATE: 1999-04-12
; EARLIER APPLICATION NUMBER: US 09/030,156
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: US 08/986,065
; EARLIER FILING DATE: 1997-12-05
; EARLIER APPLICATION NUMBER: US 08/859,644
; EARLIER FILING DATE: 1997-05-20
; EARLIER APPLICATION NUMBER: US 08/725,976
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: US 08/708,262
; EARLIER FILING DATE: 1996-09-06
; EARLIER APPLICATION NUMBER: US 08/534,454
; EARLIER FILING DATE: 1995-09-27
; EARLIER APPLICATION NUMBER: US 08/304,657
; EARLIER FILING DATE: 1994-09-09
; EARLIER APPLICATION NUMBER: US 08/271,882
; EARLIER FILING DATE: 1994-07-07
; EARLIER APPLICATION NUMBER: US 08/146,504
; EARLIER FILING DATE: 1993-11-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: DNA
; ORGANISM: human
US-09-291-129-16

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTGGCCGCGC 12
DB 11 CTGGACGCGC 1

RESULT 29
US-08-857-534-4
; Sequence 4, Application US/08857534
; Patent No. 6087170
; GENERAL INFORMATION:
; APPLICANT: George W. Kemble
; TITLE OF INVENTION: A No. 6087170el VZV Gene, Mutant VZV and Immunogenic
; TITLE OF INVENTION: Compositions
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/857,534
```

```

; MOLECULE TYPE: Oligomer DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-613-298--4

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred.No.33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCGCGCGCTG 17
Db 2 GCGCGCGCG 10

RESULT 31
PCT-US95-04971-4
; Sequence 4, Application PC/TUS9504971
; GENERAL INFORMATION:
; APPLICANT: George W. Kemble
; TITLE OF INVENTION: A Novel VZV Gene, Mutant VZV and Immunogenic
; TITLE OF INVENTION: Compositions
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04971
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,406
; FILING DATE: APRIL 28, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-004/00WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Oligomer DNA
PCT-US95-04971-4

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred.No.33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCGCGCGCTG 17
Db 2 GCGCGCGCG 10

RESULT 32
US-08-753-829A-4/c
; Sequence 4, Application US/08753829A
; Patent No.5869250
; GENERAL INFORMATION:
; APPLICANT: Juliano, Rudolph L.
; APPLICANT: Cheng, XiaoJun

```

```
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: PEPTIDES THAT RECOGNIZE SPECIFIC DNA SEQUENCES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 5869250th Carolina
; COUNTRY: United States
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,829A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-134
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-520-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-753-829A-4
;
; Query Match 35.2%; Score 7.4; DB 1; Length 10;
; Best Local Similarity 88.9%; Pred. No. 33;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
Qy 4 GCCCGCGCG 12
Db 9 GCCCGCGCG 1
;
; RESULT 33
; US-08-734-973-10/c
; Sequence 10, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 15 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
; US-08-734-973-15
;
; Query Match 35.2%; Score 7.4; DB 1; Length 10;
; Best Local Similarity 88.9%; Pred. No. 33;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
Qy 10 GCGCGCTGT 18
Db 2 GCGCGCTGT 10
```

```
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 10 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
; US-08-734-973-10
;
; Query Match 35.2%; Score 7.4; DB 1; Length 10;
; Best Local Similarity 88.9%; Pred. No. 33;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
Qy 7 CCGCGCGCG 15
Db 10 CCGCGCGCG 2
;
; RESULT 34
; US-08-734-973-15
; Sequence 15, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 15 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
; US-08-734-973-15
;
; Query Match 35.2%; Score 7.4; DB 1; Length 10;
; Best Local Similarity 88.9%; Pred. No. 33;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
Qy 10 GCGCGCTGT 18
Db 2 GCGCGCTGT 10
```

```

RESULT 35
US-08-734-973-16
; Sequence 16, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 16 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
US-08-734-973-16

```

```

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 77.8%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 10 GCGGCGTGT 18
    |||||
Db 2 GCGGCGGCU 10

```

```

RESULT 36
US-08-388-353-386/c
; Sequence 386, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 386:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-386

```

```

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2 CTGGCCCGG 10
    |||||
Db 10 CTGGCCCTG 2

```

```

RESULT 37
US-08-388-353-387/c
; Sequence 387, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 387:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-387

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCGG 10
Db 9 CTGGCCCTG 1

RESULT 38
US-08-488-551B-386/c
; Sequence 386, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 386:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-386

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCGG 10
Db 9 CTGGCCCTG 1

RESULT 39
US-08-488-551B-387/c
; Sequence 387, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 387:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-387

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCGG 10
Db 9 CTGGCCCTG 1

RESULT 40
US-08-651-472-43
; Sequence 43, Application US/08651472
; Patent No. 6103244
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: PFLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC

```



```

; TITLE OF INVENTION:  VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES:  95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Foley & Lardner
; STREET:  3000 K Street, N.W., Suite 500
; CITY:  Washington
; STATE:  D.C.
; COUNTRY:  USA
; ZIP:  20007-5109
; COMPUTER READABLE FORM:
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/651,472
; FILING DATE:
; CLASSIFICATION:  435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  US 07/914,738
; FILING DATE:  20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  US 07/750,080
; FILING DATE:  26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME:  BENT, Stephen A.
; REGISTRATION NUMBER:  29,768
; REFERENCE/DOCKET NUMBER:  30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (202)672-5300
; TELEFAX:  (202)672-5399
; TELEX:  904136
; INFORMATION FOR SEQ ID NO:  43:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  10 base pairs
; TYPE:  nucleic acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; MOLECULE TYPE:  Other nucleic acid;
; DESCRIPTION:  Synthetic DNA oligonucleotide
US-08-651-472-43

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CTGGCCCGG 10
Db      1 CTAGCCCGG 9

RESULT 41
US-08-522-384-42
; Sequence 42, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT:  LOPEZ-NIETO, CARLOS E
; APPLICANT:  NIGAM, SANTAY KUMAR
; TITLE OF INVENTION:  PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION:  CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE:  2458-4029
; CURRENT APPLICATION NUMBER:  US/08/522,384
; CURRENT FILING DATE:  1996-11-15
; NUMBER OF SEQ ID NOS:  122
; SOFTWARE:  Patent In ver. 2.1
; SEQ ID NO 42
; LENGTH:  10
; TYPE:  DNA
; ORGANISM:  Unknown Organism
; FEATURE:
; OTHER INFORMATION:  Description of Unknown Organism:  Primer
US-08-522-384-42
```

```

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CTGGCCCGG 10
Db      1 CTAGCCCGG 9

RESULT 42
US-08-358-928-43
; Sequence 43, Application US/08358928
; Patent No. 6265183
; GENERAL INFORMATION:
; APPLICANT:  DORNER, Friedrich
; APPLICANT:  SCHEIFLINGER, Friedrich
; APPLICANT:  FALKNER, Falko Gunter
; APPLICANT:  PFLEIDERER, Michael
; TITLE OF INVENTION:  DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION:  VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; TITLE OF INVENTION:  (HIV-1) ANTIGENS
; NUMBER OF SEQUENCES:  95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Foley & Lardner
; STREET:  3000 K Street, N.W., Suite 500
; CITY:  Washington
; STATE:  D.C.
; COUNTRY:  USA
; ZIP:  20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/358,928
; FILING DATE:
; CLASSIFICATION:  435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  US 07/914,738
; FILING DATE:  20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  US 07/750,080
; FILING DATE:  26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME:  BENT, Stephen A.
; REGISTRATION NUMBER:  29,768
; REFERENCE/DOCKET NUMBER:  30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (202)672-5300
; TELEFAX:  (202)672-5399
; TELEX:  904136
; INFORMATION FOR SEQ ID NO:  43:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  10 base pairs
; TYPE:  nucleic acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; MOLECULE TYPE:  Other nucleic acid;
; DESCRIPTION:  Synthetic DNA oligonucleotide
US-08-358-928-43

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CTGGCCCGG 10
Db      1 CTAGCCCGG 9

RESULT 43
```

```
US-08-899-241-240
; Sequence 240, Application US/08899241A
; Patent No. 6322995
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Huemelin, Markus
; APPLICANT: van Loon, Adolphus
; APPLICANT: Schurter, Walter
; TITLE OF INVENTION: Improved Riboflavin Production
; FILE REFERENCE: Improved Riboflavin Prod
; CURRENT APPLICATION NUMBER: US/08/899,241A
; CURRENT FILING DATE: 1997-07-23
; EARLIER APPLICATION NUMBER: 96111905.4
; EARLIER FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Ac# J01749
US-08-899-241-240

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CCCGCGCGC 14
Db      1 CCCAGCGCG 9

RESULT 44
US-08-899-241-240/c
; Sequence 240, Application US/08899241A
; Patent No. 6322995
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Huemelin, Markus
; APPLICANT: van Loon, Adolphus
; APPLICANT: Schurter, Walter
; TITLE OF INVENTION: Improved Riboflavin Production
; FILE REFERENCE: Improved Riboflavin Prod
; CURRENT APPLICATION NUMBER: US/08/899,241A
; CURRENT FILING DATE: 1997-07-23
; EARLIER APPLICATION NUMBER: 96111905.4
; EARLIER FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Ac# J01749
US-08-899-241-240

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 CGCGCTGTG 19
Db      9 CGCGCTGGG 1

RESULT 45
US-08-154-750A-12
; Sequence 12, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-12/c
; Sequence 12, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-12

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 GCCCGCGCGC 13
Db      2 GCCCGCGCGC 10

RESULT 46
US-09-154-750A-12/c
; Sequence 12, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-12

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 CGCGCGCGCT 16
Db      9 CGCGCGCGCT 1

RESULT 47
US-09-475-947A-36/c
; Sequence 36, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
```

```

; ORGANISM: human
US-09-475-947A-36

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGCGC 13
Db 9 GCCCGGCC 1

RESULT 48
US-09-475-947A-159/c
; Sequence 159, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-159

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGCGC 13
Db 9 GCCCGGCC 1

RESULT 49
US-09-537-186-5/c
; Sequence 5, Application US/09537186
; Patent No. 6534696
; GENERAL INFORMATION:
; APPLICANT: COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
; TITLE OF INVENTION: A disease resistant high yielding variety Papaver somniferum call
; FILE REFERENCE: Q58615
; CURRENT APPLICATION NUMBER: US/09/537,186
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: : Primer for generating random
US-09-537-186-5

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CCGCGCGC 15
Db 9 CCGCGGTC 1

RESULT 50
US-09-538-456-3/c
; Sequence 3, Application US/09538456
; Patent No. 6558940
; GENERAL INFORMATION:
; APPLICANT: Alam, Mansoor
; APPLICANT: Sattar, Abdul
; APPLICANT: Kumar, Suhel
; APPLICANT: Samad, Abdul
; APPLICANT: Dhawan, Om Prakash
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Singh, Seema
; APPLICANT: Kumar, Poovappallivadakehil Viswanathan Nair Ajay
; APPLICANT: Khalique, Abdul
; APPLICANT: Zaim, Mohammad
; APPLICANT: Shahabuddin, Saba
; APPLICANT: Trivedi, Mala
; TITLE OF INVENTION: A novel Streptomyces strain with potential anti-microbial
; FILE REFERENCE: activity against phytopathogenic fungi
; CURRENT APPLICATION NUMBER: US/09/538,456
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Word-97
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-538-456-3

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CCGCGCGC 15
Db 9 CCGCGGTC 1

RESULT 51
US-09-769-482-63/c
; Sequence 63, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: POYNUCLEOTIDE ARRAY
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-769-482-63

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
Qy      3 TGGCCCGGC 11
      |||||
Db      10 TGGCCCGGC 2

RESULT 52
US-09-875-453B-194
; Sequence 194, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu H. P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 2001-06-06
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-194

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      9 GGCGCGCTG 17
      |||||
Db      1 GGCGCGCGG 9

RESULT 53
US-09-875-453B-204
; Sequence 204, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu H. P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-207

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      10 GCAGCGCTGT 18
      |||||
Db      9 GCAGCGCTTT 1

RESULT 55
US-09-263-790-6/c
; Sequence 6, Application US/09263790
; Patent No. PFI2997
; GENERAL INFORMATION:
; APPLICANT: Nirmal Kumar PATRA et al.
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
```

```

; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAP 06 Primer - Primer used in RAPD analysis comparing Jal Pallav
; OTHER INFORMATION: with Jorlab-2, Manjusha, Mandakini, Bio-13, and Ceylon.
US-09-263-790-6

```

```

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 7 CCGGCGCGC 15
    |||||
Db 9 CCGGCGTGC 1

```

RESULT 56

```

US-09-538-341-4/c
; Sequence 4, Application US/09538341
; Patent No. PFI3110
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Bansal, Ravi Prakash
; APPLICANT: Niwas, Shri
; APPLICANT: Nagvi, Arif Ali
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Singh, Vikram
; APPLICANT: Sinha, Shweta
; TITLE OF INVENTION: Lippia alba plant named 'Bhurakshak'
; FILE REFERENCE: U-012701-4
; CURRENT APPLICATION NUMBER: US/09/538,341
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for generating random amplified polymorphic DNA profile of
US-09-538-341-4

```

```

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 7 CCGGCGCGC 15
    |||||
Db 9 CCGGCGTGC 1

```

RESULT 57

```

US-09-785-716A-6/c
; Sequence 6, Application US/09785716A
; Patent No. PFI4090
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; APPLICANT: Dwivedi, Samresh
; APPLICANT: Singh, Maneesha
; APPLICANT: Singh, Ajay Pratap
; APPLICANT: Singh, Vandana
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Nagvi, Ali Arif
; APPLICANT: Kuman, Sushil
; TITLE OF INVENTION: New Peppermint Plant Named 'PRANJAL'
; FILE REFERENCE: 41799/VGG/K375
; CURRENT APPLICATION NUMBER: US/09/785,716A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1

```

```

; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for RAPD profile
US-09-785-716A-6

```

```

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 7 CCGGCGCGC 15
    |||||
Db 9 CCGGCGTGC 1

```

RESULT 58

```

US-09-799-880-6/c
; Sequence 6, Application US/09799880
; Patent No. PFI4400
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Gupta, Ritika
; APPLICANT: Sastry, Kakaraparthi
; APPLICANT: Banerjee, Suchitra
; APPLICANT: Mallavarapu, Gopal
; APPLICANT: Ramesh, Srinivas
; APPLICANT: Shasany, Ajit
; APPLICANT: Darokar, Mahendra
; APPLICANT: Khanuja, Suman
; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAFA'
; FILE REFERENCE: 2734-102
; CURRENT APPLICATION NUMBER: US/09/799,880
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-799-880-6

```

```

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 7 CCGGCGCGC 15
    |||||
Db 9 CCGGCGTGC 1

```

RESULT 59

```

US-09-482-645A-6/c
; Sequence 6, Application US/09482645A
; Patent No. PFI4538
; GENERAL INFORMATION:
; APPLICANT: KHANUJA, Suman Preet Singh
; APPLICANT: SHASANY, Ajit Kumar
; APPLICANT: DHAWAN, Sunita
; APPLICANT: DAROKAR, Mahendra Pandurang
; APPLICANT: SATAPATHY, Sarita
; APPLICANT: KUMAR, Tiruppadiripuliyur Ranganathan Santha
; APPLICANT: SAIKIA, Dharmendra
; APPLICANT: PATRA, Nirmal Kumar
; APPLICANT: BAHL, Janak Raj
; APPLICANT: TRIPATHY, Arun Kumar
; TITLE OF INVENTION: Mint Plant Named 'Sambhav'
; FILE REFERENCE: U 012566-4
; CURRENT APPLICATION NUMBER: US/09/482,645A
; CURRENT FILING DATE: 2000-01-18

```

```
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAP Primer
US-09-482-645A-6

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CCGCGCGGCG 15
Db 9 CCGCGGTGC 1
      |||||
      |||||

RESULT 60
US-09-984-292-42
; Sequence 42, Application US/09984292
; Patent No. 6818747
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-09-984-292-42

Query Match      35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCGCGGCTG 17
Db 1 GCGCGCGG 9
      |||||
      |||||

RESULT 61
US-08-837-201C-40
; Sequence 40, Application US/08837201C
; Patent No. 5985558
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of
; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
US-08-837-201C-40
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,416
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,201
; FILING DATE: April 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,201C
; FILING DATE: April 14, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: ISPH-0209
; FILING DATE: April 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; COMPUTER READABLE FORM:

Query Match      34.3%; Score 7.2; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CGCGCGGCTGTG 19
Db 5 CAGCGCGCGGG 16
      |||||
      |||||

RESULT 62
US-09-364-416-40
; Sequence 40, Application US/09364416
; Patent No. 6312900
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of
; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
US-09-364-416-40
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,416
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,201
; FILING DATE: April 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; COMPUTER READABLE FORM:
```

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; ANTI-SENSE: Yes

US-09-364-416-40

Query Match

Best Local Similarity 34.3%; Score 7.2; DB 1; Length 20;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CCGCGCGCTGTG 19

DB 5 CAGCGCGCGCGG 16

RESULT 63

US-07-627-538-5/c

; Sequence 5, Application US/07627538

; Patent No. 5248600

; GENERAL INFORMATION:

; APPLICANT: Topal, Michael D.

; APPLICANT: Conrad, Michael

; TITLE OF INVENTION: Method of Cleaving DNA

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and Gibson

; STREET: Post Office Drawer 34009

; CITY: Charlotte

; STATE: No. 5248600th Carolina

; COUNTRY: U.S.A.

; ZIP: 28234

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/627,538

; FILING DATE: 19901214

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Sibley, Kenneth D.

; REGISTRATION NUMBER: 31,665

; REFERENCE/DOCKET NUMBER: 5052-24

; TELEPHONE: 919-881-3140

; TELEFAX: 919-881-3175

; TELEX: 575102

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: N

; ANTI-SENSE: N

US-07-627-538-5

Query Match

Best Local Similarity 33.3%; Score 7; DB 1; Length 10;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGCGCGC 13

DB 7 CCGCGCGC 1

RESULT 64

US-08-128-369-5/c

; Sequence 5, Application US/08128369

; Patent No. 5418150

; GENERAL INFORMATION:

; APPLICANT: Topal, Michael D.

; APPLICANT: Conrad, Michael J.

; TITLE OF INVENTION: METHOD OF CLEAVING DNA

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and

; ADDRESSEE: Gibson

; STREET: P.O. Drawer 34009

; CITY: Charlotte

; STATE: No. 5418150th Carolina

; COUNTRY: USA

; ZIP: 28234

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/128,369

; FILING DATE: 21-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Sibley, Kenneth D.

; REGISTRATION NUMBER: 31,665

; REFERENCE/DOCKET NUMBER: 5470-5A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-881-3175

; TELEFAX: 919-420-2200

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-128-369-5

Query Match

Best Local Similarity 33.3%; Score 7; DB 1; Length 10;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGCGCGC 13

DB 7 CCGCGCGC 1

RESULT 65

US-08-170-290A-1/C

; Sequence 1, Application US/08170290A

; Patent No. 5702931

; GENERAL INFORMATION:

; APPLICANT: Andrews, William H.

; APPLICANT: Morser, Michael J.

; APPLICANT: Ziehlender, Laura R.

; TITLE OF INVENTION: No. 5702931el Mutagenesis Methods and

; NUMBER OF SEQUENCES: 63

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James M. Heslin

; STREET: 379 Lytton Ave.

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/170,290A
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05573
; FILING DATE: 01-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/724,237
; FILING DATE: 01-JUL-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 11972-58-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-170-290A-1

```

```

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 9 GCGCGC 15
   |||||
Db 9 GCGCGC 3

```

```

RESULT 66
US-08-171-718-36/c
; Sequence 36, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gubella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-171-718-36

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
   |||||
Db 10 CTGTGGC 4

RESULT 67
US-08-477-396A-12
; Sequence 12, Application US/08477396A
; Patent No. 5872235
; GENERAL INFORMATION:
; APPLICANT: Chen, Lan Bo
; APPLICANT: Bao, Shideng
; APPLICANT: Liu, Yuan
; TITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF
; TITLE OF INVENTION: ISOLATING SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,396A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,488
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: US 08/448,388
; FILING DATE: 28-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12502
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCI-333BX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO

```



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; ANTI-SENSE: NO
US-08-477-396A-12

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCCCGC 11
Db 2 GCCCGC 8

RESULT 68
US-08-734-973-19/c
; Sequence 19, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 19 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
US-08-734-973-19

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCCCGC 15
Db 10 GCCCGC 4

RESULT 69
US-08-734-973-20
; Sequence 20, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; TITLE OF INVENTION: A Rapid Means For Quantitating
```

```
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 20 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
US-08-734-973-20

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCCGCGCT 16
Db 4 GCCGCGCT 10

RESULT 70
US-08-734-973-21
; Sequence 21, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
```

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (716) 856-4000
;; TELEFAX: (716) 849-0349
;; INFORMATION FOR SEQ ID NO: 21 :
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single-stranded
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; HYPOTHETICAL: No
US-08-734-973-21

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCGGCGCT 16
Db 4 GCGGCGCU 10
|||||:

RESULT 71
US-08-265-484B-6
; Sequence 6, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-265-484B-6

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
Db 4 CUGUGGC 10
|:|:|:

RESULT 72
US-08-265-484B-30/c
; Sequence 30, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-265-484B-30

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
Db 8 GCTGGCC 2
|||||:

RESULT 73
US-08-388-353-388/c
; Sequence 388, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States

```

; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-388

```

```

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 CTGGCCCC 8
        |||||
Db      8 CTGGCCCC 2

```

```

RESULT 74
US-08-388-353-389/c
; Sequence 389, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 389:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-389

```

```

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 CTGGCCCC 8
        |||||
Db      7 CTGGCCCC 1

```

```

RESULT 75
US-08-388-353-579
; Sequence 579, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 579:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-579

```

```

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 TGGCCCC 9
        |||||
Db      4 TGGCCCC 10

```

```

RESULT 76
US-08-388-353-580

```

```

; Sequence 580, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-580

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 TGGCCCG 9
        |||||
Db      3 TGGCCCG 9

```

```

RESULT 77
US-08-388-353-581
; Sequence 581, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 581:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-581

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 TGGCCCG 9
        |||||
Db      2 TGGCCCG 8

```

```

RESULT 78
US-08-388-353-582
; Sequence 582, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-582

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 3 TGGCCCG 9
   |||||
Db 1 TGGCCCG 7

```

```

RESULT 79
US-08-488-551B-388/c
; Sequence 388, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-388

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-582

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTGGCCC 8
   |||||
Db 8 CTGGCCC 2

RESULT 81
US-08-488-551B-579
; Sequence 579, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 CTGGCCC 8
   |||||
Db 8 CTGGCCC 2

```

```

RESULT 80
US-08-488-551B-389/c
; Sequence 389, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 389:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-389

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 CTGGCCC 8
   |||||
Db 7 CTGGCCC 1

```

```

RESULT 81
US-08-488-551B-579
; Sequence 579, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

```

```

; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 579:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-579

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGCCCG 9
Db 4 TGGCCCG 10

RESULT 82
US-08-488-551B-580
; Sequence 580, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-580

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGCCCG 9
Db 3 TGGCCCG 9

RESULT 83
US-08-488-551B-581
; Sequence 581, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO

```

REFERENCE/DOCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 581:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-581

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGCCCG 9
| | | | |
DB 2 TGGCCCG 8

RESULT 84
US-08-488-551B-582
; Sequence 582, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGILIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 582:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-582

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGCCCG 9
| | | | |
DB 1 TGGCCCG 7

RESULT 85
US-08-478-087-36/c
; Sequence 36, Application US/08478087
; Patent No. 6077685
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gubella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,087
FILING DATE: 07-JUN-1995

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,718
FILING DATE: 22-DEC-1993
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-FEB-1993
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 0609.3850003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-087-36

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
| | | | |
DB 10 CTGTGGC 4

RESULT 86
US-08-765-257A-6

```
; Sequence 6, Application US/08765257A
; Patent No. 6107078
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,
; TITLE OF INVENTION: Stems and Loops, tRNA Embedded Ribozymes
; TITLE OF INVENTION: and Compositions Thereof
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; MEDIUM TYPE: 3.5 INCH, 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08765,257A
; FILING DATE: June 24, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 977 9550
; TELEFAX: 212 977 9809
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-765-257A-6
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
Db 4 CUGUGGC 10
|:|:|

RESULT 87
US-08-765-257A-30/c
; Sequence 30, Application US/08765257A
; Patent No. 6107078
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,
; TITLE OF INVENTION: Stems and Loops, tRNA Embedded Ribozymes
; TITLE OF INVENTION: and Compositions Thereof
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; MEDIUM TYPE: 3.5 INCH, 1.44Mb
; COMPUTER: IBM PC
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08765,257A
; FILING DATE: June 24, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 977 9550
; TELEFAX: 212 977 9809
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-765-257A-30
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
Db 8 GCTGGCC 2
|:|:|

RESULT 88
US-08-522-384-26
; Sequence 26, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-26
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
Db 4 GCTGGCC 10
|:|:|

RESULT 89
US-08-522-384-48
; Sequence 48, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
```


; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-48

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GCTGTGG 20
Db 4 GCTGTGG 10
|||||

RESULT 90

US-08-522-384-71
; Sequence 71, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-71

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGCC 7
Db 1 GCTGCC 7
|||||

RESULT 91

US-09-307-924-10
; Sequence 10, Application US/09307924
; Patent No. 6303308
; GENERAL INFORMATION:
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: CLONING VECTORS AND THEIR PREPARATION
; TITLE OF INVENTION: AND USE FOR mRNA EXPRESSION PATTERN ANALYSIS
; FILE REFERENCE: 50125/002001
; CURRENT APPLICATION NUMBER: US/09/307,924
; CURRENT FILING DATE: 1999-05-10
; EARLIER APPLICATION NUMBER: DE 19822287.4
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-307-924-10

; OTHER INFORMATION: DNA linker
US-09-307-924-10

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCGCGC 15
Db 2 GCGCGC 8
|||||

RESULT 92

US-09-307-924-10/c
; Sequence 10, Application US/09307924
; Patent No. 6303308
; GENERAL INFORMATION:
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: CLONING VECTORS AND THEIR PREPARATION
; TITLE OF INVENTION: AND USE FOR mRNA EXPRESSION PATTERN ANALYSIS
; FILE REFERENCE: 50125/002001
; CURRENT APPLICATION NUMBER: US/09/307,924
; CURRENT FILING DATE: 1999-05-10
; EARLIER APPLICATION NUMBER: DE 19822287.4
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA linker
US-09-307-924-10

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCGCGC 15
Db 9 GCGCGC 3
|||||

RESULT 93

US-09-535-754-6
; Sequence 6, Application US/09535754
; Patent No. 6361974
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHSHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/09/535,754
; CURRENT FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-535-754-6

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CGCGCTG 17
|||||
Db 1 CGCGCTG 7

RESULT 94

US-09-336-946B-13/c
; Sequence 13, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A P1-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-336-946B-13

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CGCGCTG 18
|||||
Db 7 CGCGCTG 1

RESULT 95

US-09-508-753B-72/c
; Sequence 72, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 72
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-72

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GCTGTGG 20
|||||
Db 10 GCTGTGG 4

RESULT 96

US-09-508-753B-404
; Sequence 404, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 404
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-404

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CGCTGTG 19
|||||
Db 4 CGCTGTG 10

RESULT 97

US-10-042-111-23/c
; Sequence 23, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: primer
US-10-042-111-23

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GCTGTGG 20
|||||
Db 7 GCTGTGG 1

RESULT 98

US-09-769-482-54/c
; Sequence 54, Application US/09769482

```
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-54

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTGCC 7
Db      7 GCTGCC 1

RESULT 99
US-10-108-077-6
; Sequence 6, Application US/10108077
; Patent No. 6635449
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHSHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/10/108,077
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-108-077-6

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 CGCGCTG 17
Db      1 CGCGCTG 7

RESULT 100
US-09-867-262-5
; Sequence 6, Application US/10087426
; Patent No. 6709841
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-23
; CURRENT APPLICATION NUMBER: US/10/087,426
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-11-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-11-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
```

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; Sequence 5, Application US/09867262
; Patent No. 6696275
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-17
; CURRENT APPLICATION NUMBER: US/09/867,262
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-867-262-5

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 CGCGCTG 17
Db      1 CGCGCTG 7

RESULT 101
US-10-087-426-6
; Sequence 6, Application US/10087426
; Patent No. 6709841
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-23
; CURRENT APPLICATION NUMBER: US/10/087,426
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-11-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-11-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
```

```

; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-087-426-6

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 CGCGCTG 17
Db      1 CGCGCTG 7

RESULT 102
US-09-498-557-10
; Sequence 10, Application US/09498557
; Patent No. 6713279
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES AND ENZYMES
; FILE REFERENCE: DIVERI460-12
; CURRENT APPLICATION NUMBER: US/09/498,557
; CURRENT FILING DATE: 2000-02-04
; PRIOR FILING DATE: US 09/332,835
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-498-557-10

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 CGCGCTG 17
Db      1 CGCGCTG 7

RESULT 103
US-09-885-551A-6
; Sequence 6, Application US/09885551A
; Patent No. 6740506
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard

```

```

; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIVERI460-14
; CURRENT APPLICATION NUMBER: US/09/885,551A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-885-551A-6

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 CGCGCTG 17
Db      1 CGCGCTG 7

RESULT 104
US-09-875-453B-197
; Sequence 197, Application US/09875453B
; Patent No. 8838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungseuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurence, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-197

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 GCAGCGCT 16
Db      1 GCAGCGCT 7

RESULT 105
US-09-875-453B-203/c
; Sequence 203, Application US/09875453B

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; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu H. P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruce, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135 US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-203

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GCGCGCT 16
DB      10 GCGCGCT 4

RESULT 106
US-09-479-608A-29/c
; Sequence 29, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-29

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTGTGGC 21
DB      10 CTGTGGC 4

RESULT 107
US-09-479-608A-30/c
; Sequence 30, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-30

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTGTGGC 21
DB      9 CTGTGGC 3

RESULT 108
US-09-479-608A-31/c
; Sequence 31, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-31

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTGTGGC 21
DB      8 CTGTGGC 2

RESULT 109
US-09-479-608A-32/c
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; Sequence 32, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-32

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
Db 7 CTGTGGC 1

RESULT 110
US-10-029-221C-5
; Sequence 5, Application US/10029221C
; Patent No. 6939689
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; APPLICANT: DJAVAKHISHVILI, TSOTNE D.
; APPLICANT: FREY, GERHARD J.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-21
; CURRENT APPLICATION NUMBER: US/10/029,221C
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-029-221C-5

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CGCGCTG 17
Db 1 CGCGCTG 7

Search completed: May 10, 2006, 10:45:14
Job time : 0.001 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:44:15 ; Search time 0.001 Seconds
(without alignments)
144.438 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336

Perfect score: 21

Sequence: 1 gctgcccggcgctgtggc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 324 seqs, 3439 residues

Total number of hits satisfying chosen parameters: 648

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 356 summaries

Database : gendb1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	14.4	68.6	20	1	AR176785
C 3	12.4	59.0	16	1	CQ786323
C 4	11.4	54.3	16	1	ACCESSION:CQ786323
C 5	10.8	51.4	15	1	AR075658
C 6	10.4	49.5	14	1	ACCESSION:AR075658
C 7	10.4	47.6	11	1	AL13334
C 8	10.4	47.6	12	1	ACCESSION:AL13334
C 9	10.4	47.6	12	1	ACCESSION:CQ766472
C 10	9.8	46.7	14	1	AX081331
C 11	9.8	46.7	14	1	AR142945
C 12	9.4	44.8	11	1	CS061169
C 13	9.4	44.8	11	1	CQ936510
C 14	9.4	44.8	11	1	AX628774
C 15	9.4	44.8	11	1	AX630120
C 16	9.4	44.8	12	1	AX630373
C 17	9.4	44.8	12	1	ACCESSION:AX630373
C 18	9.4	44.8	12	1	CQ766499
C 19	9.4	44.8	13	1	AR285789
C 20	9.4	44.8	13	1	AR397780
C 21	9.4	44.8	10	1	BD161333
C 22	9.4	44.8	10	1	BD238832
C 23	9.4	44.8	10	1	AR630145
C 24	9.4	44.8	10	1	AX152988
C 25	9.4	44.8	10	1	AX153495
C 26	9.4	44.8	10	1	AX153496
C 27	9.4	44.8	11	1	CQ933102
C 28	9.4	44.8	11	1	ACCESSION:CQ933102
C 29	9.4	44.8	12	1	CS086764
C 30	9.4	44.8	12	1	AR630091
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C 41	8.4	40.0	10	1	BD238621
C 42	8.4	40.0	10	1	CQ986655
C 43	8.4	40.0	10	1	CS114173
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C 46	8.4	40.0	10	1	E54824
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C 80	8.4	40.0	11	1	AX629700
C 81	8.4	40.0	11	1	AX630546
C 82	8.4	40.0	11	1	AX631029
C 83	8.4	40.0	12	1	CQ766406
C 84	8.4	40.0	12	1	CQ766468
C 85	8.4	40.0	12	1	CQ766480
C 86	8.4	40.0	12	1	AR678905
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C 92	8.4	40.0	10	1	BD238855
C 93	8.4	40.0	10	1	BD240458
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C 96	8.4	40.0	10	1	AR630146
C 97	8.4	40.0	10	1	AX224410
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C 107	8.4	40.0	11	1	AR301724

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c 110	8	38.1	11	1	AX623347	ACCESSION:AX623347	c 183	7.4	35.2	10	1	AR071786	ACCESSION:AR071786
c 111	8	38.1	11	1	AX623827	ACCESSION:AX623827	c 184	7.4	35.2	10	1	AR105774	ACCESSION:AR105774
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c 113	8	38.1	11	1	AX627953	ACCESSION:AX627953	c 186	7.4	35.2	10	1	BD083124	ACCESSION:BD083124
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c 132	7.8	37.1	11	1	CQ835213	ACCESSION:CQ835213	c 205	7.4	35.2	10	1	CQ759089	ACCESSION:CQ759089
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c 137	7.8	37.1	11	1	AX470499	ACCESSION:AX470499	c 210	7.4	35.2	10	1	E54829	ACCESSION:E54829
c 138	7.8	37.1	11	1	AX470547	ACCESSION:AX470547	c 211	7.4	35.2	10	1	AR222959	ACCESSION:AR222959
c 139	7.8	37.1	11	1	AX471002	ACCESSION:AX471002	c 212	7.4	35.2	10	1	AR222959	ACCESSION:AR222959
c 140	7.8	37.1	11	1	AX471274	ACCESSION:AX471274	c 213	7.4	35.2	10	1	AR241748	ACCESSION:AR241748
c 141	7.8	37.1	11	1	AX471596	ACCESSION:AX471596	c 214	7.4	35.2	10	1	AR241871	ACCESSION:AR241871
c 142	7.8	37.1	11	1	AX622989	ACCESSION:AX622989	c 215	7.4	35.2	10	1	AR261814	ACCESSION:AR261814
c 143	7.8	37.1	11	1	AX623485	ACCESSION:AX623485	c 216	7.4	35.2	10	1	AR261814	ACCESSION:AR261814
c 144	7.8	37.1	11	1	AX623553	ACCESSION:AX623553	c 217	7.4	35.2	10	1	AR310513	ACCESSION:AR310513
c 145	7.8	37.1	11	1	AX623825	ACCESSION:AX623825	c 218	7.4	35.2	10	1	AR336888	ACCESSION:AR336888
c 146	7.8	37.1	11	1	AX623949	ACCESSION:AX623949	c 219	7.4	35.2	10	1	AR630150	ACCESSION:AR630150
c 147	7.8	37.1	11	1	AX624477	ACCESSION:AX624477	c 220	7.4	35.2	10	1	AR630153	ACCESSION:AR630153
c 148	7.8	37.1	11	1	AX624700	ACCESSION:AX624700	c 221	7.4	35.2	10	1	AX006877	ACCESSION:AX006877
c 149	7.8	37.1	11	1	AX625055	ACCESSION:AX625055	c 222	7.4	35.2	10	1	AX152364	ACCESSION:AX152364
c 150	7.8	37.1	11	1	AX625310	ACCESSION:AX625310	c 223	7.4	35.2	10	1	AX152365	ACCESSION:AX152365
c 151	7.8	37.1	11	1	AX626546	ACCESSION:AX626546	c 224	7.4	35.2	10	1	AX152532	ACCESSION:AX152532
c 152	7.8	37.1	11	1	AX626575	ACCESSION:AX626575	c 225	7.4	35.2	10	1	AX152671	ACCESSION:AX152671
c 153	7.8	37.1	11	1	AX626823	ACCESSION:AX626823	c 226	7.4	35.2	10	1	AX153299	ACCESSION:AX153299
c 154	7.8	37.1	11	1	AX627065	ACCESSION:AX627065	c 227	7.4	35.2	10	1	AX153300	ACCESSION:AX153300
c 155	7.8	37.1	11	1	AX627186	ACCESSION:AX627186	c 228	7.4	35.2	10	1	AX153313	ACCESSION:AX153313
c 156	7.8	37.1	11	1	AX627348	ACCESSION:AX627348	c 229	7.4	35.2	10	1	AX153316	ACCESSION:AX153316
c 157	7.8	37.1	11	1	AX627678	ACCESSION:AX627678	c 230	7.4	35.2	10	1	AX153317	ACCESSION:AX153317
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c 159	7.8	37.1	11	1	AX628416	ACCESSION:AX628416	c 232	7.4	35.2	10	1	AX153319	ACCESSION:AX153319
c 160	7.8	37.1	11	1	AX628487	ACCESSION:AX628487	c 233	7.4	35.2	10	1	AX224406	ACCESSION:AX224406
c 161	7.8	37.1	11	1	AX629263	ACCESSION:AX629263	c 234	7.4	35.2	10	1	AX224408	ACCESSION:AX224408
c 162	7.8	37.1	11	1	AX629341	ACCESSION:AX629341	c 235	7.4	35.2	10	1	AX224412	ACCESSION:AX224412
c 163	7.8	37.1	11	1	AX629452	ACCESSION:AX629452	c 236	7.4	35.2	10	1	AX224413	ACCESSION:AX224413
c 164	7.8	37.1	11	1	AX629509	ACCESSION:AX629509	c 237	7.4	35.2	10	1	AX224414	ACCESSION:AX224414
c 165	7.8	37.1	11	1	AX630130	ACCESSION:AX630130	c 238	7.4	35.2	10	1	AX224415	ACCESSION:AX224415
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c 167	7.8	37.1	11	1	AX630178	ACCESSION:AX630178	c 240	7.4	35.2	10	1	AX601650	ACCESSION:AX601650
c 168	7.8	37.1	11	1	AX630197	ACCESSION:AX630197	c 241	7.4	35.2	10	1	AX601650	ACCESSION:AX601650
c 169	7.8	37.1	11	1	AX630410	ACCESSION:AX630410	c 242	7.4	35.2	10	1	AX958217	ACCESSION:AX958217
c 170	7.8	37.1	11	1	AX630906	ACCESSION:AX630906	c 243	7.4	35.2	10	1	AX958217	ACCESSION:AX958217
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c 172	7.8	37.1	11	1	AX631246	ACCESSION:AX631246	c 245	7.4	35.2	10	1	BD007960	ACCESSION:BD007960
c 173	7.8	37.1	11	1	AX631370	ACCESSION:AX631370	c 246	7.4	35.2	10	1	AX623125	ACCESSION:AX623125
c 174	7.8	37.1	11	1	AX631647	ACCESSION:AX631647	c 247	7.4	35.2	10	1		
c 175	7.8	37.1	11	1	AX631898	ACCESSION:AX631898	c 248	7.4	35.2	10	1		
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253	7.4	35.2	11	1	AX630546	ACCESSION:AX630546
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257	7.2	34.3	20	1	AR086219	ACCESSION:AR086219
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259	7.2	34.3	20	1	E54824	ACCESSION:E54824
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263	7.2	34.3	20	1	AR071791	ACCESSION:AR071791
264	7.2	34.3	20	1	AR071792	ACCESSION:AR071792
265	7.2	34.3	20	1	AR092694	ACCESSION:AR092694
266	7.2	34.3	20	1	AR092718	ACCESSION:AR092718
267	7.2	34.3	20	1	AR098900	ACCESSION:AR098900
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270	7.2	34.3	20	1	AR107780	ACCESSION:AR107780
271	7.2	34.3	20	1	AR107802	ACCESSION:AR107802
272	7.2	34.3	20	1	AR107825	ACCESSION:AR107825
273	7.2	34.3	20	1	AR172413	ACCESSION:AR172413
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278	7.2	34.3	20	1	BD083293	ACCESSION:BD083293
279	7.2	34.3	20	1	BD161461	ACCESSION:BD161461
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281	7.2	34.3	20	1	BD161467	ACCESSION:BD161467
282	7.2	34.3	20	1	BD161475	ACCESSION:BD161475
283	7.2	34.3	20	1	BD166636	ACCESSION:BD166636
284	7.2	34.3	20	1	BD166798	ACCESSION:BD166798
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287	7.2	34.3	20	1	BD167054	ACCESSION:BD167054
288	7.2	34.3	20	1	BD225345	ACCESSION:BD225345
289	7.2	34.3	20	1	BD238618	ACCESSION:BD238618
290	7.2	34.3	20	1	BD238881	ACCESSION:BD238881
291	7.2	34.3	20	1	BD239109	ACCESSION:BD239109
292	7.2	34.3	20	1	BD239284	ACCESSION:BD239284
293	7.2	34.3	20	1	BD239353	ACCESSION:BD239353
294	7.2	34.3	20	1	BD239760	ACCESSION:BD239760
295	7.2	34.3	20	1	BD240084	ACCESSION:BD240084
296	7.2	34.3	20	1	BD240122	ACCESSION:BD240122
297	7.2	34.3	20	1	BD240437	ACCESSION:BD240437
298	7.2	34.3	20	1	BD240454	ACCESSION:BD240454
299	7.2	34.3	20	1	BD240490	ACCESSION:BD240490
300	7.2	34.3	20	1	BD240601	ACCESSION:BD240601
301	7.2	34.3	20	1	BD249594	ACCESSION:BD249594
302	7.2	34.3	20	1	BD251793	ACCESSION:BD251793
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306	7.2	34.3	20	1	CS106788	ACCESSION:CS106788
307	7.2	34.3	20	1	CS106788	ACCESSION:CS106788
308	7.2	34.3	20	1	ES9637	ACCESSION:ES9637
309	7.2	34.3	20	1	ES9637	ACCESSION:ES9637
310	7.2	34.3	20	1	E64716	ACCESSION:E64716
311	7.2	34.3	20	1	I12013	ACCESSION:I12013
312	7.2	34.3	20	1	I79740	ACCESSION:I79740
313	7.2	34.3	20	1	I86912	ACCESSION:I86912
314	7.2	34.3	20	1	AR202187	ACCESSION:AR202187
315	7.2	34.3	20	1	AR254267	ACCESSION:AR254267
316	7.2	34.3	20	1	AR303347	ACCESSION:AR303347
317	7.2	34.3	20	1	AR303679	ACCESSION:AR303679
318	7.2	34.3	20	1	AR306871	ACCESSION:AR306871
319	7.2	34.3	20	1	AR336879	ACCESSION:AR336879
320	7.2	34.3	20	1	AR351736	ACCESSION:AR351736
321	7.2	34.3	20	1	AR410161	ACCESSION:AR410161
322	7.2	34.3	20	1	AR477264	ACCESSION:AR477264
323	7.2	34.3	20	1	AR489166	ACCESSION:AR489166
324	7.2	34.3	20	1	AR490750	ACCESSION:AR490750
325	7.2	34.3	20	1	AR568611	ACCESSION:AR568611

326	7	33.3	10	1	AR630143	ACCESSION:AR630143
327	7	33.3	10	1	AR630149	ACCESSION:AR630149
328	7	33.3	10	1	AR642556	ACCESSION:AR642556
329	7	33.3	10	1	AR642557	ACCESSION:AR642557
330	7	33.3	10	1	AR642558	ACCESSION:AR642558
331	7	33.3	10	1	AR642559	ACCESSION:AR642559
332	7	33.3	10	1	AX009254	ACCESSION:AX009254
333	7	33.3	10	1	AX009254	ACCESSION:AX009254
334	7	33.3	10	1	AX147040	ACCESSION:AX147040
335	7	33.3	10	1	AX147040	ACCESSION:AX147040
336	7	33.3	10	1	AX152322	ACCESSION:AX152322
337	7	33.3	10	1	AX152346	ACCESSION:AX152346
338	7	33.3	10	1	AX152392	ACCESSION:AX152392
339	7	33.3	10	1	AX152393	ACCESSION:AX152393
340	7	33.3	10	1	AX152609	ACCESSION:AX152609
341	7	33.3	10	1	AX152706	ACCESSION:AX152706
342	7	33.3	10	1	AX153150	ACCESSION:AX153150
343	7	33.3	10	1	AX153156	ACCESSION:AX153156
344	7	33.3	10	1	AX153227	ACCESSION:AX153227
345	7	33.3	10	1	AX153234	ACCESSION:AX153234
346	7	33.3	10	1	AX302590	ACCESSION:AX302590
347	7	33.3	10	1	AX391509	ACCESSION:AX391509
348	7	33.3	10	1	AX391509	ACCESSION:AX391509
349	7	33.3	10	1	AX391511	ACCESSION:AX391511
350	7	33.3	10	1	AX391511	ACCESSION:AX391511
351	7	33.3	10	1	AX667829	ACCESSION:AX667829
352	7	33.3	10	1	AX753482	ACCESSION:AX753482
353	7	33.3	10	1	AX958222	ACCESSION:AX958222
354	7	33.3	10	1	BD007778	ACCESSION:BD007778
355	7	33.3	10	1	BD007922	ACCESSION:BD007922
356	7	33.3	10	1	BD007966	ACCESSION:BD007966

ALIGNMENTS

RESULT 1	AR086219/c	20 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AR086219	Sequence 40 from patent US 5985558.			
DEFINITION	AR086219				
ACCESSION	AR086219.1	GI:10012985			
VERSION	Unknown.				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 20)				
AUTHORS	Dean,N.M., McKay,R., Miraglia,L. and Baker,B.				
TITLE	Antisense oligonucleotide compositions and methods for the				
JOURNAL	inhibition of c-Jun and c-Fos				
FEATURES	Patent: US 5985558-A 40 16-NOV-1999;				
source	Location/Qualifiers				
	1..20				
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Query Match	68.6%;	Score 14.4;	DB 1;	Length 20;	
Best Local Similarity	93.8%;	Pred. No. 6.7;			
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
Qy	6	CCCCGGCGGCTGTGTC	21		
Db	16	CCCCGGCGGCTGTGTC	1		
RESULT 2	AR176785/c	20 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	AR176785	Sequence 40 from patent US 6312900.			
DEFINITION	AR176785				
ACCESSION	AR176785				
VERSION	AR176785.1	GI:17919140			
KEYWORDS	Unknown.				
SOURCE	Unknown.				

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Al13334
LOCUS      Al13334                11 bp    DNA        linear    PAT 18-JAN-1994
DEFINITION B.pertussis DNA for pertussis toxin (S1, AA 956-966).
ACCESSION  Al13334
VERSION     Al13334.1  GI:489617
SOURCE      Bordetella pertussis
ORGANISM    Bordetella pertussis
            Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
            Alcaligenaceae; Bordetella.
REFERENCE   1  (bases 1 to 11)
AUTHORS     Pizza, M., Rappuoli, R. and Bartoloni, A.
TITLE       Bordetella pertussis toxin with altered toxicity
JOURNAL     Patent: EP 032533-A 14 05-JUL-1989;
            SCLAVO S.p.A
FEATURES    Location/Qualifiers
            source          1..11
                        /organism="Bordetella pertussis"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:520"

Query Match      47.6%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7  CCGGCGCGCT 16
        |||||
Db       2  CCGGCGCGCT 11

RESULT 8
CQ766472/c
LOCUS      CQ766472                12 bp    DNA        linear    PAT 03-MAR-2004
DEFINITION Sequence 433 from Patent WO2004005547.
ACCESSION  CQ766472
VERSION     CQ766472.1  GI:44908732
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Weinzierl, R.
METHOD      Method
TITLE       Patent: WO 2004005547-A 433 15-JAN-2004;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
JOURNAL     Location/Qualifiers
FEATURES    Location/Qualifiers
            source          1..12
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="HS motif"

Query Match      47.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  CCGGCGCGCG 15
        |||||
Db       11 CCGGCGCGCG 2

RESULT 9
AX081331/c
LOCUS      AX081331                12 bp    DNA        linear    PAT 27-FEB-2001
DEFINITION Sequence 10 from Patent WO0108707.
ACCESSION  AX081331
VERSION     AX081331.1  GI:13170173
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Uhlmann, E., Greiner, B., Unger, E., Gothe, G. and Schwerdel, M.

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TITLE      Conjugates and methods for the production thereof, and their use
            for transporting molecules via biological membranes
JOURNAL     Patent: WO 0108707-A 10 08-FEB-2001;
            Aventis Pharma Deutschland GmbH (DE)
FEATURES    Location/Qualifiers
            source          1..12
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="modified Oligonucleotide"

Query Match      47.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4  GGCCCGCGCG 13
        |||||
Db       12 GGCCCGCGCG 3

RESULT 10
AR142945/c
LOCUS      AR142945                14 bp    DNA        linear    PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6204026.
ACCESSION  AR142945
VERSION     AR142945.1  GI:15104231
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1  (bases 1 to 14)
AUTHORS     Desjardin, L., Ellen., Cave, M., Donald, and Eisenach, K., Davis.
TITLE       Detection of M. tuberculosis complex via reverse transcriptase SDA
JOURNAL     Patent: US 6204026-A 7 20-MAR-2001;
FEATURES    Location/Qualifiers
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                        /organism="unknown"
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Query Match      46.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8  CGCGCGCGCTGTGG 20
        |||||
Db       14 CGCGCTCGCTGTGG 2

RESULT 11
CS061169
LOCUS      CS061169                14 bp    DNA        linear    PAT 13-APR-2005
DEFINITION Sequence 43 from Patent WO2005026338.
ACCESSION  CS061169
VERSION     CS061169.1  GI:62553190
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Stampfer, W., Kosjek, B., Kroutill, W., Faber, K., Niehaus, F. and Eck, J.
TITLE       Alcohol dehydrogenases with increased solvent and temperature
            stability
JOURNAL     Patent: WO 2005026338-A 43 24-MAR-2005;
            Ciba Specialty Chemicals Holding Inc. (CH)
FEATURES    Location/Qualifiers
            source          1..14
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                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Sequence used as potential probe for identifying
                                Rhodococcus ruber DSM 14855 alcohol dehydrogenase A gene"

Query Match      46.7%; Score 9.8; DB 1; Length 14;

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Best Local Similarity 84.6%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTGGCCCGCGC 13
Db 1 GCGGCCCGCGC 13

RESULT 12
LOCUS CQ836510 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1568 from Patent WO2004059001.
ACCESSION CQ836510
VERSION CQ836510.1 GI:50836044
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conrad,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1568 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/organism="Homo sapiens"
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Query Match 44.8%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTGGCCCGCGC 11
Db 1 GCGGCCCGCGC 11

RESULT 13
LOCUS AX628774 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5815 from Patent WO02053774.
ACCESSION AX628774
VERSION AX628774.1 GI:28456812
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5815 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 90.9%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTGGCCCGCGC 11
Db 1 GCGGCCCGCGC 11

RESULT 14
LOCUS AX630120/c 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7161 from Patent WO02053774.
ACCESSION AX630120
VERSION AX630120.1 GI:28458158
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7161 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/mol_type="unassigned DNA"
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Best Local Similarity 90.9%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GCGCCGCGCGC 14
Db 11 GCGCGCGCGC 1

RESULT 15
LOCUS AX630373 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7414 from Patent WO02053774.
ACCESSION AX630373
VERSION AX630373.1 GI:28458411
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7414 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
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/mol_type="unassigned DNA"
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Query Match 44.8%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GCGCGCTGTGG 20
Db 1 GGGCGCTGTGG 11

RESULT 16
LOCUS CQ766499 12 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 460 from Patent WO2004005547.
ACCESSION CQ766499
VERSION CQ766499.1 GI:44908759
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM

other sequences; artificial sequences.

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1
REFERENCE
AUTHORS Weinzierl,R.
TITLE Patent: WO 2004005547-A 460 15-JAN-2004;
JOURNAL IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
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/noe="HS motif"

Query Match 44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGCG 12
Db 2 CGGGCCCGCG 12

RESULT 17
AR576634/c
LOCUS AR576634 12 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 20 from patent US 6777180.
ACCESSION AR576634
VERSION AR576634.1 GI:56578919
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Fisher,P.B. and Kang,D.-C.
TITLE Method for full-length cDNA cloning using degenerate stem-loop
annealing primers
JOURNAL Patent: US 6777180-A 20 17-AUG-2004;
Trustees of Columbia University in the City of New York; New York,
NY;
WOX;
FEATURES
source
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Location/Qualifiers
/mol_type="unknown"
/organism="unknown"
/mol_type="genomic DNA"

Query Match 44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 15
Db 11 GCCCGCGCGC 1

RESULT 18
AR285789
LOCUS AR285789 13 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 161 from patent US 6528640.
ACCESSION AR285789
VERSION AR285789.1 GI:29723383
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 161 04-MAR-2003;
Ribozyne Pharmaceuticals, incorporated; Boulder, CO
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source
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Location/Qualifiers
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/organism="unknown"

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/mol_type="unassigned RNA"

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Query Match 44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCGC 11
Db 3 GCTGGCTCGC 13

RESULT 19
AR397780
LOCUS AR397780 13 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 161 from patent US 6617438.
ACCESSION AR397780
VERSION AR397780.1 GI:40135041
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 161 09-SEP-2003;
Sirna Therapeutics, Inc.; Boulder, CO
FEATURES
source
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Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match 44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCGC 11
Db 3 GCTGGCTCGC 13

RESULT 20
BD161333/c
LOCUS BD161333 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161333
VERSION BD161333.1 GI:27867091
KEYWORDS JP 2002186482-A/155.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 155 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/155
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
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/organism='Homo sapiens (human)'
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source
1..10
Location/Qualifiers
/mol_type="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Query Match          42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCTG 17
   |||||
Db 9 GCGCGCTG 1

RESULT 21
LOCUS BD238832/c
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238832
VERSION BD238832.1 GI:33048602
KEYWORDS JP 2002534056-A/250.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 250 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/250
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match          42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCTG 17
   |||||
Db 9 GCGCGCTG 1

RESULT 22
LOCUS AR630145
DEFINITION Sequence 199 from patent US 6838556.
ACCESSION AR630145
VERSION AR630145.1 GI:59762469
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 199 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
FEATURES
source
1..10
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match          42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCTG 17
   |||||
Db 1 GCGCGCTG 9

RESULT 23
LOCUS AX152988/c
DEFINITION Sequence 903 from Patent WO0138577.
ACCESSION AX152988
VERSION AX152988.1 GI:14534639
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Vulculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 903 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match          42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCTG 17
   |||||
Db 9 GCGCGCTG 1

RESULT 24
LOCUS AX153495
DEFINITION Sequence 1410 from Patent WO0138577.
ACCESSION AX153495
VERSION AX153495.1 GI:14535146
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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REFERENCE
1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1410 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
|||||
Db 1 CTGGCCCGG 9

RESULT 25
AX153496
LOCUS AX153496 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1411 from Patent WO0138577.
ACCESSION AX153496
VERSION AX153496.1 GI:14535147
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1411 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
|||||
Db 1 CTGGCCCGG 9

RESULT 26
CQ833102/c
LOCUS CQ833102 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 473 from Patent WO2004059002.
ACCESSION CQ833102
VERSION CQ833102.1 GI:50832709
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 473 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"

Query Match 42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
|||||
Db 1 CTGGCCCGG 9

RESULT 27
AX630364/c
LOCUS AX630364 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7405 from Patent WO2053774.
ACCESSION AX630364
VERSION AX630364.1 GI:28458402
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7405 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
|||||
Db 9 GGCGCGCTG 1

RESULT 28
CS086764
LOCUS CS086764 12 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 13 from Patent WO2005042018.
ACCESSION CS086764
VERSION CS086764.1 GI:66712215
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
1
AUTHORS Uhlmann,E., Vollmer,J., Krieg,A.M. and Noll,B.O.
TITLE C-class oligonucleotide analogs with enhanced immunostimulatory
JOURNAL potency
Patent: WO 2005042018-A 13 12-MAY-2005;
Coley Pharmaceutical GmbH (DE); Coley Pharmaceutical Group, Inc.
(US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide"

Query Match 42.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17

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Db      1  GCGCGCGCTG 9
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RESULT 29
AR630091/c
LOCUS      12 bp  DNA
DEFINITION Sequence 145 from patent US 6838556.
ACCESSION  AR630091
VERSION     AR630091.1  GI:59762360
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 12)
AUTHORS    Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
            Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
            Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE      Promoters for regulated gene expression
JOURNAL    Patent: US 6838556-A 145 04-JAN-2005;
            Genelabs Technologies, Inc.; Redwood City, CA
FEATURES   Location/Qualifiers
            source
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                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 42.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10  GCGCGCTGT 18
|||||||
Db      9  GCGCGCTGT 1

RESULT 30
CQ766472
LOCUS      12 bp  DNA
DEFINITION Sequence 433 from Patent WO2004005547.
ACCESSION  CQ766472
VERSION     CQ766472.1  GI:44908732
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Weinzierl,R.
TITLE      Method
JOURNAL    Patent: WO 2004005547-A 433 15-JAN-2004;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES   Location/Qualifiers
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="HS motif"

Query Match 41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9  GCGCGCTGTGG 20
|||||||
Db      1  GCGCGCGCGGG 12

RESULT 31
CQ766470/c
LOCUS      12 bp  DNA
DEFINITION Sequence 431 from Patent WO2004005547.
ACCESSION  CQ766470
VERSION     CQ766470.1  GI:44908730
KEYWORDS   .

Db      1  GCGCGCGCGGG 12

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SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Weinzierl,R.
TITLE      Method
JOURNAL    Patent: WO 2004005547-A 431 15-JAN-2004;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES   Location/Qualifiers
            source
              1..12
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="HS motif"

Query Match 41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CTGGCCCGCGCG 13
|||||||
Db      12  CTGGCCCGCGCG 1

RESULT 32
CQ983522
LOCUS      12 bp  DNA
DEFINITION Sequence 17 from Patent WO2005003384.
ACCESSION  CQ983522
VERSION     CQ983522.1  GI:58191883
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Bender,M. and Jacobsen,C.S.
TITLE      Method for selective detection of a target nucleic acid
JOURNAL    Patent: WO 2005003384-A 17 13-JAN-2005;
            Danmarks og Gronlands Geologiske Undersogelse (DK)
FEATURES   Location/Qualifiers
            source
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Universal Bacterial 16S primer"

Query Match 41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCTGGCCCGCGG 12
|||||||
Db      1  GCTGGCACGGAG 12

RESULT 33
CQ983659
LOCUS      12 bp  DNA
DEFINITION Sequence 154 from Patent WO2005003384.
ACCESSION  CQ983659
VERSION     CQ983659.1  GI:58192020
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Bender,M. and Jacobsen,C.S.
TITLE      Method for selective detection of a target nucleic acid
JOURNAL    Patent: WO 2005003384-A 154 13-JAN-2005;
            Danmarks og Gronlands Geologiske Undersogelse (DK)
FEATURES   Location/Qualifiers
            source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="511R2"

Query Match
Best Local Similarity 41.9%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCTGGCCCGCGC 12
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Db 1 GCTGGCAGCGG 12

RESULT 34
AX298228/c
LOCUS AX298228 12 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 9 from Patent WO0183735.
ACCESSION AX298228
VERSION AX298228.1 GI:17128282
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Dutreix,M., Sun,J.S., Biet,E., Maurisse,R. and Feugeas,J.P.
  Methods and compositions for effecting homologous recombination
  Patent: WO 0183735-A 9 08-NOV-2001;
  Institut Curie (FR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
  (CNRS) (FR); MUSEUM NATIONAL D'HISTOIRE NATURELLE (FR) ; INSTITUT
  NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR)
FEATURES
source
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/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="oligonucleotide"

Query Match
Best Local Similarity 41.9%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCTGGCCCGCGC 12
    ||||| |||
Db 12 GCTGGCCACGCG 1

RESULT 35
S88396S1/c
LOCUS S88396S1 12 bp DNA linear PRI 19-JUL-1993
DEFINITION dystrophin, dystrophin [human, Genomic Mutant; 12 nt, segment 1 of
2].
ACCESSION S88396
VERSION S88396.1 GI:247278
KEYWORDS
SEGMENT 1 of 2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
2 (bases 1 to 12)
AUTHORS Roberts,R.G., Bobrow,M. and Bentley,D.R.
TITLE Point mutations in the dystrophin gene
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (6), 2331-2335 (1992)
PUBMED 1549596
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gbbbsq 88396] from the original journal article.
FEATURES
source
1..12
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1..12

CDS

Query Match
Best Local Similarity 41.9%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCTGGCCCGCGC 12
    ||||| |||
Db 12 GCTGGCTCGGG 1

RESULT 36
AR058606
LOCUS AR058606 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 183 from patent US 5837832.
ACCESSION AR058606
VERSION AR058606.1 GI:5984183
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
  Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 183 17-NOV-1998;
FEATURES
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 40.0%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGCCCGCGCGC 13
    ||||| ||
Db 1 GGCCCGGAGC 10

RESULT 37
BD166545/c
LOCUS BD166545 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166545
VERSION BD166545.1 GI:27872357
KEYWORDS JP 2002209591-A/90.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 90 30-JUL-2002;
  JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/90
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
  YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
  PC C12P21/08,
  PC C12N15/00
  CC Human liver disease-expressing genes
  FH Key Location/Qualifiers
  FT source 1..10
  FT /organism='Homo sapiens (human)'.

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FEATURES
source
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    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

Query Match
Best Local Similarity 40.0%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGCCCGCG 10
Db 10 GCTGCCCGCAG 1

RESULT 38
BD225304
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
    OS Artificial Sequence
    PN JP 2002509706-A/3
    PD 02-APR-2002
    PF 30-MAR-1999 JP 2000540746
    PR 31-MAR-1998 US 60/080044
    PI JIN JEN, GARY A BEAUDRY, STEPHEN L MADDEN, ARTHUR H BERTELSEN PC
    C12N15/09, A61K45/00, A61K48/00, A61P35/00, C12Q1/68, G01N33/50, PC
    G01N33/574,
    PC C12N15/00
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    /organism="synthetic construct"
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Best Local Similarity 40.0%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGCGCG 12
Db 1 TGGCCCGCAG 10

RESULT 39
BD225338
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
    OS Artificial Sequence
    PN JP 2002509707-A/20
    PD 02-APR-2002
    PF 30-MAR-1999 JP 2000541180
    PR 31-MAR-1998 US 60/080037
    PI GARY A BEAUDRY, STEPHEN L MADDEN, ARTHUR H BERTELSEN PC
    C12N15/09, A01K67/027, C07H21/04, C07K14/47, C07K16/18, C12N1/15, PC
    C12N1/19,
    PC C12N1/21, C12N5/10, C12P21/08, C12Q1/68, G01N33/15, G01N33/53, PC
    G01N33/566//
    CC Compositions and methods for the identification of lung tumor
    cells

QY 1 GTCGCCCGCG 10
Db 10 GCTGCCCGCAG 1

RESULT 40
BD238621/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
    OS Homo sapiens (human)
    PN JP 2002534056-A/39
    PD 15-OCT-2002
    PF 18-JUN-1999 JP 2000554749
    PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
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    19-JUN-1998 US 60/090035, 19-JUN-1998 US 60/089993 PR
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    19-JUN-1998 US 60/090076, 19-JUN-1998 US 60/090045 PR
    08-DEC-1998 US 60/111715
    PI BRUCE L ROBERTS, SRINIVAS SHANKARA
    PC C12N15/09, C12N15/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
    C12N1/19,
    G01N37/00,

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GENZYME CORP
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PN JP 2002509707-A/20
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541180
PR 31-MAR-1998 US 60/080037
PI GARY A BEAUDRY, STEPHEN L MADDEN, ARTHUR H BERTELSEN PC
C12N15/09, A01K67/027, C07H21/04, C07K14/47, C07K16/18, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, C12P21/08, C12Q1/68, G01N33/15, G01N33/53, PC
G01N33/566//
CC Compositions and methods for the identification of lung tumor
cells

FH Key Location/Qualifiers
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/organism="synthetic construct"
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QY 3 TGGCCCGCGCG 12
Db 1 TGGCCCGCAG 10

RESULT 40
BD238621/c
LOCUS
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VERSION
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ORGANISM
REFERENCE
AUTHORS
TITLE
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    OS Homo sapiens (human)
    PN JP 2002534056-A/39
    PD 15-OCT-2002
    PF 18-JUN-1999 JP 2000554749
    PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
    19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
    19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/090079 PR
    19-JUN-1998 US 60/090035, 19-JUN-1998 US 60/089993 PR
    19-JUN-1998 US 60/089992, 19-JUN-1998 US 60/090072 PR
    19-JUN-1998 US 60/089878, 19-JUN-1998 US 60/089991 PR
    19-JUN-1998 US 60/090000, 19-JUN-1998 US 60/090048 PR
    19-JUN-1998 US 60/089999, 19-JUN-1998 US 60/090043 PR
    19-JUN-1998 US 60/090042, 19-JUN-1998 US 60/090036 PR
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    19-JUN-1998 US 60/090080, 19-JUN-1998 US 60/089833 PR
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    19-JUN-1998 US 60/090076, 19-JUN-1998 US 60/090045 PR
    08-DEC-1998 US 60/111715
    PI BRUCE L ROBERTS, SRINIVAS SHANKARA
    PC C12N15/09, C12N15/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
    C12N1/19,
    G01N37/00,

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PC      C12N15/00,C12N5/00,C12N15/00
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Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCGG 10
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Db       10 GCTGGCCCG 1

RESULT 41
CQ986655/c
LOCUS      CQ986655
DEFINITION Sequence 199 from Patent WO2005001142.
ACCESSION CQ986655
VERSION    CQ986655.1 GI:58194572
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS    Lofton-Day,C., Sledziewski,A., Thomas,J., Day,R.W.,
            Tonnes-Priddy,L. and Cardon,K.
TITLE      Methods and nucleic acids for the analysis of colorectal cell
            proliferative disorders
JOURNAL    Patent: WO 2005001142-A 199 06-JAN-2005;
            Epigenomics AG (DE)
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          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
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Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCGGGCGCGC 15
        |||||
Db       10 CGCGGGCGCG 1

RESULT 42
CS114173/c
LOCUS      CS114173
DEFINITION Sequence 931 from Patent WO2005054517.
ACCESSION CS114173
VERSION    CS114173.1 GI:68225718
KEYWORDS   .
SOURCE     synthetic construct
            other sequences; artificial sequences.
ORGANISM   1
REFERENCE   1
AUTHORS    Day,K.J., Cottrell,S., Distler,J., Morotti,A., Yamamura,S.,
            Dekker,S., Ocamp,Y. and Devos,T.
TITLE      Methods and nucleic acids for the analysis of gene expression
            associated with the development of prostate cell proliferative
            disorders
JOURNAL    Patent: WO 2005054517-A 931 16-JUN-2005;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
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          /db_xref="taxon:9606"
Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCGGGCGCGC 15
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Db       10 CGCGGGCGCG 1

RESULT 43
E39738/c
LOCUS      E39738
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39738
VERSION    E39738.1 GI:18621829
KEYWORDS   JP 2000279181-A/271.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 10)
AUTHORS    Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE      Genes with human dendritic cell expression
JOURNAL    Patent: JP 2000279181-A 271 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2000279181-A/271
            PD 10-OCT-2000
            PF 01-APR-1999 JP 1999095481
            PR
            PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
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QY      1 GCTGGCCCGG 10
        |||||
Db       10 GCTGGCCCG 1

RESULT 44
E54818
LOCUS      E54818
DEFINITION Human normal liver cell expression genes.
ACCESSION E54818
VERSION    E54818.1 GI:22556301
KEYWORDS   JP 2001211883-A/170.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human normal liver cell expression genes

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source
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Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCGGGCGCGC 15
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Db       10 CGCGGGCGCG 1

RESULT 43
E39738/c
LOCUS      E39738
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39738
VERSION    E39738.1 GI:18621829
KEYWORDS   JP 2000279181-A/271.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 10)
AUTHORS    Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE      Genes with human dendritic cell expression
JOURNAL    Patent: JP 2000279181-A 271 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2000279181-A/271
            PD 10-OCT-2000
            PF 01-APR-1999 JP 1999095481
            PR
            PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
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Query Match          40.0%; Score 8.4; DB 1; Length 10;
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QY      1 GCTGGCCCGG 10
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Db       10 GCTGGCCCG 1

RESULT 44
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LOCUS      E54818
DEFINITION Human normal liver cell expression genes.
ACCESSION E54818
VERSION    E54818.1 GI:22556301
KEYWORDS   JP 2001211883-A/170.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human normal liver cell expression genes

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JOURNAL Patent: JP 2001211883-A 170 07-AUG-2001;
 COMMENT SCIENCE & TECH AGENCY
 OS Homo sapiens (human)
 PN JP 2001211883-A/170
 PD 07-AUG-2001
 PF 31-JAN-2000 JP 2000023170
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
 YAMASHITA
 PC C12N15/09, C07K16/18, C12P21/02, C12N15/00
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 FH Key Location/Qualifiers.
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 Best Local Similarity 90.0%; Pred. No. 56;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GCGCGCTGTG 19
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 Db 1 GCGCGCTGTG 10
 RESULT 45
 E54824/c
 LOCUS Human normal liver cell expression genes. 10 bp DNA linear PAT 27-AUG-2002
 DEFINITION
 E54824 Human normal liver cell expression genes.
 E54824
 E54824.1 GI:22556307
 VERSION JP 2001211883-A/176.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 10)
 AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
 TITLE Human normal liver cell expression genes
 JOURNAL Patent: JP 2001211883-A 176 07-AUG-2001;
 COMMENT SCIENCE & TECH AGENCY
 OS Homo sapiens (human)
 PN JP 2001211883-A/176
 PD 07-AUG-2001
 PF 31-JAN-2000 JP 2000023170
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
 YAMASHITA
 PC C12N15/09, C07K16/18, C12P21/02, C12N15/00
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 FH Key Location/Qualifiers.
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 Best Local Similarity 90.0%; Pred. No. 56;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCCCGCGCGC 14
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 Db 10 GCCCGCGCGC 1
 RESULT 46
 AR630141/c
 LOCUS AR630141
 DEFINITION Sequence 195 from patent US 6838556.
 ACCESSION AR630141
 VERSION AR630141.1 GI:59762461

KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Kim, J. P., Starr, D. B., Tam, A. W., Laurance, M. E., Michelotti, E. F., Velligan, M. D., Latour, D. R., Thomas, R. L., Kongpachith, A., Sheppard, L. T., Kim, M. Y. and Bruce, T. W.
 TITLE Promoters for regulated gene expression
 JOURNAL Patent: US 6838556-A 195 04-JAN-2005;
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 1. .10
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 40.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 56;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CCCGCGCGC 15
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 Db 10 CCGGCGCGC 1
 RESULT 47
 AX152803
 LOCUS Sequence 718 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
 DEFINITION
 AX152803
 ACCESSION AX152803
 VERSION AX152803.1 GI:14534454
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE
 1
 AUTHORS Velculescu, V. E., Vogelstein, B. and Kinzler, K. W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 718 31-MAY-2001;
 The Johns Hopkins University (US)
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 Best Local Similarity 90.0%; Pred. No. 56;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GCGCGCTGTG 19
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 Db 1 GCGCGCTGTG 10
 RESULT 48
 AX224404/c
 LOCUS Sequence 11 from Patent WO0160997. 10 bp DNA linear PAT 10-SRP-2001
 DEFINITION
 AX224404
 ACCESSION AX224404
 VERSION AX224404.1 GI:15554646
 KEYWORDS Zea mays
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE
 1
 AUTHORS Albertsen, M. C., Fox, T. W., Garnaat, C. W., Huffman, G. and Kendall, T. L.
 TITLE Male tissue-preferred regulatory region and method of using same
 JOURNAL Patent: WO 0160997-A 11 23-AUG-2001;

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      /db_xref="taxon:4577"

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QY 2 CTGCCCGGC 11
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Db 10 CGGCCCGGC 1

RESULT 49
AX224407
LOCUS AX224407 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 14 from Patent WO0160997.
ACCESSION AX224407
VERSION AX224407.1 GI:15554649
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
  1. Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.
  Male tissue-preferred regulatory region and method of using same
  Patent: WO 0160997-A 14 23-AUG-2001;
  PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Db 1 CGGCCCGGC 10

RESULT 50
AX301612
LOCUS AX301612 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 326 from Patent WO0185941.
ACCESSION AX301612
VERSION AX301612.1 GI:17382695
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
  1. Versteeg, R. and Caron, H.N.
  Myc targets
  Patent: WO 0185941-A 326 15-NOV-2001;
  Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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Query Match
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QY 2 CTGCCCGGC 11
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Db 1 CGGCCCGGC 10

RESULT 51
AX339231
LOCUS AX339231 10 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 25 from Patent WO0196602.
ACCESSION AX339231
VERSION AX339231.1 GI:18135492
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
  1. Yang, A.L. and Festing, M.
  Methods and materials to determine the p53 status of a sample by
  determining the binding of p53 to a vector
  Patent: WO 0196602-A 25 20-DEC-2001;
  MEDICAL RESEARCH COUNCIL (GB)
FEATURES
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Query Match
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QY 8 CGCGCGCTG 17
   | | | | | | | |
Db 1 CGCGCGCTG 10

RESULT 52
AX753475
LOCUS AX753475 10 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 20 from Patent EP1310556.
ACCESSION AX753475
VERSION AX753475.1 GI:32166235
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
  1. Beaudry, G.A., Madden, S.L. and Bertelsen, A.H.
  Composition and methods for the identification of lung tumor cells
  Patent: EP 1310556-A 20 14-MAY-2003;
  GENZYME CORPORATION (US)
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Query Match
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  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 12
   | | | | | | | |
Db 1 TGGCCCGGC 10

RESULT 53
AX814774/c
LOCUS AX814774 10 bp DNA linear PAT 05-DEC-2003

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DEFINITION      Sequence 20 from Patent WO03064701.
ACCESSION       AX814774
VERSION         AX814774.1  GI:39103968
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        other sequences; artificial sequences.
REFERENCE
1
AUTHORS         Sledziewski,A. and Schweikhardt,R.G.
TITLE           Method for the analysis of cytosine methylation patterns
JOURNAL         Patent: WO 03064701-A 20 07-AUG-2003;
                Epigenomics AG (DE)
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                /note="AP-PCR Primer CG4"

Query Match      40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              6 CCGGGCGCGC 15
                ||||||
Db              10 CGGGCGCGC 1

RESULT 54
LOCUS           CQ833458                11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION      Sequence 829 from Patent WO2004059002.
ACCESSION       CQ833458
VERSION         CQ833458.1  GI:50833065
KEYWORDS        .
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE
1
AUTHORS         Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
                Conradt,M. and Hofmann,K.
TITLE           Method for determining the homeostasis of hairy skin
JOURNAL         Patent: WO 2004059002-A 829 15-JUL-2004;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES        Location/Qualifiers
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              12 GGCCTGTGGC 21
                ||||||
Db              2 GGCCTGTGGC 11

RESULT 55
LOCUS           CQ833790                11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION      Sequence 1161 from Patent WO2004059002.
ACCESSION       CQ833790
VERSION         CQ833790.1  GI:50833397
KEYWORDS        .
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
DEFINITION      Sequence 20 from Patent WO03064701.
ACCESSION       AX814774
VERSION         AX814774.1  GI:39103968
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        other sequences; artificial sequences.
REFERENCE
1
AUTHORS         Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
                Conradt,M. and Hofmann,K.
TITLE           Method for determining the homeostasis of hairy skin
JOURNAL         Patent: WO 2004059002-A 1161 15-JUL-2004;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES        Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              12 GGCCTGTGGC 21
                ||||||
Db              11 GGCAGTGGC 2

RESULT 57
LOCUS           CQ835396/c              11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION      Sequence 454 from Patent WO2004059001.
ACCESSION       CQ835396
VERSION         CQ835396.1  GI:50834930
KEYWORDS        .
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE
1
AUTHORS         Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
                Conradt,M. and Hofmann,K.
TITLE           Method for determining markers of human facial skin
JOURNAL         Patent: WO 2004059001-A 454 15-JUL-2004;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES        Location/Qualifiers
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              12 GGCCTGTGGC 21
                ||||||
Db              11 GGCAGTGGC 2

RESULT 57
LOCUS           CQ835396/c              11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION      Sequence 454 from Patent WO2004059001.
ACCESSION       CQ835396
VERSION         CQ835396.1  GI:50834930
KEYWORDS        .
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE
1
AUTHORS         Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
                Conradt,M. and Hofmann,K.
TITLE           Method for determining markers of human facial skin
JOURNAL         Patent: WO 2004059001-A 454 15-JUL-2004;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES        Location/Qualifiers
                1..11
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY              12 GGCCTGTGGC 21
                ||||||
Db              11 GGCAGTGGC 2

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source      1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCCCGCGCGC 14
      ||| |||||
Db      11 GCCTGCGCGC 2

RESULT 58
LOCUS      CQ835763
DEFINITION      Sequence 821 from Patent WO2004059001.
ACCESSION      CQ835763
VERSION      CQ835763.1 GI:50835297
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 821 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
source      1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCCCGCG 11
      ||| |||||
Db      2 CTGGCCCGCG 11

RESULT 59
LOCUS      CQ837774
DEFINITION      Sequence 2832 from Patent WO2004059001.
ACCESSION      CQ837774
VERSION      CQ837774.1 GI:50837308
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2832 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
source      1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCCCGCG 11
      ||| |||||
Db      2 CTGGCCCGCG 11

RESULT 60
LOCUS      CQ837882
DEFINITION      Sequence 2940 from Patent WO2004059001.
ACCESSION      CQ837882
VERSION      CQ837882.1 GI:50837416
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2940 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
source      1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCCCGCGCGC 14
      ||| |||||
Db      2 GCCCGCGCGC 11

RESULT 61
LOCUS      CQ838018
DEFINITION      Sequence 3076 from Patent WO2004059001.
ACCESSION      CQ838018
VERSION      CQ838018.1 GI:50837552
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 3076 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
source      1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 GCGCTGTGCG 21
      ||| |||||
Db      2 GCGCTGTGCG 11

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RESULT 62
CS058243/c
LOCUS          11 bp      DNA          linear          PAT 13-APR-2005
DEFINITION     Sequence 140 from Patent WO2005028671.
ACCESSION      CS058243
VERSION        CS058243.1  GI:62551426
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
               Kessler-Becker,D.
TITLE          Method for determining hair cycle markers
JOURNAL        Patent: WO 2005028671-A 140 31-MAR-2005;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
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Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5  GCCCGCGCGG 14
Db      11 GCCCGCGCGG 2

RESULT 63
CS058293
LOCUS          11 bp      DNA          linear          PAT 13-APR-2005
DEFINITION     Sequence 190 from Patent WO2005028671.
ACCESSION      CS058293
VERSION        CS058293.1  GI:62551476
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
               Kessler-Becker,D.
TITLE          Method for determining hair cycle markers
JOURNAL        Patent: WO 2005028671-A 190 31-MAR-2005;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
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               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5  GCCCGCGCGG 14
Db      11 GCCCGCGCGG 2

RESULT 64
CS058370
LOCUS          11 bp      DNA          linear          PAT 13-APR-2005
DEFINITION     Sequence 267 from Patent WO2005028671.
ACCESSION      CS058370
VERSION        CS058370.1  GI:62551553
KEYWORDS       .
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SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
               Kessler-Becker,D.
TITLE          Method for determining hair cycle markers
JOURNAL        Patent: WO 2005028671-A 267 31-MAR-2005;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
               source
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               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  TGGCCCGCGG 12
Db      1  TGGCCCGCGG 10

RESULT 65
CS058633/c
LOCUS          11 bp      DNA          linear          PAT 13-APR-2005
DEFINITION     Sequence 530 from Patent WO2005028671.
ACCESSION      CS058633
VERSION        CS058633.1  GI:62551816
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
               Kessler-Becker,D.
TITLE          Method for determining hair cycle markers
JOURNAL        Patent: WO 2005028671-A 530 31-MAR-2005;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
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               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5  GCCCGCGCGG 14
Db      11 GCCCGCGCGG 2

RESULT 66
CS058641/c
LOCUS          11 bp      DNA          linear          PAT 13-APR-2005
DEFINITION     Sequence 538 from Patent WO2005028671.
ACCESSION      CS058641
VERSION        CS058641.1  GI:62551824
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
```



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Kessler-Becker,D.
Method for determining hair cycle markers
Patent: WO 2005028671-A 538 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 40.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GCGCTGTGGC 21
Db 11 GCGCGTGGC 2

RESULT 67
AX470640/c
LOCUS AX470640 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 217 from Patent WO2053773.
ACCESSION AX470640
VERSION AX470640.1 GI:22205765
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 217 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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Query Match
Best Local Similarity 40.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCGG 10
Db 10 GCTGGCCCGG 1

RESULT 68
AX470863
LOCUS AX470863 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 440 from Patent WO2053773.
ACCESSION AX470863
VERSION AX470863.1 GI:22205988
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 440 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 40.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCGG 10
Db 10 GCTGGCCCGG 1

RESULT 69
AX471737/c
LOCUS AX471737 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1314 from Patent WO2053773.
ACCESSION AX471737
VERSION AX471737.1 GI:22206862
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1314 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 40.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGCGCGG 14
Db 11 GCCCGCGCGG 2

RESULT 70
AX482034
LOCUS AX482034 11 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 11 from Patent EP1225233.
ACCESSION AX482034
VERSION AX482034.1 GI:22316756
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1225233-A 11 24-JUL-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
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    1. .11
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="TAG sequence Hs183"

Query Match
Best Local Similarity 40.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCGGC 11
Db 2 CTGGCCCGGC 11

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RESULT 71
AX511273
LOCUS AX511273 11 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 11 from Patent WO02059558.
ACCESSION AX511273
VERSION AX511273.1 GI:23392150
SOURCE .
KEYWORDS synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: WO 02059558-A 11 01-AUG-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="TAG sequence Hs183"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGC 11
|||||
Db 2 CTGGCCCGC 11

RESULT 72
AX623125/c
LOCUS AX623125 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 166 from Patent WO02053774.
ACCESSION AX623125
VERSION AX623125.1 GI:28451066
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 166 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGC 11
|||||
Db 10 CTGGCCCGC 1

RESULT 73
AX623608
LOCUS AX623608 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 649 from Patent WO02053774.
ACCESSION AX623608
VERSION AX623608.1 GI:28451549
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 649 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGC 11
|||||
Db 10 CTGGCCCGC 1

RESULT 74
AX625821/c
LOCUS AX625821 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2862 from Patent WO02053774.
ACCESSION AX625821
VERSION AX625821.1 GI:28453762
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2862 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGC 11
|||||
Db 2 CTGGCCCGC 11

RESULT 75
AX625842
LOCUS AX625842 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2883 from Patent WO02053774.
ACCESSION AX625842
VERSION AX625842.1 GI:28453878
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2883 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 649 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGC 11
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Db 2 CTGGCCCGC 11

RESULT 74
AX625821/c
LOCUS AX625821 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2862 from Patent WO02053774.
ACCESSION AX625821
VERSION AX625821.1 GI:28453762
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2862 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCGC 10
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Db 10 GCTGGCCCGC 1

RESULT 75
AX625842
LOCUS AX625842 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2883 from Patent WO02053774.
ACCESSION AX625842
VERSION AX625842.1 GI:28453878
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2883 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGCCCGCGC 11
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Db 1 CTGCCAGGC 10

RESULT 76
AX626754/c
LOCUS AX626754 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3795 from Patent WO02053774.
ACCESSION AX626754
VERSION AX626754.1 GI:28454792
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 3795 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCGCTGTGGC 21
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Db 11 GCGCAGTGGC 2

RESULT 77
AX628541
LOCUS AX628541 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5582 from Patent WO02053774.
ACCESSION AX628541
VERSION AX628541.1 GI:28456579
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5582 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
Location/Qualifiers
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Query Match
Best Local Similarity 40.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCGCTGTGGC 21
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Db 11 GCGCAGTGGC 2

RESULT 78
AX629212
LOCUS AX629212 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6253 from Patent WO02053774.
ACCESSION AX629212
VERSION AX629212.1 GI:28457250
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 6253 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
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Query Match
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGCCCGCGC 11
    |||||
Db 2 CTGCCAGGC 11

RESULT 79
AX629295
LOCUS AX629295 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6336 from Patent WO02053774.
ACCESSION AX629295
VERSION AX629295.1 GI:28457333
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 6336 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 14
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Db 1 GCCCGCGCGC 10

RESULT 80
AX629700
LOCUS AX629700 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6741 from Patent WO02053774.
ACCESSION AX629700

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VERSION AX629700.1 GI:28457738
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6741 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
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/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCCGCG 14
Db 2 GCCCGCCGCG 11

RESULT 81
LOCUS AX630546/c 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7587 from Patent WO02053774.
ACCESSION AX630546
VERSION AX630546.1 GI:28458584
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7587 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCCGCG 14
Db 2 GCCCGCCGCG 11

RESULT 82
LOCUS AX631029 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8070 from Patent WO02053774.
ACCESSION AX631029
VERSION AX631029.1 GI:28459071
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

VERSION AX629700.1 GI:28457738
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6741 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCCGCG 14
Db 2 GCCCGCCGCG 11

RESULT 81
LOCUS AX630546/c 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7587 from Patent WO02053774.
ACCESSION AX630546
VERSION AX630546.1 GI:28458584
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7587 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCCGCG 14
Db 2 GCCCGCCGCG 11

RESULT 82
LOCUS AX631029 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8070 from Patent WO02053774.
ACCESSION AX631029
VERSION AX631029.1 GI:28459071
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8070 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCCGCG 14
Db 2 GCCCGCCGCG 11

RESULT 83
LOCUS CQ766406 12 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 367 from Patent WO2004005547.
ACCESSION CQ766406
VERSION CQ766406.1 GI:44908666
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weinzierl,R.
TITLE Method
JOURNAL Patent: WO 2004005547-A 367 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES Location/Qualifiers
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1..12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HS motif"

Query Match 40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGCG 11
Db 3 CTGGCCCGCG 12

RESULT 84
LOCUS CQ766468 12 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 429 from Patent WO2004005547.
ACCESSION CQ766468
VERSION CQ766468.1 GI:44908728
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weinzierl,R.
TITLE Method
JOURNAL Patent: WO 2004005547-A 429 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HS motif"

Query Match 40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGCG 11
Db 3 CTGGCCCGCG 12

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Matches      9;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      4  GCGCCGCGCG 13
DB      1  GTCCCGCGCG 10

RESULT 85
LOCUS      CQ766480/c
DEFINITION      Sequence 441 from Patent WO2004005547.
ACCESSION      CQ766480
VERSION      CQ766480.1
KEYWORDS      12 bp DNA linear PAT 03-MAR-2004
SOURCE      synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Weinzierl, R.
TITLE      Method
JOURNAL      Patent: WO 2004005547-A 441 15-JAN-2004;
JOURNAL      IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES      Location/Qualifiers
source      1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="HS motif"

Query Match      40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches      9;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      7  CCGCGCGCGCT 16
DB      10 CCGCGCGCGCT 1

RESULT 86
LOCUS      AR678905/c
DEFINITION      Sequence 50 from patent US 6902894.
ACCESSION      AR678905
VERSION      AR678905.1
KEYWORDS      12 bp DNA linear PAT 13-JUN-2005
SOURCE      Sequence 50 from patent US 6902894.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 12)
AUTHORS      Yang, M. and Woo, H.S.
TITLE      Mutation detection on RNA polymerase beta subunit gene having
JOURNAL      rifampin resistance
JOURNAL      Patent: US 6902894-A 50 07-JUN-2005;
JOURNAL      Genetel Pharmaceuticals Ltd.; Hong Kong;
JOURNAL      CNX;
FEATURES      Location/Qualifiers
source      1..12
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches      9;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      12 GCGCTGTGGC 21
DB      11 GCGCTGTGGGC 2

RESULT 87
LOCUS      AR103254/c
DEFINITION      Sequence 4 from patent US 6087170.

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ACCESSION      AR103254
VERSION      AR103254.1
KEYWORDS      GI:12814842
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Unclassified.
TITLE      1 (bases 1 to 10)
JOURNAL      Kemble, G. William.
JOURNAL      VZV gene, mutant VZV and immunogenic compositions
JOURNAL      Patent: US 6087170-A 4 11-JUL-2000;
FEATURES      Location/Qualifiers
source      1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      8  CGGCGCGC 15
DB      10 CGGCGCGC 3

RESULT 88
LOCUS      BD083308
DEFINITION      Human matured/activated dendritic cell expression genes.
ACCESSION      BD083308
VERSION      BD083308.1
KEYWORDS      10 bp DNA linear PAT 27-AUG-2002
SOURCE      JP 2001327293-A/229.
ORGANISM      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Matsushima, K., Hashimoto, S., Suzuki, T. and Nagai, S.
TITLE      Human matured/activated dendritic cell expression genes
JOURNAL      Patent: JP 2001327293-A 229 27-NOV-2001;
JOURNAL      JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
            PN JP 2001327293-A/229
            PD 27-NOV-2001
            PF 22-MAY-2000 JP 2000150562
            PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
            NAGAI
            PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
            CC
            FH Key Location/Qualifiers.
FEATURES      Location/Qualifiers
source      1..10
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Query Match      38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      2  CTGGCCCG 9
DB      1  CTGGCCCG 8

RESULT 89
LOCUS      BD167068/c
DEFINITION      Human liver disease-expressing genes.
ACCESSION      BD167068
VERSION      BD167068.1
KEYWORDS      10 bp DNA linear PAT 17-JAN-2003
SOURCE      JP 2002209591-A/613.
            unidentified

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankar,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 1876 15-OCT-2002;
GENZYME CORP
COMMENT     OS Homo sapiens (human)
PN JP 2002534056-A/1876
PD 15-OCT-2002
PP 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
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19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
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source
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/organism='Homo sapiens'
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/db_xref='taxon:9606'
Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCCC 8
Db 9 GCTGGCCC 2
RESULT 93
E54660/c
LOCUS      Human normal liver cell expression genes.
ACCESSION  E54660
VERSION     E54660.1 GI:22556143
KEYWORDS    JP 2001211883-A/12.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human normal liver cell expression genes
JOURNAL    Patent: JP 2001211883-A 12 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
PN JP 2001211883-A/12
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankar,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 1876 15-OCT-2002;
GENZYME CORP
COMMENT     OS Homo sapiens (human)
PN JP 2002534056-A/1876
PD 15-OCT-2002
PP 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCCC 8
Db 9 GCTGGCCC 2
RESULT 95
AR630146/c
LOCUS      Sequence 200 from patent US 6838556.
ACCESSION  AR630146
VERSION     AR630146.1 GI:59762471
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE      Promoters for regulated gene expression
JOURNAL    Patent: US 6838556-A 200 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
FEATURES
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/mol_type='genomic DNA'
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CGCGCGGC 15
Db 10 CGCGCGGC 3
RESULT 95
AR630146/c
LOCUS      Sequence 200 from patent US 6838556.
ACCESSION  AR630146
VERSION     AR630146.1 GI:59762471
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE      Promoters for regulated gene expression
JOURNAL    Patent: US 6838556-A 200 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
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/organism='unknown'
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Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCGCGCTG 17
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Db 9 GCGCGCTG 2

RESULT 96
AX224410/c
LOCUS
DEFINITION
Sequence 17 from Patent WO0160997.
ACCESSION AX224410
VERSION AX224410.1 GI:15554652
KEYWORDS
SOURCE
Zeia mayas
Zeia mayas
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
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/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGCCGGC 11
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Db 9 GCGCCGGC 2

RESULT 97
BD124175
LOCUS
DEFINITION
Compositions and method for healing wound.
ACCESSION BD124175
VERSION BD124175.1 GI:23219120
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 11)
Katz, E.H.
AUTHORS
TITLE
JOURNAL
THE WISTAR INSTITUTE
COMMENT
OS Mus musculus (mouse)
PN JP 2002503460-A/6
PP 05-FEB-2002
PR 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
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Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
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Db 1 GCTGGCCC 8

RESULT 98
BD124339
LOCUS
DEFINITION
Compositions and method for healing wound.
ACCESSION BD124339
VERSION BD124339.1 GI:23219284
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 11)
Katz, E.H.
AUTHORS
TITLE
JOURNAL
THE WISTAR INSTITUTE
COMMENT
OS Mus musculus (mouse)
PN JP 2002503460-A/170
PD 05-FEB-2002
PP 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
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Db 1 GCTGGCCC 8

RESULT 99
BD124474
LOCUS
DEFINITION
Compositions and method for healing wound.
ACCESSION BD124474
VERSION BD124474.1 GI:23219419
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 11)
Katz, E.H.
AUTHORS
TITLE
Compositions and method for healing wound


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JOURNAL Patent: JP 2002503460-A 305 05-FEB-2002;
COMMENT THE WISTAR INSTITUTE
OS Mus musculus (mouse)
PN JP 2002503460-A/305
PD 05-FEB-2002
PR 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00,PC
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CC Compositions and method for healing wound
FH Key Location/Qualifiers
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Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGGC 21
Db 1 GCTGTGGC 8

RESULT 100
CQ834999
LOCUS 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 57 from Patent WO2004059001.
ACCESSION CQ834999
VERSION CQ834999.1 GI:50834533
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 57 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTGG 20
Db 1 CGCTGTGG 8

RESULT 103
CS058186/c
LOCUS 11 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 83 from Patent WO2005028671.
ACCESSION CS058186
VERSION CS058186.1 GI:62551138
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 83 31-MAR-2005;

JOURNAL Patent: JP 2002503460-A 305 05-FEB-2002;
COMMENT THE WISTAR INSTITUTE
OS Mus musculus (mouse)
PN JP 2002503460-A/305
PD 05-FEB-2002
PR 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00,PC
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CC Compositions and method for healing wound
FH Key Location/Qualifiers
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Query Match 38.1%; Score 8; DB 1; Length 11;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGGC 21
Db 1 GCTGTGGC 8

RESULT 100
CQ834999
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DEFINITION Sequence 57 from Patent WO2004059001.
ACCESSION CQ834999
VERSION CQ834999.1 GI:50834533
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 57 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGTGGC 8
Db 3 GCTGTGGC 10

RESULT 101
CQ836944
LOCUS 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 2002 from Patent WO2004059001.
ACCESSION CQ836944
VERSION CQ836944.1 GI:50836478
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2002 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/mol_type="unassigned DNA"
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Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGTGGC 8
Db 4 GCTGTGGC 11

RESULT 102
CQ838061
LOCUS 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 3119 from Patent WO2004059001.
ACCESSION CQ838061
VERSION CQ838061.1 GI:50837595
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 3119 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/db_xref="taxon:9606"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTGG 20
Db 1 CGCTGTGG 8

RESULT 103
CS058186/c
LOCUS 11 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 83 from Patent WO2005028671.
ACCESSION CS058186
VERSION CS058186.1 GI:62551138
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 83 31-MAR-2005;

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Qy	14 GCTGTGGC 21		
Db	8 GCTGTGGC 1		
RESULT 104			
LOCUS		AR301425 11 bp DNA linear PAT 12-JUN-2003	
DEFINITION		Sequence 6 from patent US 6538173.	
ACCESSION		AR301425	
VERSION		AR301425.1 GI:31689227	
KEYWORDS		.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 11)	
AUTHORS		Heber-Katz,E.	
TITLE		Compositions and methods for wound healing	
JOURNAL		Patent: US 6538173-A 6 25-MAR-2003;	
		The Wistar Institute; Philadelphia, PA;	
WOX;			
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Query Match		38.1%; Score 8; DB 1; Length 11;	
Best Local Similarity		100.0%; Pred. No. 1e+02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCTGGCCC 8		
Db	1 GCTGGCCC 8		
RESULT 105			
LOCUS		AR301589 11 bp DNA linear PAT 12-JUN-2003	
DEFINITION		Sequence 170 from patent US 6538173.	
ACCESSION		AR301589	
VERSION		AR301589.1 GI:31689391	
KEYWORDS		.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 11)	
AUTHORS		Heber-Katz,E.	
TITLE		Compositions and methods for wound healing	
JOURNAL		Patent: US 6538173-A 170 25-MAR-2003;	
		The Wistar Institute; Philadelphia, PA;	
WOX;			
FEATURES		Location/Qualifiers	
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Query Match		38.1%; Score 8; DB 1; Length 11;	
Best Local Similarity		100.0%; Pred. No. 1e+02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCTGGCCC 8		
Db	1 GCTGGCCC 8		
RESULT 106			
LOCUS		AR301724 11 bp DNA linear PAT 12-JUN-2003	
DEFINITION		Sequence 305 from patent US 6538173.	
ACCESSION		AR301724	
VERSION		AR301724.1 GI:31689526	
KEYWORDS		.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 11)	
AUTHORS		Heber-Katz,E.	
TITLE		Compositions and methods for wound healing	
JOURNAL		Patent: US 6538173-A 305 25-MAR-2003;	
		The Wistar Institute; Philadelphia, PA;	
WOX;			
FEATURES		Location/Qualifiers	
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		/organism="unknown"	
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Query Match		38.1%; Score 8; DB 1; Length 11;	
Best Local Similarity		100.0%; Pred. No. 1e+02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	14 GCTGTGGC 21		
Db	1 GCTGTGGC 8		
RESULT 107			
LOCUS		AR605251 11 bp DNA linear PAT 15-DEC-2004	
DEFINITION		Sequence 42 from patent US 6818747.	
ACCESSION		AR605251	
VERSION		AR605251.1 GI:56656825	
KEYWORDS		.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 11)	
AUTHORS		Yao,Y. and Xu,H.	
TITLE		G.alpha.q protein variants and their use in the analysis and	
		discovery of agonists and antagonists of chemosensory receptors	
JOURNAL		Patent: US 6818747-A 42 16-NOV-2004;	
		Senomyx, Inc.; La Jolla, CA	
FEATURES		Location/Qualifiers	
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Query Match		38.1%; Score 8; DB 1; Length 11;	
Best Local Similarity		100.0%; Pred. No. 1e+02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	8 CGGCGCGC 15		
Db	9 CGGCGCGC 2		
RESULT 108			
LOCUS		AX471838 11 bp DNA linear PAT 09-AUG-2002	
DEFINITION		Sequence 1415 from Patent WO20053773.	
ACCESSION		AX471838	
VERSION		AX471838.1 GI:22206963	
KEYWORDS		.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1415 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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1. .11
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 38.1%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
Db 4 GCTGGCCC 11

RESULT 109
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LOCUS AX623061 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 102 from Patent WO02053774.
ACCESSION AX623061
VERSION AX623061.1 GI:28451002
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 102 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
Db 3 GCTGGCCC 10

RESULT 110
AX623147/c
LOCUS AX623147 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 188 from Patent WO02053774.
ACCESSION AX623147
VERSION AX623147.1 GI:28451088
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 188 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/organism="Homo sapiens"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 38.1%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGGC 21
Db 8 GCTGTGGC 1

RESULT 111
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LOCUS AX623827 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 868 from Patent WO02053774.
ACCESSION AX623827
VERSION AX623827.1 GI:28451768
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 868 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match
Best Local Similarity 38.1%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGCCGCGC 11
Db 1 GCGCCGCGC 8

RESULT 112
AX626346
LOCUS AX626346 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3387 from Patent WO02053774.
ACCESSION AX626346
VERSION AX626346.1 GI:28454384
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3387 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 38.1%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
Db 1 GCTGGCCC 8

RESULT 113
AX626346
LOCUS AX626346 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3387 from Patent WO02053774.
ACCESSION AX626346
VERSION AX626346.1 GI:28454384
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3387 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 38.1%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
Db 1 GCTGGCCC 8

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Db          3  GCTGGCCC 10
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RESULT 113
AX627953
LOCUS      AX627953          11 bp  DNA          linear  PAT 21-FEB-2003
DEFINITION Sequence 4994 from Patent WO02053774.
ACCESSION  AX627953
VERSION     AX627953.1  GI:28455991
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 4994 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
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                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  GCTGGCCC 8
    |||||
Db   4  GCTGGCCC 11

RESULT 114
AX628349/c
LOCUS      AX628349          11 bp  DNA          linear  PAT 21-FEB-2003
DEFINITION Sequence 5390 from Patent WO02053774.
ACCESSION  AX628349
VERSION     AX628349.1  GI:28456387
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5390 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  14  GCTGTGGC 21
    |||||
Db   8  GCTGTGGC 1

RESULT 115
AX628842
LOCUS      AX628842          11 bp  DNA          linear  PAT 21-FEB-2003
DEFINITION Sequence 5883 from Patent WO02053774.
ACCESSION  AX628842

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VERSION     AX628842.1  GI:28456880
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5883 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4  GGCCCGGC 11
    |||||
Db   1  GGCCCGGC 8

RESULT 116
AX629565
LOCUS      AX629565          11 bp  DNA          linear  PAT 21-FEB-2003
DEFINITION Sequence 6606 from Patent WO02053774.
ACCESSION  AX629565
VERSION     AX629565.1  GI:28457603
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 6606 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  13  CGCTGTGG 20
    |||||
Db   1  CGCTGTGG 8

RESULT 117
AX629711
LOCUS      AX629711          11 bp  DNA          linear  PAT 21-FEB-2003
DEFINITION Sequence 6752 from Patent WO02053774.
ACCESSION  AX629711
VERSION     AX629711.1  GI:28457749
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.

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TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6752 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGCGCGC 14
|||||
Db 1 CCGCGCGC 8

RESULT 118
AX630482
LOCUS AX630482 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7523 from Patent WO02053774.
ACCESSION AX630482
VERSION AX630482.1 GI:28458520
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7523 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
|||||
Db 3 GCTGGCCC 10

RESULT 119
AX630568/c
LOCUS AX630568 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7609 from Patent WO02053774.
ACCESSION AX630568
VERSION AX630568.1 GI:28458606
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7609 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGGC 21
|||||
Db 8 GCTGTGGC 1

RESULT 120
AX631248
LOCUS AX631248 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8290 from Patent WO02053774.
ACCESSION AX631248
VERSION AX631248.1 GI:28459294
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8290 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCCCGGC 11
|||||
Db 1 GGCCCGGC 8

RESULT 121
CQ836510/c
LOCUS CQ836510 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1568 from Patent WO2004059001.
ACCESSION CQ836510
VERSION CQ836510.1 GI:50836044
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1568 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGCCCGGC 11
|||||
Db 11 GCCGCGCGGC 1

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RESULT 122
AX628774/c
LOCUS          AX628774          11 bp      DNA          linear      PAT 21-FEB-2003
DEFINITION     Sequence 5815 from Patent WO02053774.
ACCESSION      AX628774
VERSION        AX628774.1  GI:28456812
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE          Hominidae; Homo.
JOURNAL        Petersohn,D., Conradt,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 5815 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
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                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match    37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGCGCCGGC 11
    |||||
Db 11 GCCGCGCGGCT 1

RESULT 123
CQ837882/c
LOCUS          CQ837882          11 bp      DNA          linear      PAT 29-JUL-2004
DEFINITION     Sequence 2940 from Patent WO2004059001.
ACCESSION      CQ837882
VERSION        CQ837882.1  GI:50837416
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE          Hominidae; Homo.
JOURNAL        Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
METHOD for determining markers of human facial skin
PATENT: WO 2004059001-A 2940 15-JUL-2004;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
                source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match    37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGCGCGGCT 16
    |||||
Db 11 CGCGCGGCT 1

RESULT 124
AX629700/c
LOCUS          AX629700          11 bp      DNA          linear      PAT 21-FEB-2003
DEFINITION     Sequence 6741 from Patent WO02053774.
ACCESSION      AX629700
VERSION        AX629700.1  GI:28457738
KEYWORDS

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SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE          Hominidae; Homo.
JOURNAL        Petersohn,D., Conradt,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 6741 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
                source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match    37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGCGCGGCT 16
    |||||
Db 11 CGCGCGGCT 1

RESULT 125
AR169386
LOCUS          AR169386          11 bp      DNA          linear      PAT 17-DEC-2001
DEFINITION     Sequence 51 from patent US 6291165.
ACCESSION      AR169386
VERSION        AR169386.1  GI:17907241
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      Borchert,T.Vedel., Kretzschmar,T. and Cherry,J.R.
AUTHORS        Shuffling of heterologous DNA sequences
TITLE          Patent: US 6291165-A 51 18-SEP-2001;
JOURNAL        Location/Qualifiers
FEATURES       Location/Qualifiers
                source
                1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match    37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGCGCGGCT 16
    |||||
Db 1 CCCGACGGCTT 11

RESULT 126
BD226182/c
LOCUS          BD226182          11 bp      DNA          linear      PAT 17-JUL-2003
DEFINITION     Glaucoma therapeutics and diagnostics based on a novel human
transcription factor.
ACCESSION      BD226182
VERSION        BD226182.1  GI:33035952
KEYWORDS       JP 2002511265-A/33.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE          Hominidae; Homo.
JOURNAL        Sheffield,V.C., Alward,W.L.M., Stone,E.M., Nishimura,D. and
                Patil,S.
                Glaucoma therapeutics and diagnostics based on a novel human
                transcription factor
                Patent: JP 2002511265-A 33 16-APR-2002;
                THE UNIVERSITY OF IOWA RESEARCH FOUNDATION

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COMMENT
OS Homo sapiens (human)
PN JP 2002511265-A/33
PD 16-APR-2002
PF 14-APR-1999 JP 2000543608
PR 15-APR-1998 US 60/081870, 22-MAY-1998 US 09/083352 PI
VAL C SHEFFIELD, WALLACE L M ALWARD, EDWIN M STONE, DARRYL PI
NISHIMURA,
PI SHIVA PATIL
PC C12N15/00,A61K45/00,A61P27/06,C07K14/47,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12Q1/68,G01N33/15,G01N33/50,C12N15/00, PC
C12N5/00
CC 11 base pair deletion
FH Key Location/Qualifiers
FT source 1..11
FT Location/Qualifiers
/organism="Homo sapiens (human)".

FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGCGC 15
Db 11 GCTCGCGCTGC 1

RESULT 127
BD250406/c
LOCUS
DEFINITION
Methods for determination of single nucleic acid polymorphisms
using a bioelectric microchip.
ACCESSION
BD250406
VERSION
BD250406.1 GI:33060176
KEYWORDS
JP 2002541823-A/16.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 11)
Nerenberg, M. I., Canter, D. M., Radtkey, R. R., O'Connell, J. P., Wang, L.
and Sosnowski, R. G.
TITLE
Methods for determination of single nucleic acid polymorphisms
using a bioelectric microchip
JOURNAL
Patent: JP 2002541823-A 16 10-DEC-2002;
NANOGEN INC
COMMENT
OS Homo sapiens (human)
PN JP 2002541823-A/16
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000611727
PR 12-APR-1999 US 09/290129
PI MICHAEL I NERENBERG, DAVID M CANTER, RAY R RADTKEY, JAMES P PI
O'CONNELL,
PI LING, WANG, RONALD G SOSNOWSKI
PC C12N15/09,C12Q1/68,G01N33/53,G01N37/00,C12N15/00 CC Methods
for determination of single nucleic
acid polymorphisms
CC using a
CC bioelectric microchip
FH Key Location/Qualifiers
FT source 1..11
FT Location/Qualifiers
/organism="Homo sapiens (human)".

FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTGGCCCGCGCG 12
Db 11 CTGGACAGGCG 1

RESULT 128
CQ833470
LOCUS
DEFINITION
Sequence 841 from Patent WO2004059002.
ACCESSION
CQ833470
VERSION
CQ833470.1 GI:50833077
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
Conradt, M. and Hofmann, K.
TITLE
Method for determining the homeostasis of hairy skin
JOURNAL
Patent: WO 2004059002-A 841 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGCGCGCGCT 16
Db 1 CCCACGCGCT 11

RESULT 129
CQ835047/c
LOCUS
DEFINITION
Sequence 105 from Patent WO2004059001.
ACCESSION
CQ835047
VERSION
CQ835047.1 GI:50834581
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
Conradt, M. and Hofmann, K.
TITLE
Method for determining markers of human facial skin
JOURNAL
Patent: WO 2004059001-A 105 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
Db 11 GAGCGCAGTGG 1

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RESULT 130
CQ835073/c
LOCUS          11 bp      DNA          linear          PAT 29-JUL-2004
DEFINITION     Sequence 131 from Patent WO2004059001.
ACCESSION      CQ835073
VERSION        CQ835073.1  GI:50834607
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
                Conradt,M. and Hofmann,K.
TITLE          Method for determining markers of human facial skin
JOURNAL        Patent: WO 2004059001-A 131 15-JUL-2004;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
                source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match    37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CTGGCCCGCGC 12
Db      11  CTGGCCCTCG 1

RESULT 131
CQ835177
LOCUS          11 bp      DNA          linear          PAT 29-JUL-2004
DEFINITION     Sequence 235 from Patent WO2004059001.
ACCESSION      CQ835177
VERSION        CQ835177.1  GI:50834711
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
                Conradt,M. and Hofmann,K.
TITLE          Method for determining markers of human facial skin
JOURNAL        Patent: WO 2004059001-A 235 15-JUL-2004;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
                source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match    37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CTGGCCCGCGC 12
Db      11  CTGGCCCTCG 1

RESULT 132
CQ835213/c
LOCUS          11 bp      DNA          linear          PAT 29-JUL-2004
DEFINITION     Sequence 271 from Patent WO2004059001.
ACCESSION      CQ835213
VERSION        CQ835213.1  GI:50834717
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
                Conradt,M. and Hofmann,K.
TITLE          Method for determining markers of human facial skin
JOURNAL        Patent: WO 2004059001-A 271 15-JUL-2004;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
                source
                1..11
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match    37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6  CCGGCGCGCGCT 16
Db      1  CCAGGCACGCT 11

RESULT 133
CQ835213.1
LOCUS          11 bp      DNA          linear          PAT 29-JUL-2004
DEFINITION     Sequence 131 from Patent WO2004059001.
ACCESSION      CQ835213
VERSION        CQ835213.1  GI:50834747
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
                Conradt,M. and Hofmann,K.
TITLE          Method for determining markers of human facial skin
JOURNAL        Patent: WO 2004059001-A 271 15-JUL-2004;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
                source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match    37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCTGGCCCGGC 11
Db      11  GCTGGGCTGGC 1

RESULT 134
CQ837783
LOCUS          11 bp      DNA          linear          PAT 29-JUL-2004
DEFINITION     Sequence 2841 from Patent WO2004059001.
ACCESSION      CQ837783
VERSION        CQ837783.1  GI:50837317
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
                Conradt,M. and Hofmann,K.
TITLE          Method for determining markers of human facial skin
JOURNAL        Patent: WO 2004059001-A 2841 15-JUL-2004;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
                source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match    37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCTGGCCCGGC 11
Db      11  GATGGCCAGGC 1

RESULT 135
CQ837783
LOCUS          11 bp      DNA          linear          PAT 29-JUL-2004
DEFINITION     Sequence 2841 from Patent WO2004059001.
ACCESSION      CQ837783
VERSION        CQ837783.1  GI:50837317
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
                Conradt,M. and Hofmann,K.
TITLE          Method for determining markers of human facial skin
JOURNAL        Patent: WO 2004059001-A 2841 15-JUL-2004;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
                source
                1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match    37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches        9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCTGGCCCGGC 11
Db      11  GATGGCCAGGC 1

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REFERENCE
AUTHORS      Petersohn,D., Schlottmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2841 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       Location/Qualifiers
              1. .11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match   37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 CTGCCCCGGCG 12
    |||||
Db   1 CTGCCCCGGCG 11

RESULT 135
AX470499
LOCUS        AX470499 11 bp DNA linear PAT 13-APR-2005
DEFINITION   Sequence 176 from Patent WO2005028671.
ACCESSION    AX470499
VERSION      AX470499.1 GI:62551462
KEYWORDS     Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominoidea; Homo.
REFERENCE    1
AUTHORS      Holtkoetter,O., Petersohn,D., Schlottmann,K., Giesen,M. and
              Kessler-Becker,D.
TITLE        Method for determining hair cycle markers
JOURNAL      Patent: WO 2005028671-A 176 31-MAR-2005;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       Location/Qualifiers
              1. .11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match   37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  9 GCGCGCGTGTG 19
    |||||
Db   1 GCGGTGCTGTG 11

RESULT 136
AR238595/c
LOCUS        AR238595 11 bp DNA linear PAT 20-DEC-2002
DEFINITION   Sequence 16 from patent US 6468742.
ACCESSION    AR238595
VERSION      AR238595.1 GI:27283665
KEYWORDS     Unknown.
ORGANISM     Unknown.
              Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Nerenberg,M.I., Canter,D.M., Radtkey,R.R., Wang,L., O'connell,J.P.
              and Sosnowski,R.G.
TITLE        Methods for determination of single nucleic acid polymorphisms
              using bioelectronic microchip
JOURNAL      Patent: US 6468742-A 16 22-OCT-2002;
              Nanogen, Inc.; San Diego, CA
FEATURES
source       Location/Qualifiers
              1. .11

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                /organism="unknown"
                /mol_type="genomic DNA"

Query Match   37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 CTGCCCCGGCG 12
    |||||
Db   11 CTGACACGGCG 1

RESULT 137
AX470499
LOCUS        AX470499 11 bp DNA linear PAT 09-AUG-2002
DEFINITION   Sequence 76 from Patent WO02053773.
ACCESSION    AX470499
VERSION      AX470499.1 GI:22205624
KEYWORDS     Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominoidea; Homo.
REFERENCE    1
AUTHORS      Hofmann,K., Conradt,M. and Petersohn,D.
TITLE        Method for determining skin stress or skin ageing in vitro
JOURNAL      Patent: WO 02053773-A 76 11-JUL-2002;
              HENKEL KGAA (DE)
FEATURES
source       Location/Qualifiers
              1. .11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match   37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  6 CCGCGCGCGCT 16
    |||||
Db   1 CCAGGCACGCT 11

RESULT 138
AX470547/c
LOCUS        AX470547 11 bp DNA linear PAT 09-AUG-2002
DEFINITION   Sequence 124 from Patent WO02053773.
ACCESSION    AX470547
VERSION      AX470547.1 GI:22205672
KEYWORDS     Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominoidea; Homo.
REFERENCE    1
AUTHORS      Hofmann,K., Conradt,M. and Petersohn,D.
TITLE        Method for determining skin stress or skin ageing in vitro
JOURNAL      Patent: WO 02053773-A 124 11-JUL-2002;
              HENKEL KGAA (DE)
FEATURES
source       Location/Qualifiers
              1. .11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match   37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  10 GCGCGCTGTGG 20
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Db      11 GAGCGCAGTGG 1

RESULT 139
LOCUS   AX471002
DEFINITION Sequence 579 from Patent WO02053773.
ACCESSION AX471002
VERSION   AX471002.1 GI:22206127
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.
REFERENCE
AUTHORS  Hofmann,K., Conradt,M. and Petersohn,D.
TITLE    Method for determining skin stress or skin ageing in vitro
JOURNAL  Patent: WO 02053773-A 579 11-JUL-2002;
          HENKEL KGAA (DE)
FEATURES
source   Location/Qualifiers
          1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GGCCCGGCGCG 14
        |||||
Db      1 GGCCCTGAGCG 11

RESULT 140
LOCUS   AX471274/c
DEFINITION Sequence 851 from Patent WO02053773.
ACCESSION AX471274
VERSION   AX471274.1 GI:22206399
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.
REFERENCE
AUTHORS  Hofmann,K., Conradt,M. and Petersohn,D.
TITLE    Method for determining skin stress or skin ageing in vitro
JOURNAL  Patent: WO 02053773-A 851 11-JUL-2002;
          HENKEL KGAA (DE)
FEATURES
source   Location/Qualifiers
          1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      11 CGCGCTGTGGC 21
        | |||||
Db      11 CTCGCTGGGCG 1

RESULT 141
LOCUS   AX471596/c
DEFINITION Sequence 1173 from Patent WO02053773.
ACCESSION AX471596
VERSION   AX471596.1 GI:22206721

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KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.
REFERENCE
AUTHORS  Hofmann,K., Conradt,M. and Petersohn,D.
TITLE    Method for determining skin stress or skin ageing in vitro
JOURNAL  Patent: WO 02053773-A 1173 11-JUL-2002;
          HENKEL KGAA (DE)
FEATURES
source   Location/Qualifiers
          1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 GCGCGCTGTGG 20
        |||||
Db      11 GCGTGCAGTGG 1

RESULT 142
LOCUS   AX622989
DEFINITION Sequence 30 from Patent WO02053774.
ACCESSION AX622989
VERSION   AX622989.1 GI:28450930
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.
REFERENCE
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 30 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source   Location/Qualifiers
          1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      11 CGCGCTGTGGC 21
        | |||||
Db      1 CAGCGAGTGGC 11

RESULT 143
LOCUS   AX623485/c
DEFINITION Sequence 526 from Patent WO02053774.
ACCESSION AX623485
VERSION   AX623485.1 GI:28451426
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.
REFERENCE
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin

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JOURNAL Patent: WO 02053774-A 526 11-JUL-2002;
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGCT 15
Db 11 GCCAGGCGCCC 1

RESULT 144
AX623553
LOCUS AX623553 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 594 from Patent WO02053774.
ACCESSION AX623553
VERSION AX623553.1 GI:28451494
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 594 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCGCGCGCGCT 16
Db 1 CCCAACGCGCT 11

RESULT 145
AX623825
LOCUS AX623825 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 866 from Patent WO02053774.
ACCESSION AX623825
VERSION AX623825.1 GI:28451766
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 866 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGCCGCGCGCT 14
Db 1 GCGCAGCGCTG 11

RESULT 147
AX624226/c
LOCUS AX624226 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1267 from Patent WO02053774.
ACCESSION AX624226
VERSION AX624226.1 GI:28452167
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1267 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGCCGCGCGCT 14
Db 1 GCGCAGCGCTG 11

RESULT 148
AX624226/c
LOCUS AX624226 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1267 from Patent WO02053774.
ACCESSION AX624226
VERSION AX624226.1 GI:28452167
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1267 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
Db 11 GAGTGTGTGG 1

RESULT 149

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AX624477
LOCUS AX624477 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1518 from Patent WO02053774.
ACCESSION AX624477
VERSION AX624477.1 GI:28452418
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1518 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGCGCGCGC 13
||| ||| |||
Db 1 TGACCGCGCGC 11

RESULT 149
AX624700/c
LOCUS AX624700 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1741 from Patent WO02053774.
ACCESSION AX624700
VERSION AX624700.1 GI:28452641
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1741 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGCGCGCGC 13
||| ||| |||
Db 1 TGACCGCGCGC 11

RESULT 150
AX625055
LOCUS AX625055 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2096 from Patent WO02053774.
ACCESSION AX625055
VERSION AX625055.1 GI:28452996
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 2096 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
||| ||| |||
Db 11 GAGCGCAGTGG 1

RESULT 151
AX625310/c
LOCUS AX625310 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2351 from Patent WO02053774.
ACCESSION AX625310
VERSION AX625310.1 GI:28453251
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 2351 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 15
||||| |||
Db 1 GCCCGGTGCC 11

RESULT 152
AX626546
LOCUS AX626546 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3587 from Patent WO02053774.
ACCESSION AX626546
VERSION AX626546.1 GI:28454584
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 3587 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 2096 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 15
||||| |||
Db 1 GCCCGGTGCC 11

RESULT 151
AX625310/c
LOCUS AX625310 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2351 from Patent WO02053774.
ACCESSION AX625310
VERSION AX625310.1 GI:28453251
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 2351 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
||||| |||
Db 11 GCGTCAGTGG 1

RESULT 152
AX626546
LOCUS AX626546 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3587 from Patent WO02053774.
ACCESSION AX626546
VERSION AX626546.1 GI:28454584
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 3587 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CCGGGCGGCT 16
Db 1 CCAGGCAGCT 11

RESULT 153
AX626575/c
LOCUS
DEFINITION
Sequence 3616 from Patent WO02053774.
ACCESSION
AX626575.1 GI:28454613
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 3616 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGGCCCGGCG 12
Db 11 CTGGCCCGCTCG 1

RESULT 154
AX626823
LOCUS
DEFINITION
Sequence 3864 from Patent WO02053774.
ACCESSION
AX626823
VERSION
AX626823.1 GI:28454861
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 3864 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGGCCCGGCGC 13

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|||||
1 TGGTCCAGCGC 11

RESULT 155
AX627065/c
LOCUS
DEFINITION
Sequence 4106 from Patent WO02053774.
ACCESSION
AX627065
VERSION
AX627065.1 GI:28455103
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 4106 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GCGCGCTGTGG 20
Db 11 GAGAGCTGTGG 1

RESULT 156
AX627186/c
LOCUS
DEFINITION
Sequence 4227 from Patent WO02053774.
ACCESSION
AX627186
VERSION
AX627186.1 GI:28455224
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 4227 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 GCGCGCTGTGTG 19
Db 11 GCGAGGCTGTG 1

RESULT 157
AX627348
LOCUS
DEFINITION
Sequence 4389 from Patent WO02053774.
ACCESSION
AX627348

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VERSION      AX627348.1  GI:28455386
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens

REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4389 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              source
                1..11
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"

Query Match  37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy           9  GCGCGCGCTGTG 19
              ||| |||||
Db           1  GGAGGGCTGTG 11

RESULT 158
LOCUS       AX627678                      11 bp  DNA          linear  PAT 21-FEB-2003
DEFINITION  Sequence 4719 from Patent WO02053774.
ACCESSION   AX627678
VERSION     AX627678.1  GI:28455716
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominiidae; Homo.

REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4719 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              source
                1..11
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"

Query Match  37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy           9  GCGCGCGCTGTG 19
              ||| |||||
Db           1  GGCGCACTCTG 11

RESULT 159
LOCUS       AX628416                      11 bp  DNA          linear  PAT 21-FEB-2003
DEFINITION  Sequence 5457 from Patent WO02053774.
ACCESSION   AX628416
VERSION     AX628416.1  GI:28456454
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominiidae; Homo.

REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.

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TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 5457 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              source
                1..11
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                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"

Query Match  37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy           9  GCGCGCGCTGTG 19
              ||| |||||
Db           1  GGGGTGCTGTG 11

RESULT 160
LOCUS       AX628487                      11 bp  DNA          linear  PAT 21-FEB-2003
DEFINITION  Sequence 5528 from Patent WO02053774.
ACCESSION   AX628487
VERSION     AX628487.1  GI:28456525
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominiidae; Homo.

REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 5528 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
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                1..11
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"

Query Match  37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy           11  CGCGCTGTGGC 21
                ||||| |||
Db           11  CTCGCTGGGC 1

RESULT 161
LOCUS       AX629263                      11 bp  DNA          linear  PAT 21-FEB-2003
DEFINITION  Sequence 6304 from Patent WO02053774.
ACCESSION   AX629263
VERSION     AX629263.1  GI:28457301
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominiidae; Homo.

REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6304 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              source
                1..11
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"

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Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CTGGCCCGCGC 12
Db      1 CTGGCCCGCAG 11

RESULT 162
LOCUS      AX629341
DEFINITION Sequence 6382 from Patent WO02053774.
ACCESSION  AX629341
VERSION     AX629341.1 GI:28457379
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 6382 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 GCGCGCCTGTG 19
Db      1 GCGAGGCTGTG 11

RESULT 163
LOCUS      AX629452
DEFINITION Sequence 6493 from Patent WO02053774.
ACCESSION  AX629452
VERSION     AX629452.1 GI:28457490
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 6493 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 GCGCGCCTGTG 19
Db      1 GCGAGGCTGTG 11

RESULT 164
LOCUS      AX629509/c
DEFINITION Sequence 6550 from Patent WO02053774.
ACCESSION  AX629509
VERSION     AX629509.1 GI:28457547
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 6550 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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                /mol_type="unassigned DNA"
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Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCTGGCCCGGC 11
Db      11 GCTGGGCTGGC 1

RESULT 165
LOCUS      AX630130
DEFINITION Sequence 7171 from Patent WO02053774.
ACCESSION  AX630130
VERSION     AX630130.1 GI:28458168
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 7171 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 GCGCGCCTGTG 19
Db      1 GGAGCTCTGTG 11

RESULT 166
LOCUS      AX630139/c
DEFINITION Sequence 7180 from Patent WO02053774.
ACCESSION  AX630139
VERSION     AX630139.1 GI:28458177
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 7180 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 GCGCGCCTGTG 19
Db      1 GGAGCAGCTGTG 11
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7180 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCGCGC 11

Db 11 GATGCCAGGC 1

RESULT 167

AX630178 AX630178 11 bp DNA linear PAT 21-FEB-2003
LOCUS Sequence 7219 from Patent WO02053774.
DEFINITION AX630178
ACCESSION AX630178
VERSION AX630178.1 GI:28458216

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7219 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGCCGCGCGC 14

Db 1 GGCCTGAGCG 11

RESULT 168

AX630197/c AX630197 11 bp DNA linear PAT 21-FEB-2003
LOCUS Sequence 7238 from Patent WO02053774.
DEFINITION AX630197
ACCESSION AX630197
VERSION AX630197.1 GI:28458235

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7238 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

Location/Qualifiers

source

1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGCCGCGCGC 13

Db 11 TGGGCGCGCGC 1

RESULT 169

AX630410 AX630410 11 bp DNA linear PAT 21-FEB-2003
LOCUS Sequence 7451 from Patent WO02053774.
DEFINITION AX630410
ACCESSION AX630410
VERSION AX630410.1 GI:28458448

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7451 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

Location/Qualifiers

source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CGCGCTGTGGC 21

Db 1 CACGCAGTGGC 11

RESULT 170

AX630906/c AX630906 11 bp DNA linear PAT 21-FEB-2003
LOCUS Sequence 7947 from Patent WO02053774.
DEFINITION AX630906
ACCESSION AX630906
VERSION AX630906.1 GI:28458946

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7947 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

Location/Qualifiers

source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match

Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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QY      5  GCCCGCGCGC 15
Db      11  GCCAGCGCCC 1

RESULT 171
AX630974
LOCUS   AX630974                11 bp  DNA    linear    PAT 21-FEB-2003
DEFINITION
Sequence 8015 from Patent WO02053774.
ACCESSION
AX630974
VERSION  AX630974.1  GI:28459016
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1. Petersohn,D., Conradt,M. and Hofmann,K.
   Method for determining homeostasis of the skin
   Patent: WO 02053774-A 8015 11-JUL-2002;
   Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      Location/Qualifiers
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6  CCCGCGCGCT 16
Db      1  CCCACGCGCT 11

RESULT 172
AX631246
LOCUS   AX631246                11 bp  DNA    linear    PAT 21-FEB-2003
DEFINITION
Sequence 8288 from Patent WO02053774.
ACCESSION
AX631246
VERSION  AX631246.1  GI:28459292
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1. Petersohn,D., Conradt,M. and Hofmann,K.
   Method for determining homeostasis of the skin
   Patent: WO 02053774-A 8288 11-JUL-2002;
   Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      Location/Qualifiers
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  GCGCCGCGCG 14
Db      1  GGCTGGCGCG 11

RESULT 173
AX631370
LOCUS   AX631370                11 bp  DNA    linear    PAT 21-FEB-2003
DEFINITION
Sequence 8412 from Patent WO02053774.

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ACCESSION  AX631370
VERSION    AX631370.1  GI:28459416
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 8412 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
source     1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  GCGCCGCGCG 14
Db      1  GCGCAGCGCTG 11

RESULT 174
AX631647/c
LOCUS   AX631647                11 bp  DNA    linear    PAT 21-FEB-2003
DEFINITION
Sequence 8689 from Patent WO02053774.
ACCESSION
AX631647
VERSION  AX631647.1  GI:28459723
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 8689 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
source     1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 GCGCGCTGTGG 20
Db      11 GAGTCTGTGG 1

RESULT 175
AX631898
LOCUS   AX631898                11 bp  DNA    linear    PAT 21-FEB-2003
DEFINITION
Sequence 8940 from Patent WO02053774.
ACCESSION
AX631898
VERSION  AX631898.1  GI:28460036
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE  1

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Dorner,F., Scheiflinger,F., Falkner,F.Gunter. and Pfleiderer,M.
TITLE        Methods for generating immune responses employing modified vaccinia
              of fowlpox viruses
JOURNAL      Patent: US 6103244-A 43 15-AUG-2000;
FEATURES     Location/Qualifiers
              source
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                /mol_type="unassigned DNA"
Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGCCCCCG 10
    |||||||
Db 1 CTAGCCCTG 9

RESULT 186
LOCUS      AR107796
DEFINITION Sequence 42 from patent US 6110667.
ACCESSION  AR107796
VERSION     AR107796
KEYWORDS    AR107796.1 GI:12823283
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE        Processes, apparatus and compositions for characterizing nucleotide
              sequences based on K-tuple analysis
JOURNAL      Patent: US 6110667-A 42 29-AUG-2000;
FEATURES     Location/Qualifiers
              source
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGCCCCCG 10
    |||||||
Db 1 CTAGCCCTG 9

RESULT 187
LOCUS      BD083124
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION  BD083124
VERSION     BD083124.1 GI:22628734
KEYWORDS    JP 2001327293-A/45.
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE        Human matured/activated dendritic cell expression genes
JOURNAL      Patent: JP 2001327293-A 45 27-NOV-2001;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2001327293-A/45
              PD 27-NOV-2001
              PF 22-MAY-2000 JP 2000150562
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Dorner,F., Scheiflinger,F., Falkner,F.Gunter. and Pfleiderer,M.
TITLE        Methods for generating immune responses employing modified vaccinia
              of fowlpox viruses
JOURNAL      Patent: US 6103244-A 43 15-AUG-2000;
FEATURES     Location/Qualifiers
              source
                1..10
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGCCCCCG 10
    |||||||
Db 1 CTAGCCCTG 9

RESULT 188
LOCUS      BD091134
DEFINITION P53-induced apoptosis.
ACCESSION  BD091134
VERSION     BD091134.1 GI:22636744
KEYWORDS    JP 2001523441-A/12.
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Vogelstein,B., Kinzler,K.W. and Polyak,K.
TITLE        P53-induced apoptosis
JOURNAL      Patent: JP 2001523441-A 12 27-NOV-2001;
              THE JOHNS HOPKINS UNIVERSITY
COMMENT      OS Homo sapiens (human)
              PN JP 2001523441-A/12
              PD 27-NOV-2001
              PF 17-SEP-1997 US 60/059153,30-MAR-1998 US 60/079817 PI
              BERT VOGELSTEIN,KENNETH W KINZLER,KORNELIA POLYAK PC
              C12Q1/68,C07K16/32,C12P21/08//C12N15/09,C12N15/00 CC P53-induced
              apoptosis
              FH Key
              FT source
              Location/Qualifiers
                1..10
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FEATURES     Location/Qualifiers
              source
                1..10
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGCCGC 13
    |||||||
Db 2 GCCCGCCGC 10

RESULT 189
LOCUS      BD091134/c
DEFINITION P53-induced apoptosis.
ACCESSION  BD091134
VERSION     BD091134.1 GI:22636744
KEYWORDS    JP 2001523441-A/12.
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE        Human matured/activated dendritic cell expression genes
JOURNAL      Patent: JP 2001327293-A 45 27-NOV-2001;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2001327293-A/45
              PD 27-NOV-2001
              PF 22-MAY-2000 JP 2000150562
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI

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NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers.
FEATURES     Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGC 11
    |||||||
Db 2 TGGCCCGC 10

RESULT 188
LOCUS      BD091134
DEFINITION P53-induced apoptosis.
ACCESSION  BD091134
VERSION     BD091134.1 GI:22636744
KEYWORDS    JP 2001523441-A/12.
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Vogelstein,B., Kinzler,K.W. and Polyak,K.
TITLE        P53-induced apoptosis
JOURNAL      Patent: JP 2001523441-A 12 27-NOV-2001;
              THE JOHNS HOPKINS UNIVERSITY
COMMENT      OS Homo sapiens (human)
              PN JP 2001523441-A/12
              PD 27-NOV-2001
              PF 17-SEP-1997 US 60/059153,30-MAR-1998 US 60/079817 PI
              BERT VOGELSTEIN,KENNETH W KINZLER,KORNELIA POLYAK PC
              C12Q1/68,C07K16/32,C12P21/08//C12N15/09,C12N15/00 CC P53-induced
              apoptosis
              FH Key
              FT source
              Location/Qualifiers
                1..10
                /organism="Homo sapiens (human)".
FEATURES     Location/Qualifiers
              source
                1..10
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGCCGC 13
    |||||||
Db 2 GCCCGCCGC 10

RESULT 189
LOCUS      BD091134/c
DEFINITION P53-induced apoptosis.
ACCESSION  BD091134
VERSION     BD091134.1 GI:22636744
KEYWORDS    JP 2001523441-A/12.
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE        Human matured/activated dendritic cell expression genes
JOURNAL      Patent: JP 2001327293-A 45 27-NOV-2001;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2001327293-A/45
              PD 27-NOV-2001
              PF 22-MAY-2000 JP 2000150562
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI

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REFERENCE
AUTHORS      Vogelsstein,B., Kinzler,K.W. and Polyak,K.
TITLE        P53-induced apoptosis
JOURNAL      Patent: JP 2001523441-A 12 27-NOV-2001;
              THE JOHNS HOPKINS UNIVERSITY
COMMENT      OS Homo sapiens (human)
              PN JP 2001523441-A/12
              PD 27-NOV-2001
              PF 17-SEP-1998 JP 2000511894
              PR 17-SEP-1997 US 60/059153,30-NOV-1998 US 60/079817 PI
              BERT VOGELSTEIN KENNETH W KINZLER, KORNELIA POLYAK PC
              C12Q1/68,C07K16/32,C12P21/08//C12N15/09,C12N15/00 CC P53-induced
              apoptosis
              FH Key
              FT source
              FT 1..10
              Location/Qualifiers
              /organism='Homo sapiens (human)'.
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCGCGGCT 16
   |||||
Db 9 CGCGCGGCT 1

RESULT 190
BD161262
LOCUS          BD161262          10 bp DNA linear PAT 17-JAN-2003
DEFINITION    Human activated Th1 and Th2 cell expression genes.
ACCESSION     BD161262
VERSION       JP 2002186482-A/84.
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     Nagai,S., Matsushima,K. and Hashimoto,S.
AUTHORS      Human activated Th1 and Th2 cell expression genes
TITLE        Patent: JP 2002186482-A 84 02-JUL-2002;
JOURNAL      JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002186482-A/84
              PD 02-JUL-2002
              PF 19-DEC-2000 JP 2000385816
              PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
              C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
              activated Th1 and Th2 cell expression genes FH Key
              Location/Qualifiers
              FT source
              FT 1..10
              /organism='Homo sapiens (human)'.
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCGCGGCT 16
   |||||
Db 9 CGCGCGGCT 1

RESULT 190
BD161262
LOCUS          BD161262          10 bp DNA linear PAT 17-JAN-2003
DEFINITION    Human activated Th1 and Th2 cell expression genes.
ACCESSION     BD161262
VERSION       JP 2002186482-A/84.
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     Nagai,S., Matsushima,K. and Hashimoto,S.
AUTHORS      Human activated Th1 and Th2 cell expression genes
TITLE        Patent: JP 2002186482-A 84 02-JUL-2002;
JOURNAL      JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002186482-A/84
              PD 02-JUL-2002
              PF 19-DEC-2000 JP 2000385816
              PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
              C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
              activated Th1 and Th2 cell expression genes FH Key
              Location/Qualifiers
              FT source
              FT 1..10
              /organism='Homo sapiens (human)'.
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
   |||||
Db 2 TGGCCAGGC 10

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RESULT 191
BD161390
LOCUS          BD161390          10 bp DNA linear PAT 17-JAN-2003
DEFINITION    Human activated Th1 and Th2 cell expression genes.
ACCESSION     BD161390
VERSION       JP 2002186482-A/212.
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     Nagai,S., Matsushima,K. and Hashimoto,S.
AUTHORS      Human activated Th1 and Th2 cell expression genes
TITLE        Patent: JP 2002186482-A 212 02-JUL-2002;
JOURNAL      JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002186482-A/212
              PD 02-JUL-2002
              PF 19-DEC-2000 JP 2000385816
              PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
              C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
              activated Th1 and Th2 cell expression genes FH Key
              Location/Qualifiers
              FT source
              FT 1..10
              /organism='Homo sapiens (human)'.
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCG 13
   |||||
Db 1 GCGCGCGCG 9

RESULT 192
BD166463/c
LOCUS          BD166463          10 bp DNA linear PAT 17-JAN-2003
DEFINITION    Human liver disease-expressing genes.
ACCESSION     BD166463
VERSION       BD166463.1 GI:27872275
KEYWORDS      JP 2002209591-A/8.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE        Human liver disease-expressing genes
JOURNAL      Patent: JP 2002209591-A 8 30-JUL-2002;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2002209591-A/8
              PD 30-JUL-2002
              PF 19-JAN-2001 JP 2001012328
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
              YAMASHITA
              PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
              PC C12P21/08,
              PC C12N15/00
              CC Human liver disease-expressing genes
              FH Key
              FT source
              FT 1..10
              Location/Qualifiers
              /organism='Homo sapiens (human)'.
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
   |||||
Db 2 TGGCCAGGC 10

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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCGCGCGCT 16
        |||||
Db       10 CCGCGCTCT 2

RESULT 193
BD166486      10 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166486
VERSION BD166486.1 GI:27872298
KEYWORDS JP 2002209591-A/31.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 31 30-JUL-2002;
        JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
        PN JP 2002209591-A/31
        PD 30-JUL-2002
        PF 19-JAN-2001 JP 2001012328
        PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
        YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
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Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCGCGCGCG 14
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Db       10 CCGCGCGGG 2

RESULT 195
BD166712/C
LOCUS
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166712
VERSION BD166712.1 GI:27872524
KEYWORDS JP 2002209591-A/257.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 257 30-JUL-2002;
        JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
        PN JP 2002209591-A/257
        PD 30-JUL-2002
        PF 19-JAN-2001 JP 2001012328
        PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
        YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
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Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCGCGCGCG 14
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Db       10 CCGCGCGGG 2

RESULT 196
BD166714/C
LOCUS
DEFINITION Human liver disease-expressing genes.

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ACCESSION      BD166714
VERSION        BD166714.1 GI:27872526
KEYWORDS       JP 2002209591-A/259.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE          Human liver disease-expressing genes
JOURNAL        Patent: JP 2002209591-A 259 30-JUL-2002;
               JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT        OS Homo sapiens (human)
               PN JP 2002209591-A/259
               PD 30-JUL-2002
               PF 19-JAN-2001 JP 2001012328
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Query Match    35.2%; Score 7.4; DB 1; Length 10;
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QY 8 CGCGCGCT 16
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Db 10 CGCGCTCT 2

RESULT 197
LOCUS          BD166826
DEFINITION     Human liver disease-expressing genes.
ACCESSION      BD166826
VERSION        BD166826.1 GI:27872638
KEYWORDS       JP 2002209591-A/371.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE          Human liver disease-expressing genes
JOURNAL        Patent: JP 2002209591-A 371 30-JUL-2002;
               JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT        OS Homo sapiens (human)
               PN JP 2002209591-A/371
               PD 30-JUL-2002
               PF 19-JAN-2001 JP 2001012328
               PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
               YAMASHITA
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               PC C12N15/00
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Query Match    35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCGCGCT 16
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Db 10 CGCGCTCT 2

RESULT 197
LOCUS          BD166826
DEFINITION     Human liver disease-expressing genes.
ACCESSION      BD166826
VERSION        BD166826.1 GI:27872638
KEYWORDS       JP 2002209591-A/371.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE          Human liver disease-expressing genes
JOURNAL        Patent: JP 2002209591-A 371 30-JUL-2002;
               JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT        OS Homo sapiens (human)
               PN JP 2002209591-A/371
               PD 30-JUL-2002
               PF 19-JAN-2001 JP 2001012328
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Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGC 14
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Db 2 CCAGGCGC 10

RESULT 198
LOCUS          BD166993
DEFINITION     Human liver disease-expressing genes.
ACCESSION      BD166993
VERSION        BD166993.1 GI:27872805
KEYWORDS       JP 2002209591-A/538.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE          Human liver disease-expressing genes
JOURNAL        Patent: JP 2002209591-A 538 30-JUL-2002;
               JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT        OS Homo sapiens (human)
               PN JP 2002209591-A/538
               PD 30-JUL-2002
               PF 19-JAN-2001 JP 2001012328
               PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
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               PC C12N15/00
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FEATURES       source
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Query Match    35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGC 14
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Db 2 CCAGGCGC 10

RESULT 199
LOCUS          BD167029
DEFINITION     Human liver disease-expressing genes.
ACCESSION      BD167029
VERSION        BD167029.1 GI:27872841
KEYWORDS       JP 2002209591-A/574.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE          Human liver disease-expressing genes
JOURNAL        Patent: JP 2002209591-A 574 30-JUL-2002;
               JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT        OS Homo sapiens (human)
               PN JP 2002209591-A/574
               PD 30-JUL-2002
               PF 19-JAN-2001 JP 2001012328
               PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
               YAMASHITA

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PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
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CC Human liver disease-expressing genes
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCGGCGCTG 17
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Db 2 GACGGCTG 10

RESULT 200
BD167035
LOCUS Human liver disease-expressing genes.
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167035
VERSION BD167035.1 GI:27872847
KEYWORDS JP 2002209591-A/580.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 580 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/580
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.le+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CCGGCGCGC 15
| | | | |
Db 2 CCGGCGCCC 10

RESULT 201
BD167212
LOCUS Human liver disease-expressing genes.
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167212
VERSION BD167212.1 GI:27873024
KEYWORDS JP 2002209591-A/757.
SOURCE unidentified
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ORGANISM unidentified
REFERENCE unclassified.
AUTHORS 1 (bases 1 to 10)
TITLE Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
JOURNAL Human liver disease-expressing genes
Patent: JP 2002209591-A 757 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/757
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.le+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
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Db 2 TGGCCAGGC 10

RESULT 202
BD238593/c
LOCUS Preparation and use of superior vaccines.
DEFINITION BD238593
ACCESSION BD238593.1 GI:33048363
VERSION JP 2002534056-A/11.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 11 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/11
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/089977,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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C12N1/19,
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G01N37/00,
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Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCGGCGCG 14
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Db 10 CCGGCGCG 2

RESULT 203
BD240040/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240040
VERSION BD240040.1 GI:33049810
KEYWORDS JP 2002534056-A/1458.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1458 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1458
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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G01N37/00,
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Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCGGCGCG 14
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Db 10 CCGGCGCG 2

RESULT 204
BD240685
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240685
VERSION BD240685.1 GI:33050455
KEYWORDS JP 2002534056-A/2103.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 2103 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/2103
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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CC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GCGCTGTGG 20
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Db 2 GCGCTGTGG 10

RESULT 205

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/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCGG 9
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 Db 9 GCTGGCCGG 1

RESULT 204
 BD240685

LOCUS
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD240685
 VERSION BD240685.1 GI:33050455
 KEYWORDS JP 2002534056-A/2103.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE
 AUTHORS Roberts,B.L. and Shankara,S.
 TITLE Preparation and use of superior vaccines
 JOURNAL Patent: JP 2002534056-A 2103 15-OCT-2002;
 GENZYME CORP

COMMENT
 OS Homo sapiens (human)
 PN JP 2002534056-A/2103
 PD 15-OCT-2002
 PF 18-JUN-1999 JP 2000554749
 PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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 PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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 C12N1/19,
 G01N37/00,
 PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
 G01N37/00,
 CC C12N15/00,C12N5/00,C12N15/00
 CC Preparation and use of superior vaccines
 FH Key Location/Qualifiers
 FT source 1..10
 FT /organism='Homo sapiens (human)'.
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 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GCGCTGTGG 20
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 Db 2 GCGCTGTGG 10

RESULT 205

CQ759089
 LOCUS CQ759089 10 bp DNA linear PAT 01-MAR-2004
 DEFINITION Sequence 1 from Patent WO2003106681.
 ACCESSION CQ759089
 VERSION CQ759089.1 GI:44849080
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Rattus.
 REFERENCE 1
 AUTHORS Altan,O., Kurreck,J., Gruenweller,A. and Erdmann,V.
 TITLE Antisense oligonucleotides against pml
 JOURNAL Patent: WO 2003106681-A 1 24-DEC-2003;
 Gruenenthal GmbH (DE)
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 /organism="Rattus norvegicus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:10116"
 Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TGGCCCGCGC 11
 Db | |||||
 2 TTGCCCGCGC 10
 RESULT 206
 CQ772477/c
 LOCUS CQ772477 10 bp DNA linear PAT 04-MAR-2004
 DEFINITION Sequence 78 from Patent WO2004011677.
 ACCESSION CQ772477
 VERSION CQ772477.1 GI:45126203
 KEYWORDS Equid herpesvirus 1 (Equine herpesvirus 1)
 SOURCE Equid herpesvirus 1
 ORGANISM Equid herpesvirus 1
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Alphaherpesvirinae; Varicelloviruses.
 REFERENCE 1
 AUTHORS Davis Poynter,N., Nugent,J., Birch-Machin,I. and Allen,G.
 TITLE Viral marker
 JOURNAL Patent: WO 2004011677-A 78 05-FEB-2004;
 ANIMAL HEALTH TRUST (GB)
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 /organism="Equid herpesvirus 1"
 /mol_type="unassigned DNA"
 /db_xref="taxon:10326"
 Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CTGCCCGCG 10
 Db | |||||
 10 CTGGCTCGG 2
 RESULT 207
 CQ945058
 LOCUS CQ945058 10 bp DNA linear PAT 01-DEC-2004
 DEFINITION Sequence 205 from Patent WO2004099445.
 ACCESSION CQ945058
 VERSION CQ945058.1 GI:56294399
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1

AUTHORS Kahl,G., Winter,P., Krueger,D., Reich,S., Matsumura,H. and Terauchi,R.
 TITLE Use of a type iii restriction enzyme to isolate identification tags comprising more than 25 nucleotides
 JOURNAL Patent: WO 2004099445-A 205 18-NOV-2004;
 Iwate Prefectural Government (JP)
 FEATURES
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Description of Artificial Sequence:Synthetic DNA (Tag Sequence)"
 Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 GGCCCGCGC 12
 Db || |||||
 2 GGCCCGCGC 10
 RESULT 208
 CS128776/c
 LOCUS CS128776 10 bp DNA linear PAT 02-AUG-2005
 DEFINITION Sequence 9 from Patent WO2005064015.
 ACCESSION CS128776
 VERSION CS128776.1 GI:71794797
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Khanuja,S.P.
 JOURNAL Patent: WO 2005064015-A 9 14-JUL-2005;
 Council of Scientific and Industrial Research (IN)
 FEATURES
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 1..10
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="A primer used in RAPD for identifying plants having high content of artemisinin"
 Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 CCGCGCGCGC 15
 Db |||||
 9 CCGCGCTGC 1
 RESULT 209
 E39489
 LOCUS E39489 10 bp DNA linear PAT 31-JAN-2002
 DEFINITION Genes with human dendritic cell expression.
 ACCESSION E39489
 VERSION E39489.1 GI:18621580
 KEYWORDS JP 2000279181-A/22.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
 TITLE Genes with human dendritic cell expression
 JOURNAL Patent: JP 2000279181-A 22 10-OCT-2000;
 SCIENCE & TECH AGENCY
 COMMENT OS Homo sapiens (human)
 PN JP 2000279181-A/22

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PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR
PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
1..10
/organism="Homo sapiens (human)"
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
DB 2 TGGCCAGGC 10

RESULT 210
E54829
LOCUS Human normal liver cell expression genes. 10 bp DNA linear PAT 27-AUG-2002
DEFINITION
ACCESSION E54829
VERSION E54829.1 GI:22556312
KEYWORDS JP 2001211883-A/181.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 181 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/181
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
DB 2 TGGCCAGGC 10

RESULT 211
AR222959
LOCUS Sequence 12 from patent US 6432640. 10 bp DNA linear PAT 26-SEP-2002
DEFINITION
ACCESSION AR222959
VERSION AR222959.1 GI:23330797
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Polyak,K., Vogelstein,B. and Kinzler,K.W.
TITLE P53-induced apoptosis
JOURNAL Patent: US 6432640-A 12 13-AUG-2002;
The Johns Hopkins University; Baltimore, MD;
WOX;

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGGC 13
DB 2 GCCCGCGGC 10

RESULT 212
AR222959/c
LOCUS Sequence 12 from patent US 6432640. 10 bp DNA linear PAT 26-SEP-2002
DEFINITION
ACCESSION AR222959
VERSION AR222959.1 GI:23330797
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Polyak,K., Vogelstein,B. and Kinzler,K.W.
TITLE P53-induced apoptosis
JOURNAL Patent: US 6432640-A 12 13-AUG-2002;
The Johns Hopkins University; Baltimore, MD;
WOX;

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCGCGGCT 16
DB 9 CGCGCGGCT 1

RESULT 213
AR241748/c
LOCUS Sequence 36 from patent US 6472154. 10 bp DNA linear PAT 20-DEC-2002
DEFINITION
ACCESSION AR241748
VERSION AR241748.1 GI:27287560
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 36 29-OCT-2002;
Board of Regents, The University of Texas System; Austin, TX

Query Match 35.2%; Score 7.4; DB 1; Length 10;

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Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGGC 13
Db 9 GCCCGGCC 1

RESULT 214
AR241871/c
LOCUS AR241871 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 159 from patent US 6472154.
ACCESSION AR241871
VERSION AR241871.1 GI:27287683
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 159 29-OCT-2002;
Board of Regents, The University of Texas System; Austin, TX
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGGC 13
Db 9 GCCCGGCC 1

RESULT 215
AR261814/c
LOCUS AR261814 10 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 240 from patent US 6322995.
ACCESSION AR261814
VERSION AR261814.1 GI:28072954
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Hohmann,H.-P., Humbelin,M., van Loon,A. and Schurter,W.
TITLE Riboflavin production
JOURNAL Patent: US 6322995-A 240 27-NOV-2001;
F. Hoffmann-La Roche AG; Basel;
EPX;
FEATURES
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGCGCGC 14
Db 1 CCCAGCGCG 9

RESULT 216
AR261814/c
LOCUS AR261814 10 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 240 from patent US 6322995.
ACCESSION AR261814
VERSION AR261814.1 GI:28072954

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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hohmann,H.-P., Humbelin,M., van Loon,A. and Schurter,W.
TITLE Riboflavin production
JOURNAL Patent: US 6322995-A 240 27-NOV-2001;
F. Hoffmann-La Roche AG; Basel;
EPX;
FEATURES
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 CCGCGCTGTG 19
Db 9 CCGCGTGG 1

RESULT 217
AR310513/c
LOCUS AR310513 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3 from patent US 6558940.
ACCESSION AR310513
VERSION AR310513.1 GI:31703523
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Alam,M., Sattar,A., Kumar,S., Samad,A., Dhawan,O.P.,
Khanuja,S.P.S., Shasany,A.K., Singh,S., Kumar,P.V.N.A., Khaliq,A.,
Zaim,M., Shahabuddin,S. and Trivedi,W.
TITLE Streptomyces strain with potential anti-microbial activity against
phytopathogenic fungi
JOURNAL Patent: US 6558940-A 3 06-MAY-2003;
Council of Scientific and Industrial Research;;
INX;
FEATURES
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGCGCGCG 15
Db 9 CCGCGGTGC 1

RESULT 218
AR336888/c
LOCUS AR336888 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 63 from patent US 6566130.
ACCESSION AR336888
VERSION AR336888.1 GI:33722738
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 63 20-MAY-2003;
Henry M. Jackson Foundation for the Advancement of Military
Medicine; Rockville, MD

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    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 3 TGGCCCGC 11
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  Db 10 TGGCCCGC 2

RESULT 219
AR630140
LOCUS
  DEFINITION
    Sequence 194 from patent US 6838556.
  ACCESSION
    AR630140
  VERSION
    AR630140.1 GI:59762459
  KEYWORDS
    .
  SOURCE
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 10)
    AUTHORS
      Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
      Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
      Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
    TITLE
      Promoters for regulated gene expression
    JOURNAL
      Patent: US 6838556-A 194 04-JAN-2005;
      Genelabs Technologies, Inc.; Redwood City, CA
  FEATURES
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        /organism="unknown"
        /mol_type="genomic DNA"

  Query Match
    Best Local Similarity 35.2%; Score 7.4; DB 1; Length 10;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 9 GCGCGCGT 17
      |||||
  Db 1 GCGCGCGG 9

RESULT 220
AR630150
LOCUS
  DEFINITION
    Sequence 204 from patent US 6838556.
  ACCESSION
    AR630150
  VERSION
    AR630150.1 GI:59762479
  KEYWORDS
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  SOURCE
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 10)
    AUTHORS
      Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
      Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
      Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
    TITLE
      Promoters for regulated gene expression
    JOURNAL
      Patent: US 6838556-A 204 04-JAN-2005;
      Genelabs Technologies, Inc.; Redwood City, CA
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        /organism="unknown"
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  Query Match
    Best Local Similarity 35.2%; Score 7.4; DB 1; Length 10;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 9 GCGCGCGT 17
      |||||
  Db 1 GCGCGCGG 9

RESULT 221
AR630153/C
LOCUS
  DEFINITION
    Sequence 207 from patent US 6838556.
  ACCESSION
    AR630153
  VERSION
    AR630153.1 GI:59762485
  KEYWORDS
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  SOURCE
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 10)
    AUTHORS
      Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
      Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
      Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
    TITLE
      Promoters for regulated gene expression
    JOURNAL
      Patent: US 6838556-A 207 04-JAN-2005;
      Genelabs Technologies, Inc.; Redwood City, CA
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        /organism="unknown"
        /mol_type="genomic DNA"

  Query Match
    Best Local Similarity 35.2%; Score 7.4; DB 1; Length 10;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 10 GCGCGCGT 18
      |||||
  Db 9 GCGCGCTT 1

RESULT 222
AX006877/C
LOCUS
  DEFINITION
    Sequence 30 from Patent WO0001832.
  ACCESSION
    AX006877
  VERSION
    AX006877.1 GI:9994892
  KEYWORDS
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  SOURCE
    synthetic construct
    ORGANISM
      other sequences; artificial sequences.
  REFERENCE
    1
    AUTHORS
      Fenoll-Comes,C. and Munoz-Martin,M.D.
    TITLE
      Inducible promoters
    JOURNAL
      Patent: WO 0001832-A 30 13-JAN-2000;
      FENOLL COMES CARMEN (ES); MUNOZ MARTIN MARIA DE LOS ANGE (ES);
      PLANT BIOSCIENCE LIMITED (GB)
  FEATURES
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          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="Synthetic"

  Query Match
    Best Local Similarity 35.2%; Score 7.4; DB 1; Length 10;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 2 CTGGCCCG 10
      |||||
  Db 10 CCGGCCCG 2

RESULT 223
AX152364
LOCUS
  DEFINITION
    Sequence 279 from Patent WO0138577.
  ACCESSION
    AX152364
  VERSION
    AX152364.1 GI:14534015
  KEYWORDS
    .

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptsomes
JOURNAL    Patent: WO 0138577-A 279 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 GCGCTGTGG 20
        | | | | |
Db       2 GGGCTGTGG 10

RESULT 224
AX152365      35.2%; Score 7.4; DB 1; Length 10;
LOCUS         AX152365      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION    Sequence 280 from Patent WO0138577.
ACCESSION     AX152365
VERSION       AX152365.1 GI:14534016
KEYWORDS      .
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptsomes
JOURNAL    Patent: WO 0138577-A 280 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 GCGCTGTGG 20
        | | | | |
Db       2 GGGCTGTGG 10

RESULT 225
AX152532/c    35.2%; Score 7.4; DB 1; Length 10;
LOCUS         AX152532/c    10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION    Sequence 447 from Patent WO0138577.
ACCESSION     AX152532
VERSION       AX152532.1 GI:14534183
KEYWORDS      .
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptsomes
JOURNAL    Patent: WO 0138577-A 447 31-MAY-2001;

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FEATURES   Location/Qualifiers
            source
            1..10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      13 CGCTGTGGC 21
        | | | | |
Db       9 CGCTGGGC 1

RESULT 226
AX152671/c    35.2%; Score 7.4; DB 1; Length 10;
LOCUS         AX152671/c    10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION    Sequence 586 from Patent WO0138577.
ACCESSION     AX152671
VERSION       AX152671.1 GI:14534322
KEYWORDS      .
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptsomes
JOURNAL    Patent: WO 0138577-A 586 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
            source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      13 CGCTGTGGC 21
        | | | | |
Db       10 CGCAGTGGC 2

RESULT 227
AX153299/c    35.2%; Score 7.4; DB 1; Length 10;
LOCUS         AX153299/c    10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION    Sequence 1214 from Patent WO0138577.
ACCESSION     AX153299
VERSION       AX153299.1 GI:14534950
KEYWORDS      .
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptsomes
JOURNAL    Patent: WO 0138577-A 1214 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      13 CGCTGTGGC 21
        | | | | |
Db       10 CGCAGTGGC 2

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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
 ||||| |||
 Db 9 TGGCCAGGC 1

RESULT 228
 AX153300/c
 LOCUS AX153300 10 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 1215 from Patent WO0138577.
 ACCESSION AX153300
 VERSION AX153300.1 GI:14534951
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 JOURNAL Hominidae; Homo.

REFERENCE
 AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 1215 31-MAY-2001;
 The Johns Hopkins University (US)

FEATURES
 source
 1. .10
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
 ||||| |||
 Db 9 TGGCCAGGC 1

RESULT 229
 AX153313
 LOCUS AX153313 10 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 1228 from Patent WO0138577.
 ACCESSION AX153313
 VERSION AX153313.1 GI:14534964
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 JOURNAL Hominidae; Homo.

REFERENCE
 AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 1228 31-MAY-2001;
 The Johns Hopkins University (US)

FEATURES
 source
 1. .10
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
 ||||| |||
 Db 2 TGGCCAGGC 10

RESULT 230
 AX153314

LOCUS AX153314 10 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 1229 from Patent WO0138577.
 ACCESSION AX153314
 VERSION AX153314.1 GI:14534965
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 JOURNAL Hominidae; Homo.

REFERENCE
 AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 1229 31-MAY-2001;
 The Johns Hopkins University (US)

FEATURES
 source
 1. .10
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
 ||||| |||
 Db 2 TGGCCAGGC 10

RESULT 231
 AX153315
 LOCUS AX153315 10 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 1230 from Patent WO0138577.
 ACCESSION AX153315
 VERSION AX153315.1 GI:14534966
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 JOURNAL Hominidae; Homo.

REFERENCE
 AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
 TITLE Human transcriptomes
 JOURNAL Patent: WO 0138577-A 1230 31-MAY-2001;
 The Johns Hopkins University (US)

FEATURES
 source
 1. .10
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
 ||||| |||
 Db 2 TGGCCAGGC 10

RESULT 232
 AX153316
 LOCUS AX153316 10 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 1231 from Patent WO0138577.
 ACCESSION AX153316
 VERSION AX153316.1 GI:14534967
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1231 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
Hominidae; Homo.
1
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
Db 2 TGGCCAGGC 10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

RESULT 233
AX153317
LOCUS AX153317 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1232 from Patent WO0138577.
ACCESSION AX153317
VERSION AX153317.1 GI:14534968
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1232 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
Homo sapiens
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
Db 2 TGGCCAGGC 10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

RESULT 234
AX153318
LOCUS AX153318 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1233 from Patent WO0138577.
ACCESSION AX153318
VERSION AX153318.1 GI:14534969
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1233 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
Homo sapiens
1. .10
/organism="Homo sapiens"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
Db 2 TGGCCAGGC 10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

RESULT 235
AX153319
LOCUS AX153319 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1234 from Patent WO0138577.
ACCESSION AX153319
VERSION AX153319.1 GI:14534970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1234 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
Homo sapiens
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
Db 2 TGGCCAGGC 10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

RESULT 236
AX224406
LOCUS AX224406 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 13 from Patent WO0160997.
ACCESSION AX224406
VERSION AX224406.1 GI:15554648
KEYWORDS
SOURCE Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 13 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
Homo sapiens
1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGCGCCG 9
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Db      1  GCGGGCCCCG 9

RESULT 237
AX224406/c
LOCUS   AX224406          10 bp      DNA      linear      PAT 10-SEP-2001
DEFINITION
Sequence 13 from Patent WO0160997.
ACCESSION
AX224406
VERSION  AX224406.1  GI:15554648
KEYWORDS
SOURCE   Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1
AUTHORS  Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE    Male tissue-preferred regulatory region and method of using same
JOURNAL  Patent: WO 0160997-A 13 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers
source
1..10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTGGCCCCG 9
      || || || || ||
Db      1  GCGGGCCCCG 9

RESULT 240
AX224412/c
LOCUS   AX224412          10 bp      DNA      linear      PAT 10-SEP-2001
DEFINITION
Sequence 19 from Patent WO0160997.
ACCESSION
AX224412
VERSION  AX224412.1  GI:15554654
KEYWORDS
SOURCE   Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1
AUTHORS  Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE    Male tissue-preferred regulatory region and method of using same
JOURNAL  Patent: WO 0160997-A 19 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers
source
1..10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTGGCCCCG 9
      || || || || ||
Db      1  GCGGGCCCCG 9

RESULT 241
AX224413
LOCUS   AX224413          10 bp      DNA      linear      PAT 10-SEP-2001
DEFINITION
Sequence 20 from Patent WO0160997.
ACCESSION
AX224413
VERSION  AX224413.1  GI:15554655
KEYWORDS
SOURCE   Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1
AUTHORS  Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE    Male tissue-preferred regulatory region and method of using same
JOURNAL  Patent: WO 0160997-A 15 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers
source
1..10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTGGCCCCG 9
      || || || || ||
Db      1  GCGGGCCCCG 9

RESULT 238
AX224408
LOCUS   AX224408          10 bp      DNA      linear      PAT 10-SEP-2001
DEFINITION
Sequence 15 from Patent WO0160997.
ACCESSION
AX224408
VERSION  AX224408.1  GI:15554650
KEYWORDS
SOURCE   Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1
AUTHORS  Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE    Male tissue-preferred regulatory region and method of using same
JOURNAL  Patent: WO 0160997-A 15 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers
source
1..10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTGGCCCCG 9
      || || || || ||
Db      1  GCGGGCCCCG 9

RESULT 239
AX224412
LOCUS   AX224412          10 bp      DNA      linear      PAT 10-SEP-2001
DEFINITION
Sequence 19 from Patent WO0160997.
ACCESSION
AX224412
VERSION  AX224412.1  GI:15554654

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JOURNAL Patent: WO 0160997-A 20 23-AUG-2001;
FEATURES PIONEER HI-BRED INTERNATIONAL, INC. (US)
source Location/Qualifiers
1..10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 9
||| |||||
Db 1 GCGGGCCCG 9

RESULT 242
AX224413/c
LOCUS AX224413 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 20 from Patent WO0160997.
ACCESSION AX224413
VERSION AX224413.1 GI:15554655
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 20 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
1..10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 9
||| |||||
Db 10 GCGGGCCCG 2

RESULT 243
AX224414
LOCUS AX224414 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 21 from Patent WO0160997.
ACCESSION AX224414
VERSION AX224414.1 GI:15554656
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 21 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
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/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 9
||| |||||
Db 10 GCGGGCCCG 2

RESULT 244
AX224415/c
LOCUS AX224415 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 22 from Patent WO0160997.
ACCESSION AX224415
VERSION AX224415.1 GI:15554657
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 22 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
1..10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 9
||| |||||
Db 9 GCGGGCCCG 1

RESULT 245
AX224416/c
LOCUS AX224416 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 23 from Patent WO0160997.
ACCESSION AX224416
VERSION AX224416.1 GI:15554658
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 23 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
1..10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 9
||| |||||
Db 9 GCGGGCCCG 1

RESULT 246
AX224417/c
LOCUS AX224417 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 24 from Patent WO0160997.
ACCESSION AX224417
VERSION AX224417.1 GI:15554659
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 24 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
1..10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 9
||| |||||
Db 9 GCGGGCCCG 1

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AX601650
LOCUS AX601650 10 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 32 from Patent WO02092825.
ACCESSION AX601650
VERSION AX601650.1 GI:28401695
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Mikkelsen,J.G., Rasmussen,S.V., Duch,M., Pedersen,F.S. and
Aagaard,L.
TITLE Improved vectors for gene therapy
JOURNAL Patent: WO 02092825-A 32 21-NOV-2002;
Aarhus University (DK)
FEATURES
source
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTGGCCCG 9
|||||||
Db 1 GCTGGCCAG 9

RESULT 247
AX601650/c
LOCUS AX601650 10 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 32 from Patent WO02092825.
ACCESSION AX601650
VERSION AX601650.1 GI:28401695
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Mikkelsen,J.G., Rasmussen,S.V., Duch,M., Pedersen,F.S. and
Aagaard,L.
TITLE Improved vectors for gene therapy
JOURNAL Patent: WO 02092825-A 32 21-NOV-2002;
Aarhus University (DK)
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/db_xref="taxon:32630"
/notes="palindrome at position 209-218 in Akv/AkvB"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTGGCCCG 9
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Db 1 GCTGGCCAG 9

RESULT 248
AX958217
LOCUS AX958217 10 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 20 from Patent WO03046156.
ACCESSION AX958217
VERSION AX958217.1 GI:40785870
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE
AUTHORS Claude,P.P.
TITLE Novel bacterial biomassess, method for obtaining same and uses
thereof for bacterization of soils and crop residues
JOURNAL Patent: WO 03046156-A 20 05-JUN-2003;
Valbios (FR)
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CCCGCGCGC 14
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Db 2 CCCAGCGCG 10

RESULT 249
AX958217/c
LOCUS AX958217 10 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 20 from Patent WO03046156.
ACCESSION AX958217
VERSION AX958217.1 GI:40785870
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE
AUTHORS Claude,P.P.
TITLE Novel bacterial biomassess, method for obtaining same and uses
thereof for bacterization of soils and crop residues
JOURNAL Patent: WO 03046156-A 20 05-JUN-2003;
Valbios (FR)
FEATURES
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/db_xref="taxon:32644"
/notes="Azobacter"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 CGCGCTGTG 19
|||||||
Db 10 CGCGCTGGG 2

RESULT 250
BD007953/c
LOCUS BD007953 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007953
VERSION BD007953.1 GI:18636326
KEYWORDS JP 2001069993-A/229.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 10)
TITLE Matsuhashima,K., Hashimoto,S. and Suzuki,T.
JOURNAL LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 229 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/229

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REFERENCE
AUTHORS Claude,P.P.
TITLE Novel bacterial biomassess, method for obtaining same and uses
thereof for bacterization of soils and crop residues
JOURNAL Patent: WO 03046156-A 20 05-JUN-2003;
Valbios (FR)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/notes="Azobacter"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CCCGCGCGC 14
|||||||
Db 2 CCCAGCGCG 10

RESULT 249
AX958217/c
LOCUS AX958217 10 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 20 from Patent WO03046156.
ACCESSION AX958217
VERSION AX958217.1 GI:40785870
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE
AUTHORS Claude,P.P.
TITLE Novel bacterial biomassess, method for obtaining same and uses
thereof for bacterization of soils and crop residues
JOURNAL Patent: WO 03046156-A 20 05-JUN-2003;
Valbios (FR)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/notes="Azobacter"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 CGCGCTGTG 19
|||||||
Db 10 CGCGCTGGG 2

RESULT 250
BD007953/c
LOCUS BD007953 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007953
VERSION BD007953.1 GI:18636326
KEYWORDS JP 2001069993-A/229.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 10)
TITLE Matsuhashima,K., Hashimoto,S. and Suzuki,T.
JOURNAL LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 229 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/229

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PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00, C12P21/08, C12N15/00
CC
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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source
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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TGGCCCGC 11
Db 9 TGGCCAGC 1
RESULT 251
BD007960/c
LOCUS
DEFINITION LPS activated human monocyte expressing genes. PAT 31-JAN-2002
ACCESSION BD007960 10 bp DNA linear
VERSION BD007960.1 GI:18636333
KEYWORDS JP 2001069993-A/236.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima.K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 236 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/236
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00, C12P21/08, C12N15/00
CC
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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/organism='Homo sapiens'
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/db_xref='taxon:9606'
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CCGCGTGC 14
Db 9 CCGGTGCG 1
RESULT 252
AX623125

LOCUS AX623125 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 166 from Patent WO02053774.
ACCESSION AX623125
VERSION AX623125.1 GI:28451066
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 166 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Location/Qualifiers
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
Query Match 35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CTGGCCCG 10
Db 3 CTGGCCAG 11
RESULT 253
AX630546
LOCUS
DEFINITION Sequence 7587 from Patent WO02053774. PAT 21-FEB-2003
ACCESSION AX630546 11 bp DNA linear
VERSION AX630546.1 GI:28458584
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7587 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Location/Qualifiers
/organism='Homo sapiens'
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/db_xref='taxon:9606'
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Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CTGGCCCG 10
Db 3 CTGGCCAG 11
RESULT 254
AR605251
LOCUS
DEFINITION Sequence 42 from patent US 6818747. PAT 15-DEC-2004
ACCESSION AR605251 11 bp DNA linear
VERSION AR605251.1 GI:56656825
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)

AUTHORS Yao, Y. and Xu, H.
 TITLE G.alpha.q protein variants and their use in the analysis and discovery of agonists and antagonists of chemosensory receptors
 JOURNAL Senomyx, Inc.; La Jolla, CA
 FEATURES source 1..11
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGGCGCGCTG 17
 Db 1 GGGCGCGCG 9

RESULT 255
 LOCUS CQ766499/c
 DEFINITION Sequence 460 from Patent WO2004005547.
 ACCESSION CQ766499
 VERSION CQ766499.1 GI:44908759
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Weinzierl, R.
 TITLE Method
 JOURNAL IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
 FEATURES source 1..12
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="HS motif"

Query Match 35.2%; Score 7.4; DB 1; Length 12;
 Best Local Similarity 88.9%; Pred. No. 1.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
 Db 9 CGGGCCCGG 1

RESULT 256
 LOCUS CQ786323/c
 DEFINITION Sequence 131 from Patent WO2004020668.
 ACCESSION CQ786323
 VERSION CQ786323.1 GI:45721425
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Nakamura, Y. and Katagiri, T.
 TITLE Method for treating synovial sarcoma
 JOURNAL Patent: WO 2004020668-A 131 11-MAR-2004;
 Oncotherapy Science, Inc. (JP); The University of Tokyo (JP)
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 /organism="synthetic construct"
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 /db_xref="taxon:32630"
 /note="Description of Artificial Sequence: synthetic oligonucleotide"

AUTHORS Yao, Y. and Xu, H.
 TITLE G.alpha.q protein variants and their use in the analysis and discovery of agonists and antagonists of chemosensory receptors
 JOURNAL Senomyx, Inc.; La Jolla, CA
 FEATURES source 1..11
 /organism="unknown"
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Query Match 35.2%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGGCGCGCTG 17
 Db 1 GGGCGCGCG 9

RESULT 255
 LOCUS CQ766499/c
 DEFINITION Sequence 460 from Patent WO2004005547.
 ACCESSION CQ766499
 VERSION CQ766499.1 GI:44908759
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Weinzierl, R.
 TITLE Method
 JOURNAL IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="HS motif"

Query Match 35.2%; Score 7.4; DB 1; Length 12;
 Best Local Similarity 88.9%; Pred. No. 1.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
 Db 9 CGGGCCCGG 1

RESULT 256
 LOCUS CQ786323/c
 DEFINITION Sequence 131 from Patent WO2004020668.
 ACCESSION CQ786323
 VERSION CQ786323.1 GI:45721425
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Nakamura, Y. and Katagiri, T.
 TITLE Method for treating synovial sarcoma
 JOURNAL Patent: WO 2004020668-A 131 11-MAR-2004;
 Oncotherapy Science, Inc. (JP); The University of Tokyo (JP)
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Query Match 34.3%; Score 7.2; DB 1; Length 16;
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 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGGC 21
 Db 16 GCGCGCGCGCC 5

RESULT 257
 LOCUS AR086219
 DEFINITION Sequence 40 from patent US 5985558.
 ACCESSION AR086219
 VERSION AR086219.1 GI:10012985
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dean, N.M., McKay, R., Miraglia, L. and Baker, B.
 TITLE Antisense oligonucleotide compositions and methods for the inhibition of c-Jun and c-Fos
 JOURNAL Patent: US 5985558-A 40 16-NOV-1999;
 FEATURES Location/Qualifiers
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Query Match 34.3%; Score 7.2; DB 1; Length 20;
 Best Local Similarity 75.0%; Pred. No. 3.4e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CGCGCGCTGTG 19
 Db 5 CAGCGCGCGGG 16

RESULT 258
 LOCUS AR176785
 DEFINITION Sequence 40 from patent US 6312900.
 ACCESSION AR176785
 VERSION AR176785.1 GI:17919140
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dean, N.M., McKay, R., Miraglia, L. and Baker, B.
 TITLE Antisense oligonucleotide compositions and methods for the modulation of activating protein 1
 JOURNAL Patent: US 6312900-A 40 06-NOV-2001;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 34.3%; Score 7.2; DB 1; Length 20;
 Best Local Similarity 75.0%; Pred. No. 3.4e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CGCGCGCTGTG 19
 Db 5 CAGCGCGCGGG 16

RESULT 259
 LOCUS ES4824
 DEFINITION Human normal liver cell expression genes.
 ACCESSION ES4824
 VERSION ES4824.1 GI:22556307

QY 10 GCGCGCT 16
Db 4 GCGCGCT 10

RESULT 264
AR071792
LOCUS AR071792 10 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 21 from patent US 5912147.
ACCESSION AR071792
VERSION AR071792.1 GI:7222680
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 21 15-JUN-1999;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCGCGCT 16
Db 4 GCGCGCT 10

RESULT 265
AR092694
LOCUS AR092694 10 bp DNA linear PAT 08-SRP-2000
DEFINITION Sequence 6 from patent US 5998193.
ACCESSION AR092694
VERSION AR092694.1 GI:10019446
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 5998193-A 6 07-DEC-1999;
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
Db 4 CTGTGGC 10

RESULT 266
AR092718/c
LOCUS AR092718/c 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 30 from patent US 5998193.
ACCESSION AR092718
VERSION AR092718.1 GI:10019470
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)

AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 5998193-A 30 07-DEC-1999;
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 8 GCTGGCC 2

RESULT 267
AR098900/c
LOCUS AR098900 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 36 from patent US 6077685.
ACCESSION AR098900
VERSION AR098900.1 GI:12808666
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE Tumor suppressor merlin and antibodies thereof
JOURNAL Patent: US 6077685-A 36 20-JUN-2000;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
Db 10 CTGTGGC 4

RESULT 268
AR106678
LOCUS AR106678 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 6 from patent US 6107078.
ACCESSION AR106678
VERSION AR106678.1 GI:12821208
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 6107078-A 6 22-AUG-2000;
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
Db 4 CTGTGGC 10

RESULT 269
AR092718/c
LOCUS AR092718/c 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 30 from patent US 5998193.
ACCESSION AR092718
VERSION AR092718.1 GI:10019470
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)

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RESULT 269
AR106702/C
LOCUS AR106702 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 30 from patent US 6107078.
ACCESSION AR106702
VERSION AR106702.1 GI:12821232
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Keese, P., Stapper, M. and Perriman, R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
embedded ribozymes and compositions thereof
JOURNAL Patent: US 6107078-A 30 22-AUG-2000;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 8 GCTGGCC 2

RESULT 270
AR107780
LOCUS AR107780 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 26 from patent US 6110667.
ACCESSION AR107780
VERSION AR107780.1 GI:12823267
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Lopez-Nieto, C. Eduardo, and Nigam, S. Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 26 29-AUG-2000;
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Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 8 GCTGGCC 2

RESULT 271
AR107802
LOCUS AR107802 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 48 from patent US 6110667.
ACCESSION AR107802
VERSION AR107802.1 GI:12823289
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Lopez-Nieto, C. Eduardo, and Nigam, S. Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 26 29-AUG-2000;
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 4 GCTGGCC 10

RESULT 272
AR107825
LOCUS AR107825 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 71 from patent US 6110667.
ACCESSION AR107825
VERSION AR107825.1 GI:12823312
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Lopez-Nieto, C. Eduardo, and Nigam, S. Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 71 29-AUG-2000;
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
Db 4 GCTGTGG 10

RESULT 273
AR172413
LOCUS AR172413 10 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 10 from patent US 6303308.
ACCESSION AR172413
VERSION AR172413.1 GI:17911904
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Halle, J.-P., Regenbogen, J., and Goppelt, A.
TITLE Cloning vectors and their preparation and use for mRNA expression
pattern analysis
JOURNAL Patent: US 6303308-A 10 16-OCT-2001;
FEATURES
source
Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCC 15
Db 2 GCGCGCC 8

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sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 48 29-AUG-2000;
FEATURES
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/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
Db 4 GCTGTGG 10

RESULT 272
AR107825
LOCUS AR107825 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 71 from patent US 6110667.
ACCESSION AR107825
VERSION AR107825.1 GI:12823312
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Lopez-Nieto, C. Eduardo, and Nigam, S. Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide
sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 71 29-AUG-2000;
FEATURES
source
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 1 GCTGGCC 7

RESULT 273
AR172413
LOCUS AR172413 10 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 10 from patent US 6303308.
ACCESSION AR172413
VERSION AR172413.1 GI:17911904
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Halle, J.-P., Regenbogen, J., and Goppelt, A.
TITLE Cloning vectors and their preparation and use for mRNA expression
pattern analysis
JOURNAL Patent: US 6303308-A 10 16-OCT-2001;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCC 15
Db 2 GCGCGCC 8

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RESULT 274
 ARI172413/C
 LOCUS 10 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 10 from patent US 6303308.
 ACCESSION ARI172413
 VERSION ARI172413.1 GI:17911904
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 Unclassified.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Halle, J.-P., Regenhogen, J. and Coppel, A.
 TITLE Cloning vectors and their preparation and use for mRNA expression
 pattern analysis
 JOURNAL Patent: US 6303308-A 10 16-OCT-2001;
 FEATURES
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Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCGCGGC 15
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 Db 9 GCGCGGC 3

RESULT 275
 BD065207
 LOCUS 10 bp DNA linear PAT 27-AUG-2002
 DEFINITION Characterization of the yeast transcriptome.
 ACCESSION BD065207
 VERSION BD065207.1 GI:22610810
 KEYWORDS JP 2001509017-A/143.
 SOURCE Saccharomyces cerevisiae (baker's yeast)
 ORGANISM Saccharomycetes
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 REFERENCE 1 (bases 1 to 10);
 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
 AUTHORS Characterization of the yeast transcriptome
 TITLE Patent: JP 2001509017-A 143 10-JUL-2001;
 JOURNAL THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 COMMENT OS Saccharomyces cerevisiae (yeast)
 PN JP 2001509017-A/143
 PD 10-JUL-2001
 PF 22-JAN-1998 JP 1998532117
 PR 23-JAN-1997 US 60/035917
 PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
 C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC
 Characterization of the yeast transcriptome
 FH Key Location/Qualifiers
 FT source 1. .10
 /organism="Saccharomyces cerevisiae (yeast)".

FEATURES
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 /organism="Saccharomyces cerevisiae"
 /mol_type="genomic DNA"
 /db_xref="taxon:4932"

Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CGCTGTG 19
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 Db 4 CGCTGTG 10

RESULT 276

BD083127
 LOCUS 10 bp DNA linear PAT 27-AUG-2002
 DEFINITION Human matured/activated dendritic cell expression genes.
 ACCESSION BD083127
 VERSION BD083127.1 GI:22628737
 KEYWORDS JP 2001327293-A/48.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima, K., Hashimoto, S., Suzuki, T. and Nagai, S.
 TITLE Human matured/activated dendritic cell expression genes
 JOURNAL Patent: JP 2001327293-A 48 27-NOV-2001;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2001327293-A/48
 PD 27-NOV-2001
 PF 22-MAY-2000 JP 2000150562
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
 NAGAI
 PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
 CC
 FH Key Location/Qualifiers.

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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
 |||||
 Db 2 CTGTGGC 8

RESULT 277
 BD083229
 LOCUS 10 bp DNA linear PAT 27-AUG-2002
 DEFINITION Human matured/activated dendritic cell expression genes.
 ACCESSION BD083229
 VERSION BD083229.1 GI:22628839
 KEYWORDS JP 2001327293-A/150.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima, K., Hashimoto, S., Suzuki, T. and Nagai, S.
 TITLE Human matured/activated dendritic cell expression genes
 JOURNAL Patent: JP 2001327293-A 150 27-NOV-2001;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2001327293-A/150
 PD 27-NOV-2001
 PF 22-MAY-2000 JP 2000150562
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
 NAGAI
 PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
 CC
 FH Key Location/Qualifiers.

FEATURES
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
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Query Match 33.3%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
|||||

Db 2 CTGTGGC 8

RESULT 278
BD083293
LOCUS BD083293 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083293
VERSION BD083293.1 GI:22628903
KEYWORDS JP 2001327293-A/214.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
Human matured/activated dendritic cell expression genes
Patent: JP 2001327293-A 214 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/214
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI
NAGAI

PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
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Db 3 GCTGGCC 9

RESULT 279
BD161461
LOCUS BD161461 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161461
VERSION BD161461.1 GI:27867219
KEYWORDS JP 2002186482-A/283.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 10)
Nagai,S., Matsushima,K. and Hashimoto,S.
Human activated Th1 and Th2 cell expression genes
Patent: JP 2002186482-A 283 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/283
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key

Location/Qualifiers
FT source 1..10
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FEATURES
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Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
|||||

Db 3 GCGCGGC 9

RESULT 280
BD161461/c
LOCUS BD161461 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161461
VERSION BD161461.1 GI:27867219
KEYWORDS JP 2002186482-A/283.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 10)
Nagai,S., Matsushima,K. and Hashimoto,S.
Human activated Th1 and Th2 cell expression genes
Patent: JP 2002186482-A 283 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/283
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key

Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
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source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
|||||

Db 10 GCGCGGC 4

RESULT 281
BD161467
LOCUS BD161467 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161467
VERSION BD161467.1 GI:27867225
KEYWORDS JP 2002186482-A/289.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)

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AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 289 02-JUL-2002;
COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/289
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers 1..10
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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGC 15
DB 3 GCGCGC 9

RESULT 282
BD161475/c
LOCUS
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161475
VERSION BD161475.1 GI:27867233
KEYWORDS JP 2002186482-A/297.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 297 02-JUL-2002;
COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/297
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers 1..10
FT source /organism='Homo sapiens (human)'.
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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
DB 7 GCTGTGG 1

RESULT 283
BD166636/c
LOCUS
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166636
VERSION BD166636.1 GI:27872448
KEYWORDS JP 2002209591-A/181.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 181 30-JUL-2002;
COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/181
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGCTGT 18
DB 7 GCGCTGT 1

RESULT 284
BD166798/c
LOCUS
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166798
VERSION BD166798.1 GI:27872610
KEYWORDS JP 2002209591-A/343.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 343 30-JUL-2002;
COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/343
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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/organism='Homo sapiens (human)'.
FEATURES
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/organism='unidentified'
/mol_type='genomic DNA'

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/db_xref="taxon:32644"

Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
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 Db 7 GCTGGCC 1

RESULT 285
 BD166944/c
 LOCUS Human liver disease-expressing genes. 10 bp DNA linear PAT 17-JAN-2003
 DEFINITION BD166944
 ACCESSION BD166944.1 GI:27872756
 VERSION JP 2002209591-A/489.
 KEYWORDS Human liver disease-expressing genes
 SOURCE unclassified
 ORGANISM Homo sapiens (human)
 unclassified.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 489 30-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 FN JP 2002209591-A/489
 PD 30-JUL-2002
 PF 19-JAN-2001 JP 2001012328
 PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
 YAMASHITA
 PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
 PC C12P21/08,
 PC C12N15/00
 CC Human liver disease-expressing genes
 FH Key Location/Qualifiers
 FT source 1..10
 FT source 7 GCTGGCC 1

FEATURES
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 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
 |||||
 Db 7 GCTGGCC 1

RESULT 286
 BD166997/c
 LOCUS Human liver disease-expressing genes. 10 bp DNA linear PAT 17-JAN-2003
 DEFINITION BD166997
 ACCESSION BD166997.1 GI:27872809
 VERSION JP 2002209591-A/542.
 KEYWORDS Human liver disease-expressing genes
 SOURCE unclassified
 ORGANISM Homo sapiens (human)
 unclassified.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 542 30-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 FN JP 2002209591-A/542
 PD 30-JUL-2002
 PF 19-JAN-2001 JP 2001012328

PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
 YAMASHITA
 PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
 PC C12P21/08,
 PC C12N15/00
 CC Human liver disease-expressing genes
 FH Key Location/Qualifiers
 FT source 1..10
 FT source 7 GCTGGCC 1

FEATURES
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 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
 |||||
 Db 7 GCTGGCC 1

RESULT 287
 BD167054/c
 LOCUS Human liver disease-expressing genes. 10 bp DNA linear PAT 17-JAN-2003
 DEFINITION BD167054
 ACCESSION BD167054.1 GI:27872866
 VERSION JP 2002209591-A/599.
 KEYWORDS Human liver disease-expressing genes
 SOURCE unclassified
 ORGANISM Homo sapiens (human)
 unclassified.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 599 30-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 FN JP 2002209591-A/599
 PD 30-JUL-2002
 PF 19-JAN-2001 JP 2001012328
 PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
 YAMASHITA
 PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
 PC C12P21/08,
 PC C12N15/00
 CC Human liver disease-expressing genes
 FH Key Location/Qualifiers
 FT source 1..10
 FT source 7 GCTGGCC 1

FEATURES
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RESULT 288
 BD225345/c
 LOCUS Compositions and methods for the identification of lung tumor cells. 10 bp DNA linear PAT 17-JUL-2003
 DEFINITION BD225345
 ACCESSION BD225345

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VERSION      BD225345.1 GI:33035115
KEYWORDS     JP 2002509707-A/27.
SOURCE       synthetic construct
ORGANISM     synthetic construct
REFERENCE    1 (bases 1 to 10)
AUTHORS      Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE        Compositions and methods for the identification of lung tumor cells
JOURNAL      Patent: JP 2002509707-A 27 02-APR-2002;
COMMENT      GENZYME CORP
OS           Artificial Sequence
PN           JP 2002509707-A/27
PD           02-APR-2002
PF           30-MAR-1999 JP 2000541180
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C12N15/09,A01K67/027,C07H21/04,C07K14/47,C07K16/18,C12N1/15, PC
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PC           C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/15,G01N33/53, PC
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CTGTGGC 21
Db 9 CTGTGGC 3
RESULT 289
BD238618
LOCUS
DEFINITION      Preparation and use of superior vaccines.
ACCESSION      BD238618
VERSION        BD238618.1 GI:33048388
KEYWORDS       JP 2002534056-A/36.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS         Roberts,B.L. and Shankara,S.
TITLE           Preparation and use of superior vaccines
JOURNAL         Patent: JP 2002534056-A 36 15-OCT-2002;
GENZYME CORP
COMMENT         OS Homo sapiens (human)
PN JP 2002534056-A/36
PD 15-OCT-2002
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19-DEC-1998 US 60/111715
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QY 1 GCTGGCC 7
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RESULT 290
BD238881
LOCUS
DEFINITION      Preparation and use of superior vaccines.
ACCESSION      BD238881
VERSION        BD238881.1 GI:33048651
KEYWORDS       JP 2002534056-A/299.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS         Roberts,B.L. and Shankara,S.
TITLE           Preparation and use of superior vaccines
JOURNAL         Patent: JP 2002534056-A 299 15-OCT-2002;
GENZYME CORP
COMMENT         OS Homo sapiens (human)
PN JP 2002534056-A/299
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
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19-DEC-1998 US 60/111715
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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QY 13 CGCTGTG 19
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RESULT 291
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239109.1 GI:33048879
VERSION JP 2002534056-A/527.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 527 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/527
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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QY 5 GCCCGGC 11
Db 4 GCCCGGC 10

RESULT 293
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239353
VERSION BD239353.1 GI:33049123
KEYWORDS JP 2002534056-A/771.

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCCCGGC 11
Db 4 GCCCGGC 10

RESULT 293
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LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239353
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KEYWORDS JP 2002534056-A/771.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 771 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/771
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
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QY 5 GCCCGGC 11
Db 1 GCCCGGC 7
RESULT 294
BD239760/c
LOCUS 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239760
VERSION BD239760.1 GI:33049530
KEYWORDS JP 2002534056-A/1178.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1178 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1178

PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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QY 9 GCCCGGC 15
Db 8 GCCCGGC 2
RESULT 295
BD240084/c
LOCUS 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240084
VERSION BD240084.1 GI:33049854
KEYWORDS JP 2002534056-A/1502.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1502 15-OCT-2002;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
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RESULT 301
BD249594/C
LOCUS 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Pi-ta gene imparting disease resistance to plants.
ACCESSION BD249594
VERSION BD249594.1 GI:33059364
KEYWORDS JP 2002525033-A/9.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Valent B.S. and Bryan,G.T.
TITLE Pi-ta gene imparting disease resistance to plants
JOURNAL Patent: JP 2002525033-A 9 13-AUG-2002;
EI DU PONT DE NEMOURS AND CO
COMMENT OS Artificial Sequence
PN JP 2002525033-A/9
PD 13-AUG-2002
PF 03-AUG-1999 JP 2000563786
PR 04-AUG-1998 US 60/095229,21-JUN-1999 US 09/336946 PI
BARBARA SUE VALENT,GREGORY T BRYAN
PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC
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PN JP 2002534056-A/2019
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGCTGT 18
Db 7 GCGCTGT 1

RESULT 302
BD251793
LOCUS 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Endo-selection in orthogenesis.
ACCESSION BD251793
VERSION BD251793.1 GI:33061563
KEYWORDS JP 2002537836-A/3.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Short,J.M. and Frey,G.J.
TITLE Endo-selection in orthogenesis
JOURNAL Patent: JP 2002537836-A 3 12-NOV-2002;
DIVERSA CORP
COMMENT OS Artificial Sequence
PN JP 2002537836-A/3
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603365
PR 09-MAR-1999 US 09/267118,26-MAR-1999 US 09/276860 PR
14-JUN-1999 US 09/332835
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QY 11 GCGCTGT 17
Db 1 GCGCTGT 7

RESULT 303
CS101365
LOCUS 10 bp DNA linear PAT 10-JUN-2005
DEFINITION Sequence 14 from Patent WO2005045021.
ACCESSION CS101365
VERSION CS101365.1 GI:67509811
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Desire,L.
TITLE Bace455, an alternative splice variant of the human beta-secretase
JOURNAL Patent: WO 2005045021-A 14 19-MAY-2005;
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Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
    |||||
DB 3 GCTGGCC 9

/note="primer"

RESULT 304
CS106787
LOCUS      CS106787
DEFINITION Sequence 5 from Patent WO2005042781.
ACCESSION  CS106787
VERSION     CS106787.1 GI:67513715
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Smith,D.R., Malek,J.A. and Mckernan,K.J.
TITLE      Methods for producing a paired tag from a nucleic acid sequence and
JOURNAL    Patent: WO 2005042781-A 5 12-MAY-2005;
           Agencourt Bioscience Corporation (US)
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="ASCII Linker - top strand"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCC 15
    |||||
DB 1 GCGCGCC 7

RESULT 305
CS106787/c
LOCUS      CS106787
DEFINITION Sequence 5 from Patent WO2005042781.
ACCESSION  CS106787
VERSION     CS106787.1 GI:67513715
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Smith,D.R., Malek,J.A. and Mckernan,K.J.
TITLE      Methods for producing a paired tag from a nucleic acid sequence and
JOURNAL    Patent: WO 2005042781-A 5 12-MAY-2005;
           Agencourt Bioscience Corporation (US)
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="ASCII Linker - top strand"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCC 15
    |||||
DB 1 GCGCGCC 7

RESULT 306
CS106788
LOCUS      CS106788
DEFINITION Sequence 6 from Patent WO2005042781.
ACCESSION  CS106788
VERSION     CS106788.1 GI:67513716
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Smith,D.R., Malek,J.A. and Mckernan,K.J.
TITLE      Methods for producing a paired tag from a nucleic acid sequence and
JOURNAL    Patent: WO 2005042781-A 6 12-MAY-2005;
           Agencourt Bioscience Corporation (US)
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="ASCII Linker - bottom strand"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCC 15
    |||||
DB 1 GCGCGCC 7

RESULT 307
CS106788/c
LOCUS      CS106788
DEFINITION Sequence 6 from Patent WO2005042781.
ACCESSION  CS106788
VERSION     CS106788.1 GI:67513716
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Smith,D.R., Malek,J.A. and Mckernan,K.J.
TITLE      Methods for producing a paired tag from a nucleic acid sequence and
JOURNAL    Patent: WO 2005042781-A 6 12-MAY-2005;
           Agencourt Bioscience Corporation (US)
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="ASCII Linker - bottom strand"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCC 15
    |||||
DB 8 GCGCGCC 2

RESULT 308
CS106787
LOCUS      CS106787
DEFINITION Cloning vector for mRNA-expressing pattern analysis, and
ACCESSION  ES9637
VERSION     ES9637
           ES9637.1 GI:13019440

```



```

Db          7 CCGCGGC 1
|||||||
RESULT 312
I79740/c
LOCUS      I79740          10 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 36 from patent US 5707863.
ACCESSION  I79740
VERSION     I79740.1 GI:3208030
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE     Tumor suppressor gene merlin
JOURNAL   Patent: US 5707863-A 36 13-JAN-1998;
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTGTGGC 21
|||||||
Db      10 CTGTGGC 4

RESULT 313
I86912/c
LOCUS      I86912          10 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 1 from patent US 5702931.
ACCESSION  I86912
VERSION     I86912.1 GI:3206630
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Andrews,W.H., Morser,M.J. and Vilander,L.R.
TITLE     Mutagenesis methods and compositions
JOURNAL   Patent: US 5702931-A 1 30-DEC-1997;
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTGTGGC 21
|||||||
Db      10 CTGTGGC 4

RESULT 314
AR202187
LOCUS      AR202187          10 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 6 from patent US 6361974.
ACCESSION  AR202187
VERSION     AR202187.1 GI:20256726
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Short,J.M., Djavakhishvili,T.David. and Frey,G.Johann.
TITLE     Exonuclease-mediated nucleic acid reassembly in directed evolution

JOURNAL   Patent: US 6361974-A 6 26-MAR-2002;
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CCGCGCTG 17
|||||||
Db      1 CCGCGCTG 7

RESULT 315
AR254267/c
LOCUS      AR254267          10 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 13 from patent US 6479731.
ACCESSION  AR254267
VERSION     AR254267.1 GI:27303040
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Valent,B.S. and Bryan,G.T.
TITLE     Pi-ta gene conferring fungal disease resistance to plants
JOURNAL   Patent: US 6479731-A 13 12-NOV-2002;
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GCGCTGT 18
|||||||
Db      7 GCGCTGT 1

RESULT 316
AR303347/c
LOCUS      AR303347          10 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 72 from patent US 6544736.
ACCESSION  AR303347
VERSION     AR303347.1 GI:31692123
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
          Watahiki,M.
TITLE     Method for synthesizing cDNA from mRNA sample
JOURNAL   Patent: US 6544736-A 72 08-APR-2003;
          Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.;
          Tokyo;
          JPX;
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 GCTGTGG 20
|||||||

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Db          10 GCTGTGG 4

RESULT 317
LOCUS      AR303679          10 bp      DNA          linear      PAT 12-JUN-2003
DEFINITION Sequence 404 from patent US 6544736.
ACCESSION  AR303679
VERSION     AR303679.1 GI:31692455
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Shinamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
TITLE       Method for synthesizing cDNA from mRNA sample
JOURNAL     Patent: US 6544736-A 404 08-APR-2003;
            Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.;
            Tokyo;
            JPX;

FEATURES   Location/Qualifiers
            source          1..10
                        /organism="unknown"
                        /mol_type="genomic DNA"

            Query Match    33.3%; Score 7; DB 1; Length 10;
            Best Local Similarity 100.0%; Pred. No. 1.5e+02;
            Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY         13 CGCTGTG 19
            |||||
            4 CGCTGTG 10

Db          AR306871          10 bp      DNA          linear      PAT 12-JUN-2003
LOCUS      AR306871/c
DEFINITION Sequence 23 from patent US 6551476.
ACCESSION  AR306871
VERSION     AR306871.1 GI:31697271
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Scherba,E.S.
TITLE       Noble-metal coated inert anode for aluminum production
JOURNAL     Patent: US 6551476-A 23 22-APR-2003;
            Location/Qualifiers
FEATURES   Location/Qualifiers
            source          1..10
                        /organism="unknown"
                        /mol_type="genomic DNA"

            Query Match    33.3%; Score 7; DB 1; Length 10;
            Best Local Similarity 100.0%; Pred. No. 1.5e+02;
            Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY         14 GCTGTGG 20
            |||||
            7 GCTGTGG 1

Db          AR336879/c
LOCUS      AR336879          10 bp      DNA          linear      PAT 17-AUG-2003
DEFINITION Sequence 54 from patent US 6566130.
ACCESSION  AR336879
VERSION     AR336879.1 GI:33722729
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.

            Query Match    33.3%; Score 7; DB 1; Length 10;
            Best Local Similarity 100.0%; Pred. No. 1.5e+02;
            Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY         14 GCTGTGG 20
            |||||
            7 GCTGTGG 1

Db          AR410161
LOCUS      AR410161          10 bp      DNA          linear      PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6635449.
ACCESSION  AR410161
VERSION     AR410161.1 GI:40161386
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Short,J.M.
TITLE       Exonuclease-mediated nucleic acid reassembly in directed evolution
JOURNAL     Patent: US 6635449-A 6 21-OCT-2003;
            Diversa Corporation; San Diego, CA

FEATURES   Location/Qualifiers
            source          1..10
                        /organism="unknown"
                        /mol_type="genomic DNA"

            Query Match    33.3%; Score 7; DB 1; Length 10;
            Best Local Similarity 100.0%; Pred. No. 1.5e+02;
            Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY         14 GCTGTGG 20
            |||||
            4 GCTGTGG 10

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REFERENCE   1 (bases 1 to 10)
AUTHORS     Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE       Androgen-regulated gene expressed in prostate tissue
JOURNAL     Patent: US 6566130-A 54 20-MAY-2003;
            Henry M. Jackson Foundation for the Advancement of Military
            Medicine; Rockville, MD

FEATURES   Location/Qualifiers
            source          1..10
                        /organism="unknown"
                        /mol_type="genomic DNA"

            Query Match    33.3%; Score 7; DB 1; Length 10;
            Best Local Similarity 100.0%; Pred. No. 1.5e+02;
            Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY         1 GCTGGCC 7
            |||||
            7 GCTGGCC 1

Db          AR351736
LOCUS      AR351736          10 bp      DNA          linear      PAT 17-AUG-2003
DEFINITION Sequence 1278 from patent US 6588746.
ACCESSION  AR351736
VERSION     AR351736.1 GI:33753532
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Dobrindt,D. and Fischer,U.
TITLE       Device for generating an offset of transported flexible sheet
            material
JOURNAL     Patent: US 6588746-A 1278 08-JUL-2003;
            NexPress Solutions LLC; Rochester, NY;
            DEX;

FEATURES   Location/Qualifiers
            source          1..10
                        /organism="unknown"
                        /mol_type="genomic DNA"

            Query Match    33.3%; Score 7; DB 1; Length 10;
            Best Local Similarity 100.0%; Pred. No. 1.5e+02;
            Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY         14 GCTGTGG 20
            |||||
            4 GCTGTGG 10

Db          AR410161
LOCUS      AR410161          10 bp      DNA          linear      PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6635449.
ACCESSION  AR410161
VERSION     AR410161.1 GI:40161386
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Short,J.M.
TITLE       Exonuclease-mediated nucleic acid reassembly in directed evolution
JOURNAL     Patent: US 6635449-A 6 21-OCT-2003;
            Diversa Corporation; San Diego, CA

FEATURES   Location/Qualifiers
            source          1..10
                        /organism="unknown"
                        /mol_type="genomic DNA"

            Query Match    33.3%; Score 7; DB 1; Length 10;
            Best Local Similarity 100.0%; Pred. No. 1.5e+02;
            Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY         14 GCTGTGG 20
            |||||
            4 GCTGTGG 10

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Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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QY	11	CGCGCTG 17							
Db	1	CGCGCTG 7							

RESULT 322									
AR477264									
LOCUS	AR477264	Sequence 5 from patent US 6696275.	10 bp	DNA	linear			PAT 14-MAY-2004	
DEFINITION	AR477264								
ACCESSION	AR477264								
VERSION	AR477264.1	GI:47234597							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 10)								
AUTHORS	Short, J.M. and Frey, G.J.								
TITLE	End selection in directed evolution								
JOURNAL	Patent: US 6696275-A 5 24-FEB-2004;								
FEATURES	Diversa Corporation; San Diego, CA								
source	Location/Qualifiers								
	1..10								
	/organism="unknown"								
	/mol_type="genomic DNA"								

Query Match	33.3%;	Score 7;	DB 1;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 1.5e+02;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	11	CGCGCTG 17							
Db	1	CGCGCTG 7							

RESULT 323									
AR489166									
LOCUS	AR489166	Sequence 6 from patent US 6709841.	10 bp	DNA	linear			PAT 15-MAY-2004	
DEFINITION	AR489166								
ACCESSION	AR489166								
VERSION	AR489166.1	GI:47256094							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 10)								
AUTHORS	Short, J.M.								
TITLE	Exonuclease-mediated gene assembly in directed evolution								
JOURNAL	Patent: US 6709841-A 6 23-MAR-2004;								
FEATURES	Diversa Corporation; San Diego, CA								
source	Location/Qualifiers								
	1..10								
	/organism="unknown"								
	/mol_type="genomic DNA"								

Query Match	33.3%;	Score 7;	DB 1;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 1.5e+02;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	11	CGCGCTG 17							
Db	1	CGCGCTG 7							

RESULT 324									
AR490750									
LOCUS	AR490750	Sequence 10 from patent US 6713279.	10 bp	DNA	linear			PAT 15-MAY-2004	
DEFINITION	AR490750								
ACCESSION	AR490750								
VERSION	AR490750.1	GI:47258162							
KEYWORDS									
SOURCE	Unknown.								

Query Match	33.3%;	Score 7;	DB 1;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 1.5e+02;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	11	CGCGCTG 17							
Db	1	CGCGCTG 7							

RESULT 325									
AR568611									
LOCUS	AR568611	Sequence 6 from patent US 6740506.	10 bp	DNA	linear			PAT 14-DEC-2004	
DEFINITION	AR568611								
ACCESSION	AR568611								
VERSION	AR568611.1	GI:56568059							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 10)								
AUTHORS	Short, J.M. and Frey, G.J.								
TITLE	End selection in directed evolution								
JOURNAL	Patent: US 6740506-A 6 25-MAY-2004;								
FEATURES	Diversa Corporation; San Diego, CA								
source	Location/Qualifiers								
	1..10								
	/organism="unknown"								
	/mol_type="genomic DNA"								

Query Match	33.3%;	Score 7;	DB 1;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 1.5e+02;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	11	CGCGCTG 17							
Db	1	CGCGCTG 7							

RESULT 326									
AR630143									
LOCUS	AR630143	Sequence 197 from patent US 6838556.	10 bp	DNA	linear			PAT 14-FEB-2005	
DEFINITION	AR630143								
ACCESSION	AR630143								
VERSION	AR630143.1	GI:59762465							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 10)								
AUTHORS	Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.E., Michelotti, E.F., Velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Kim, M.Y. and Bruice, R.W.								
TITLE	Promoters for regulated gene expression								
JOURNAL	Patent: US 6838556-A 197 04-JAN-2005;								
FEATURES	Genelabs Technologies, Inc.; Redwood City, CA								
source	Location/Qualifiers								
	1..10								
	/organism="unknown"								
	/mol_type="genomic DNA"								

Query Match	33.3%;	Score 7;	DB 1;	Length 10;
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Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCGCGCT 16
 Db 1 GCGCGCT 7

RESULT 327
 AR630149/c
 LOCUS Sequence 203 from patent US 6838556.
 DEFINITION AR630149
 ACCESSION AR630149
 VERSION AR630149.1 GI:59762477
 KEYWORDS
 SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 10)
 REFERENCE Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
 AUTHORS Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
 Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
 TITLE Promoters for regulated gene expression
 JOURNAL Patent: US 6838556-A 203 04-JAN-2005;
 Genelabs Technologies, Inc.; Redwood City, CA
 FEATURES
 Location/Qualifiers
 source
 1..10
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCGCGCT 16
 Db 10 GCGCGCT 4

RESULT 328
 AR642556/c
 LOCUS Sequence 29 from patent US 6864052.
 DEFINITION AR642556
 ACCESSION AR642556
 VERSION AR642556.1 GI:62779710
 KEYWORDS
 SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 10)
 REFERENCE Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
 AUTHORS Enhanced sequencing by hybridization using pools of probes
 TITLE Patent: US 6864052-A 29 08-MAR-2005;
 JOURNAL Callida Genomics, Inc.; Sunnyvale, CA
 FEATURES
 Location/Qualifiers
 source
 1..10
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
 Db 10 CTGTGGC 4

RESULT 329
 AR642557/c
 LOCUS Sequence 30 from patent US 6864052.
 DEFINITION AR642557
 ACCESSION

VERSION AR642557.1 GI:62779711
 KEYWORDS
 SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 10)
 REFERENCE Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
 AUTHORS Enhanced sequencing by hybridization using pools of probes
 TITLE Patent: US 6864052-A 30 08-MAR-2005;
 JOURNAL Callida Genomics, Inc.; Sunnyvale, CA
 FEATURES
 Location/Qualifiers
 source
 1..10
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
 Db 9 CTGTGGC 3

RESULT 330
 AR642558/c
 LOCUS Sequence 31 from patent US 6864052.
 DEFINITION AR642558
 ACCESSION AR642558
 VERSION AR642558.1 GI:62779712
 KEYWORDS
 SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 10)
 REFERENCE Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
 AUTHORS Enhanced sequencing by hybridization using pools of probes
 TITLE Patent: US 6864052-A 31 08-MAR-2005;
 JOURNAL Callida Genomics, Inc.; Sunnyvale, CA
 FEATURES
 Location/Qualifiers
 source
 1..10
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
 Db 8 CTGTGGC 2

RESULT 331
 AR642559/c
 LOCUS Sequence 32 from patent US 6864052.
 DEFINITION AR642559
 ACCESSION AR642559.1 GI:62779713
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 10)
 REFERENCE Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
 AUTHORS Enhanced sequencing by hybridization using pools of probes
 TITLE Patent: US 6864052-A 32 08-MAR-2005;
 JOURNAL Callida Genomics, Inc.; Sunnyvale, CA
 FEATURES
 Location/Qualifiers
 source
 1..10
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
 Db 8 CTGTGGC 2

RESULT 331
 AR642559/c
 LOCUS Sequence 32 from patent US 6864052.
 DEFINITION AR642559
 ACCESSION AR642559.1 GI:62779713
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 10)
 REFERENCE Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
 AUTHORS Enhanced sequencing by hybridization using pools of probes
 TITLE Patent: US 6864052-A 32 08-MAR-2005;
 JOURNAL Callida Genomics, Inc.; Sunnyvale, CA
 FEATURES
 Location/Qualifiers
 source
 1..10
 /organism="unknown"
 /mol_type="genomic DNA"


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Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
Db      |||||
7 CTGTGGC 1

RESULT 332
AX009254
LOCUS      AX009254      10 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 10 from Patent EP0965642.
ACCESSION  AX009254
VERSION     AX009254.1 GI:9996585
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Goppelt,A.D., Halle,J.P. and Regenbogen,J.D.
TITLE      Cloning vector, its production and use for the analysis of mrna
JOURNAL    Patent: EP 0965642-A 10 22-DEC-1999;
           SWITCH BIOTECH GMBH (DE)
FEATURES   Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
Db      |||||
2 GCGCGGC 8

RESULT 333
AX009254/c
LOCUS      AX009254      10 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 10 from Patent EP0965642.
ACCESSION  AX009254
VERSION     AX009254.1 GI:9996585
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Goppelt,A.D., Halle,J.P. and Regenbogen,J.D.
TITLE      Cloning vector, its production and use for the analysis of mrna
JOURNAL    Patent: EP 0965642-A 10 22-DEC-1999;
           SWITCH BIOTECH GMBH (DE)
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
Db      |||||
2 GCGCGGC 8

RESULT 334
AX147040
LOCUS      AX147040      10 bp      DNA      linear      PAT 08-JUN-2001
DEFINITION Sequence 1 from Patent WO0136482.
ACCESSION  AX147040
VERSION     AX147040.1 GI:14346308
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Enikolopov,G.N. and Mignone,J.
TITLE      Transgenic mice expressing fluorescent protein under the control of
           the nestin promoter
JOURNAL    Patent: WO 0136482-A 1 25-MAY-2001;
           COLD SPRING HARBOR LABORATORY (US)
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic Linker"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
Db      |||||
2 GCGCGGC 8

RESULT 335
AX147040/c
LOCUS      AX147040      10 bp      DNA      linear      PAT 08-JUN-2001
DEFINITION Sequence 1 from Patent WO0136482.
ACCESSION  AX147040
VERSION     AX147040.1 GI:14346308
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Enikolopov,G.N. and Mignone,J.
TITLE      Transgenic mice expressing fluorescent protein under the control of
           the nestin promoter
JOURNAL    Patent: WO 0136482-A 1 25-MAY-2001;
           COLD SPRING HARBOR LABORATORY (US)
FEATURES   Location/Qualifiers
            source
              1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic Linker"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
Db      |||||
2 GCGCGGC 3

RESULT 336
AX152322
LOCUS      AX152322      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 237 from Patent WO0138577.
ACCESSION  AX152322
VERSION     AX152322.1 GI:14533973
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```

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REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 237 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
Db 7 GCTGGCC 1

RESULT 337
AX152346/c
LOCUS AX152346 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 261 from Patent WO0138577.
ACCESSION AX152346
VERSION AX152346.1 GI:14533997
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 261 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCGGGCC 13
Db 10 CCGGGCC 4

RESULT 338
AX152392/c
LOCUS AX152392 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 307 from Patent WO0138577.
ACCESSION AX152392
VERSION AX152392.1 GI:14534043
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 307 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCGGGCC 13
Db 10 CCGGGCC 4

RESULT 339
AX152393/c
LOCUS AX152393 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 308 from Patent WO0138577.
ACCESSION AX152393
VERSION AX152393.1 GI:14534044
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 308 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
Db 7 GCTGGCC 1

RESULT 340
AX152609
LOCUS AX152609 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 524 from Patent WO0138577.
ACCESSION AX152609
VERSION AX152609.1 GI:14534260
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 524 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
Db 7 GCTGGCC 1

RESULT 341
AX152609
LOCUS AX152609 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 524 from Patent WO0138577.
ACCESSION AX152609
VERSION AX152609.1 GI:14534260
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 524 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
Db 15 CTGTGGC 21

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Db 4 CTGTGGC 10

RESULT 341
AX152706/c
LOCUS
DEFINITION Sequence 621 from Patent WO0138577.
ACCESSION AX152706
VERSION AX152706.1 GI:14534357
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 1071 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 4 GCTGGCC 10

RESULT 344
AX153227
LOCUS
DEFINITION Sequence 1142 from Patent WO0138577.
ACCESSION AX153227
VERSION AX153227.1 GI:14534878
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 1142 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
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1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGCGC 13
Db 3 CCGGCGC 9

RESULT 345
AX153234
LOCUS
DEFINITION Sequence 1149 from Patent WO0138577.
ACCESSION AX153234
VERSION AX153234.1 GI:14534885
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 1149 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCCCGG 10
Db 7 GGCCCGG 1

RESULT 343
AX153156
LOCUS
DEFINITION Sequence 1071 from Patent WO0138577.
ACCESSION AX153156
VERSION AX153156.1 GI:14534807
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JOURNAL Patent: WO 0138577-A 1149 31-MAY-2001;
FEATURES   The Johns Hopkins University (US)
source     Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCCCGC 11
Db 4 GCCCGC 10

RESULT 346
AX302590
LOCUS AX302590 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 108 from Patent WO0175177.
ACCESSION AX302590
VERSION AX302590.1 GI:17383117
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patent: WO 0175177-A 108 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CGCGCTG 17
Db 3 CGCGCTG 9

RESULT 347
AX391509
LOCUS AX391509 10 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 3 from Patent EP1184462.
ACCESSION AX391509
VERSION AX391509.1 GI:19700117
KEYWORDS Staphylococcus aureus
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
REFERENCE 1
AUTHORS Fan,F.G., He,Y.G., Huang,J.G., Jiang,X.G., Mcdevitt,D.G.,
Rosenberg,M.G. and St John,A.G.
TITLE Identification of targets of antimicrobial compounds
JOURNAL Patent: EP 1184462-A 3 06-MAR-2002;
SmithKline Beecham Corporation (US) ; SMITHKLINE BEECHAM PLC (GB)
FEATURES
source
1. .10
/organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCGCGC 15
Db 3 GCGCGC 9

RESULT 348
AX391509/c
LOCUS AX391509 10 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 3 from Patent EP1184462.
ACCESSION AX391509
VERSION AX391509.1 GI:19700117
KEYWORDS Staphylococcus aureus
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
REFERENCE 1
AUTHORS Fan,F.G., He,Y.G., Huang,J.G., Jiang,X.G., Mcdevitt,D.G.,
Rosenberg,M.G. and St John,A.G.
TITLE Identification of targets of antimicrobial compounds
JOURNAL Patent: EP 1184462-A 3 06-MAR-2002;
SmithKline Beecham Corporation (US) ; SMITHKLINE BEECHAM PLC (GB)
FEATURES
source
1. .10
/organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCGCGC 15
Db 3 GCGCGC 9

RESULT 350
AX391511/c
LOCUS AX391511 10 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 5 from Patent EP1184462.

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ACCESSION      AX391511
VERSION        AX391511.1  GI:19700119
KEYWORDS
SOURCE
ORGANISM       Staphylococcus aureus
REFERENCE      Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS       Fan, F.G., He, Y.G., Huang, J.G., Jiang, X.G., Medevitt, D.G.,
              Rosenberg, M.G. and St John, A.G.
TITLE         Identification of targets of antimicrobial compounds
JOURNAL       Patent: EP 1184462-A 5 06-MAR-2002;
              SmithKline Beecham Corporation (US) ; SMITHKLINE BEECHAM PLC (GB)
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source
1. .10
   /organism="Staphylococcus aureus"
   /mol_type="unassigned DNA"
   /db_xref="taxon:1280"
Query Match   33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9  GCGCGCG 15
    |||||
Db   10 GCGCGCG 4

RESULT 351
AX667829
LOCUS         AX667829
DEFINITION   Sequence 1278 from Patent WO0242459.
ACCESSION    AX667829
VERSION      AX667829.1  GI:29291366
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Liu, Q.
TITLE        Position dependent recognition of gnn nucleotide triplets by zinc
              fingers
JOURNAL      Patent: WO 0242459-A 1278 30-MAY-2002;
              Sangamo Biosciences Inc. (US)
FEATURES
source
1. .10
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="example target DNA"
Query Match   33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  14 GCTGTGG 20
    |||||
Db   4  GCTGTGG 10

RESULT 352
AX753482/c
LOCUS         AX753482
DEFINITION   Sequence 27 from Patent EP1310556.
ACCESSION    AX753482
VERSION      AX753482.1  GI:32166242
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Beaudry, G.A., Madden, S.L. and Bertelsen, A.H.
TITLE        Composition and methods for the identification of lung tumor cells
JOURNAL      Patent: EP 1310556-A 27 14-MAY-2003;

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GENZYME CORPORATION (US)
Location/Qualifiers
1. .10
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
Query Match   33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15 CTGTGGC 21
    |||||
Db   9  CTGTGGC 3

RESULT 353
AX958222
LOCUS         AX958222
DEFINITION   Sequence 25 from Patent WO03046156.
ACCESSION    AX958222
VERSION      AX958222.1  GI:40785875
KEYWORDS     unidentified
SOURCE       unidentified
ORGANISM     unclassified sequences.
REFERENCE    1
AUTHORS      Claude, P.P.
TITLE        Novel bacterial biomasses, method for obtaining same and uses
              thereof for bacterization of soils and crop residues
JOURNAL      Patent: WO 03046156-A 25 05-JUN-2003;
              Valbios (FR)
FEATURES
source
1. .10
   /organism="unidentified"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32644"
   /note="Azobacter"
Query Match   33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches       7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8  CGCGCGC 14
    |||||
Db   3  CGCGCGC 9

RESULT 354
BD007778
LOCUS         BD007778
DEFINITION   LPS activated human monocyte expressing genes.
ACCESSION    BD007778
VERSION      BD007778.1  GI:18636151
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominiidae; Homo.
              1 (bases 1 to 10)
REFERENCE    1
AUTHORS      Matsushima, K., Hashimoto, S. and Suzuki, T.
TITLE        LPS activated human monocyte expressing genes
JOURNAL      Patent: JP 2001069993-A 54 21-MAR-2001;
              JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT      OS Homo sapiens (human)
              PN JP 2001069993-A/54
              PD 21-MAR-2001
              PF 28-APR-2000  JP 2000131079
              PR
              PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI
              C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
              A61P29/00,

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PC A61P31/00,C12P21/08,C12N15/00
CC Key Location/Qualifiers
FH source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
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        1..10
            Location/Qualifiers
            /organism='Homo sapiens'
            /mol_type='genomic DNA'
            /db_xref='taxon:9606'

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
    |||||
Db 2 CTGTGGC 8

RESULT 355
BD007922/c
LOCUS BD007922 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007922
VERSION BD007922.1 GI:18636295
KEYWORDS JP 2001069993-A/198.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 198 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/198
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 CTGGCCC 1

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DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007966
VERSION BD007966.1 GI:18636339
KEYWORDS JP 2001069993-A/242.
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 242 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/242
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: May 10, 2006, 10:44:15
Job time : 0.001 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:47:25 ; Search time 0.001 Seconds
(without alignments)
88.242 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336

Perfect score: 21

Sequence: 1 gctgcccgcgcgtgtggc 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 194 seqs, 2101 residues

Total number of hits satisfying chosen parameters: 388

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 221 summaries

Database : pubmaindb1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	12.8	61.0	17	1	US-10-430-882-739
C 5	12.4	59.0	17	1	US-09-827-395A-442
C 6	12.4	59.0	17	1	US-09-827-395A-443
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C 11	12.2	58.1	17	1	US-09-745-237A-389
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Published - Applications - NFA - Main

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RESULT 1

US-09-923-517-40/c

; Sequence 40, Application US/09923517

; Publication No. US20020039741A1

; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.

; Miraglias, Brenda F. Baker

; TITLE OF INVENTION: Antisense Oligonucleotide

; Compositions and Methods for the Modulation of

; Activating Protein 1

; NUMBER OF SEQUENCES: 139

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Jane Massey Licata

; STREET: 66 East Main Street

; CITY: Marlton

; STATE: NJ

; COUNTRY: USA

; ZIP: 08053

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: WINDOWS 95

; SOFTWARE: WORDPERFECT 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/923,517

; FILING DATE: 07-Aug-2001


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; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
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; Sequence 739, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 739
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-739

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DB      17  TTGCCCGCGCGCTGT 2

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; Sequence 739, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03

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; NUMBER OF SEQ ID NOS: 2617
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; SEQ ID NO 739
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-739
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; Sequence 442, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
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US-09-827-395A-443/c
; Sequence 443, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 443
; LENGTH: 17
; TYPE: RNA
```

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; ORGANISM: Homo sapiens
US-09-827-395A-443
```

```
Query Match          59.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 17;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 GCCCGCGCGCTGT 18
    |||||
Db 16 GCCCGCGGGCTGT 3
```

RESULT 7

```
US-10-430-882-442/c
; Sequence 442, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 442
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-442
```

```
Query Match          59.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 17;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 GCCCGCGCGCTGT 18
    |||||
Db 17 GCCCGCGGGCTGT 4
```

RESULT 8

```
US-10-430-882-443/c
; Sequence 443, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
```

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; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 443
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-443

Query Match      59.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 17;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  5 GCCCGCGCGCTGT 18
Db  16 GCCCGCGCGCTGT 3

RESULT 9
US-09-895-040A-61
; Sequence 61, Application US/09895040A
; Patent No. US20020123474A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Ji, Yonggang
; TITLE OF INVENTION: HUMAN GTP-RHO BINDING PROTEIN 2
; FILE REFERENCE: AROMICA-11
; CURRENT APPLICATION NUMBER: US/09/895,040A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 61
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-040A-61

Query Match      58.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  5 GCCCGCGCGCTGTGC 21
Db  1 GACCGACGCGCTGTGC 17

RESULT 10
US-09-930-423-389
; Sequence 389, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 389
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-930-423-389

Query Match      58.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 20;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  1 GCTGGCCCGCGCGCTG 17
Db  1 GCUGGCCAGGGCCUG 17

RESULT 11
US-09-745-237A-389
; Sequence 389, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 389
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-389

Query Match      58.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 20;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  1 GCTGGCCCGCGCGCTG 17
Db  1 GCUGGCCAGGGCCUG 17

RESULT 12
US-10-402-099-14
; Sequence 14, Application US/10402099
; Publication No. US20030220287A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, M. Ian
; APPLICANT: Mohuczy, Dagmara
; TITLE OF INVENTION: Antisense Nucleic Acids
; FILE REFERENCE: 5853-235
; CURRENT APPLICATION NUMBER: US/10/402,099
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-402-099-14

Query Match      49.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 33;

```

```
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGCGC 13
Db 3 CTGGCCCGCGC 14

RESULT 13
US-10-666-205-43
; Sequence 43, Application US/10666205
; Publication No. US20040157305A1
; GENERAL INFORMATION:
; APPLICANT: Stampfer, Wolfgang
; APPLICANT: Kosjek, Birgit
; APPLICANT: Kroutil, Wolfgang
; APPLICANT: Faber, Kurt
; APPLICANT: Niehaus, Frank
; APPLICANT: Eck, Juergen
; TITLE OF INVENTION: Alcohol dehydrogenases with increased solvent and temperature sta
; FILE REFERENCE: HL/95-22634/Cip
; CURRENT APPLICATION NUMBER: US/10/666,205
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/EP03/02439
; PRIOR FILING DATE: March 10, 2003
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence used as potential probe for identifying Rhodococcus ruber
; OTHER INFORMATION: r DSM 14855 alcohol dehydrogenase A gene
US-10-666-205-43

Query Match 46.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 50;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGCGC 13
Db 1 GCGCCCGCGCGC 13

RESULT 14
US-09-990-762-97/c
; Sequence 97, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: nucleotide sequence
US-09-990-762-97

Query Match 44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 38;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 15
Db 11 GCCCAGCGCGC 1

RESULT 15
US-10-257-017B-290182
; Sequence 290182, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290182
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014238
US-10-257-017B-290182

Query Match 44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 38;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
Db 1 GCGCGCGTGTG 11

RESULT 16
US-10-257-017B-304177
; Sequence 304177, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 304177
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020811
US-10-257-017B-304177

Query Match 44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 38;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCGCGCTGTG 19
Db 1 GCGCGTGTG 11
```

RESULT 17

US-10-257-017B-321157/c
 ; Sequence 321157, Application US/10257017B
 ; Publication No. US20040241651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
 ; FILE OF INVENTION: methylations
 ; FILE REFERENCE: E01/1193/WO
 ; CURRENT APPLICATION NUMBER: US/10/257,017B
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 382046
 ; SEQ ID NO 321157
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030082
 US-10-257-017B-321157

Query Match 44.8%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 38;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGCGCGCTGTG 19
 |||||
 Db 12 GGCGCGATGTG 2

RESULT 18

US-10-915-233-97/c
 ; Sequence 97, Application US/10915233
 ; Publication No. US2005008477A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOUNG, J. KEITH
 ; APPLICANT: MILLER, JEFFREY
 ; APPLICANT: PABO, CARL O.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
 ; FILE REFERENCE: MTV-030.02 (20021-3002)
 ; CURRENT APPLICATION NUMBER: US/10/915,233
 ; CURRENT FILING DATE: 2004-08-10
 ; PRIOR APPLICATION NUMBER: US/09/990,762
 ; PRIOR FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 09/858,852
 ; PRIOR FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: 60/204,509
 ; PRIOR FILING DATE: 2000-05-16
 ; NUMBER OF SEQ ID NOS: 97
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 97
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
 US-10-915-233-97

Query Match 44.8%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 38;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 15
 |||||
 Db 11 GCCCAGCGCGC 1

RESULT 19

US-09-825-805-161

; Sequence 161, Application US/09825805
 ; Publication No. US20030004122A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Beigelman, Leo
 ; APPLICANT: Beaudry, Amber
 ; APPLICANT: Karpeisky, Alex
 ; APPLICANT: Adamic, Jasenka Matulic
 ; APPLICANT: Sweedler, Dave
 ; APPLICANT: Zinnen, Shawn
 ; TITLE OF INVENTION: Nucleotide Triphosphate and their incorporation into Oligonucleo
 ; FILE REFERENCE: MEH800-831-F (400/009)
 ; CURRENT APPLICATION NUMBER: US/09/825,805
 ; CURRENT FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: 09/578,223
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 09/476,387
 ; PRIOR FILING DATE: 1999-12-30
 ; PRIOR APPLICATION NUMBER: 09/474,432
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: 09/301,511
 ; PRIOR FILING DATE: 1999-04-28
 ; PRIOR APPLICATION NUMBER: 09/186,675
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR APPLICATION NUMBER: 60/083,727
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/064,866
 ; PRIOR FILING DATE: 1997-11-05
 ; NUMBER OF SEQ ID NOS: 1558
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 161
 ; LENGTH: 13
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-825-805-161

Query Match 44.8%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 81.8%; Pred. No. 50;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCGGC 11
 ||:||||
 Db 3 GCGGCGCUGC 13

RESULT 20

US-10-257-017B-66113/c
 ; Sequence 66113, Application US/10257017B
 ; Publication No. US20040241651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
 ; FILE OF INVENTION: methylations
 ; FILE REFERENCE: E01/1193/WO
 ; CURRENT APPLICATION NUMBER: US/10/257,017B
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 382046
 ; SEQ ID NO 66113
 ; LENGTH: 13
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017381
 US-10-257-017B-66113

Query Match 44.8%; Score 9.4; DB 1; Length 13;
 Best Local Similarity 90.9%; Pred. No. 50;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY      6 CCGCGCGCGCT 16
Db      12 CCGAGCGCGCT 2

RESULT 21
US-10-257-017B-66114
; Sequence 66114, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 66114
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017381
US-10-257-017B-66114

Query Match      44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 50;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCGCGCGCGCT 16
Db      2 CCGAGCGCGCT 12

RESULT 22
US-10-033-145-250/c
; Sequence 250, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 250
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-250

Query Match      42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCGCGCGCTG 17
Db      9 GCGCGCGCTG 1

RESULT 23
US-10-330-627-903/c
; Sequence 903, Application US/10330627
; Publication No. US20030175771A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 903
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-903

Query Match      42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCGCGCGCTG 17
Db      9 GCGCGCGCTG 1

RESULT 24
US-10-330-627-1410
; Sequence 1410, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1410
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1410

Query Match      42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTGGCCCGG 10
Db      1 CTGGCCCGG 9

RESULT 25
US-10-330-627-1411
; Sequence 1411, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1411
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1411

Query Match      42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 CTGGCCCGG 10
    |||||
Db   1 CTGGCCCGG 9

RESULT 26
US-10-978-283-13
; Sequence 13, Application US/10978283
; Publication No. US20050239734A1
; GENERAL INFORMATION:
; APPLICANT: Uhlmann, Eugen
; APPLICANT: Vollmer, Jorg
; APPLICANT: Krieg, Arthur M
; APPLICANT: Noll, Bernhard O
; TITLE OF INVENTION: C-CLASS OLIGONUCLEOTIDE ANALOGS WITH ENHANCED IMMUNOSTIMULATORY
; FILE REFERENCE: C1041.70034US01
; CURRENT APPLICATION NUMBER: US/10/978,283
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/516,913
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-978-283-13

Query Match      42.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 GCGCGCTG 17
    |||||
Db   1 GCGCGCTG 9

RESULT 27
US-10-053-526A-9/c
; Sequence 9, Application US/10053526A
; Publication No. US20030003547A1
; GENERAL INFORMATION:
; APPLICANT: INSTITUT CURIE; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (C.N.R.S.);
; APPLICANT: MUSEUM NATIONAL D'HISTOIRE NATURELLE; INSTITUT NATIONAL DE LA SANTE ET DE
; APPLICANT: RECHERCHE MEDICALE (INSERM)
; APPLICANT: Dutreix, Marie
; APPLICANT: Sun, Jian-Sheng
; APPLICANT: Biet, Elodie
; APPLICANT: Maurisse, Rosalie
; APPLICANT: Feugas, Jean-Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EFFECTING HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 3754/0K213
; CURRENT APPLICATION NUMBER: US/10/053,526A
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/IB01/00749
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: EP 00401218.3
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 11
```

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-053-526A-9

Query Match      41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 GCTGGCCCGCG 12
    |||||
Db   12 GCTGGCCCGCG 1

RESULT 28
US-10-836-670-14/c
; Sequence 14, Application US/10836670
; Publication No. US20040235031A1
; GENERAL INFORMATION:
; APPLICANT: Schultz, Gregory Scott
; APPLICANT: Lewin, Alfred Samuel
; APPLICANT: Blalock, Timothy D.
; TITLE OF INVENTION: ANTI-SCARRING RIBOZYMES AND METHODS
; FILE REFERENCE: 5853-303
; CURRENT APPLICATION NUMBER: US/10/836,670
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Human adenovirus type 1
US-10-836-670-14

Query Match      41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5 GCCCGCGCGCT 16
    |||||
Db   12 GCTGGAGCGCT 1

RESULT 29
US-10-033-145-39/c
; Sequence 39, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-39

Query Match      40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GCTGGCCCG 10
    |||||
Db 10 GCTGGCCCG 1

RESULT 30
US-10-140-763A-6/c
; Sequence 6, Application US/10140763A
; Publication No. US20030104420A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Methods and Compositions for Modulating
; FILE REFERENCE: SIER-012
; CURRENT APPLICATION NUMBER: US/10/140,763A
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/289,641
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-140-763A-6

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 10
    |||||
Db 10 GCTGGCCCG 1

RESULT 31
US-10-330-627-718
; Sequence 718, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 718
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-718

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGTG 19
    |||||
Db 1 GCGCGCTGTG 10

RESULT 32
US-10-091-281-362
; Sequence 362, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 362
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative EBOX/MYCMAX.03 motif
US-10-091-281-362

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 14
    |||||
Db 1 GCCAGCGCGC 10

RESULT 33
US-10-356-792-20/c
; Sequence 20, Application US/10356792
; Publication No. US20030215842A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej
; APPLICANT: Schweikhardt, Gary
; TITLE OF INVENTION: METHOD FOR THE ANALYSIS OF CYTOSINE METHYLATION PATTERNS
; FILE REFERENCE: 47675-33
; CURRENT APPLICATION NUMBER: US/10/356,792
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 60/352,944
; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: AP-PCR Primer CG4
US-10-356-792-20

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCGCGCGCGC 15
    |||||
Db 10 CCGCGCGCGC 1

RESULT 34
US-10-293-222-326
; Sequence 326, Application US/10293222
; Publication No. US2004003392A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
```



```
; PRIOR APPLICATION NUMBER: EP 0020284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 326
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-326

Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGTGTG 19
   |||||
Db 1 GCGCGTGTG 10

RESULT 35
US-10-418-414-4/c
; Sequence 4, Application US/10418414
; Publication No. US20040072202A1
; GENERAL INFORMATION:
; APPLICANT: McGall, Glenn Hugh
; Miyada, Charles Garrett
; Cronin, Maureen T.
; Tan, Jennifer Dee
; Chee, Mark
; TITLE OF INVENTION: Modified Nucleic Acid Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/418,414
; FILING DATE: 22-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/608,691
; FILING DATE: 29-Jun-2000
; APPLICATION NUMBER: US/08/630,427
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/440,742
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: WO PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 16528X-012510
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; PRIOR APPLICATION NUMBER: EP 0020284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 326
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-326

Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGTGTG 19
   |||||
Db 1 GCGCGTGTG 10

RESULT 36
US-10-816-079-20
; Sequence 20, Application US/10816079
; Publication No. US20040166527A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Beaudry, Gary A
; APPLICANT: Madden, Stephen L
; APPLICANT: Bertelsen, Arthur H
; TITLE OF INVENTION: Composition and Methods for the Identification of Lung Tumor
; TITLE OF INVENTION: Cells
; FILE REFERENCE: GA0129C2
; CURRENT APPLICATION NUMBER: US/10/816,079
; PRIOR FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: 09/663,516
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/080,037
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SAGE tag
US-10-816-079-20

Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCGCGCG 12
   |||||
Db 1 TGGCCGCGCG 10

RESULT 37
US-10-713-381-11/c
; Sequence 11, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
```

US-10-713-381-11

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
| | | | | | | |
Db 10 CGGGCCCGGC 1

RESULT 38

US-10-713-381-14
; Sequence 14, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-14

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
| | | | | | | |
Db 1 CGGGCCCGGC 10

RESULT 39

US-10-487-934-245
; Sequence 245, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-245

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCGG 10
| | | | | | | |
Db 1 GCTGGCCCGG 10

RESULT 40

US-10-487-934-266
; Sequence 266, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 266
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-266

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGTG 19
| | | | | | | | | |
Db 1 GCGCGCTGTG 10

RESULT 41

US-10-602-494-359/c
; Sequence 359, Application US/10602494
; Publication No. US20040265833A1
; GENERAL INFORMATION:
; APPLICANT: Cathy Lofton-Day
; APPLICANT: Andrew Sledziewski
; APPLICANT: Jeff Thomas
; APPLICANT: Robert W. Day
; APPLICANT: Lori Tonnes-Priddy
; APPLICANT: Karen Cardon
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of colorectal cell
; FILE REFERENCE: 47675-45
; CURRENT APPLICATION NUMBER: US/10/602,494
; CURRENT FILING DATE: 2003-06-23
; NUMBER OF SEQ ID NOS: 385
; SEQ ID NO 359
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-602-494-359

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCGGCGCGGC 15
| | | | | | | | | |
Db 10 CGGCGCGGC 1

RESULT 42

```
US-10-055-728-11
; Sequence 11, Application US/10055728
; Publication No. US20030170720A1
; GENERAL INFORMATION:
; APPLICANT: van der Kuyl, Antoinette C.
; TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
; FILE REFERENCE: 5244US (REN/P55190US00)
; CURRENT APPLICATION NUMBER: US/10/055,728
; CURRENT FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 0120373.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TAG sequence Hs183
US-10-055-728-11

Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 CTGGCCCGGC 11
    |||||
DB 2 CTGGCCCGGC 11

RESULT 43
US-10-310-677-11
; Sequence 11, Application US/10310677
; Publication No. US20030219772A1
; GENERAL INFORMATION:
; APPLICANT: Kuyl v.d., Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: Means and methods for treatment evaluation
; FILE REFERENCE: P55190US10
; CURRENT APPLICATION NUMBER: US/10/310,677
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: EP 01203703.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/325,722
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TAG sequence
; OTHER INFORMATION: Hs183
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(11)
US-10-310-677-11

Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 CTGGCCCGGC 11
    |||||
DB 2 CTGGCCCGGC 11

US-10-450-797-217/c
; Sequence 217, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-217

Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GCTGGCCCGG 10
    |||||
DB 10 GCTGGCCCGG 1

RESULT 44
US-10-450-797-440
; Sequence 440, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 440
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-440

Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 CTGGCCCGGC 11
    |||||
DB 2 CTGGCCCGGC 11

RESULT 45
US-10-450-797-1314/c
; Sequence 1314, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 440
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1314/c

Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 CTGGCCCGGC 11
    |||||
DB 2 CTGGCCCGGC 11

RESULT 46
US-10-450-797-1314/c
; Sequence 1314, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1314
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1314

Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      5  GCCCGCGCGG 14
        |||||
Db      11  GCCCGCGGG  2

RESULT 47
US-09-990-762-97
; Sequence 97, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: nucleotide sequence
US-09-990-762-97

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      10  GCGCGCTGTG 19
        |||||
Db      11  GCGCGCTGG 10

RESULT 48
US-10-915-233-97
; Sequence 97, Application US/10915233
; Publication No. US20050064477A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
```

```
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/10/915,233
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US/09/990,762
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: nucleotide sequence
US-10-915-233-97

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      10  GCGCGCTGTG 19
        |||||
Db      11  GCGCGCTGG 10

RESULT 49
US-09-263-959-437/c
; Sequence 437, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 437:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-437

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
```

Qy 2 CTGGCCCGGC 11
 Db 11 CTGGCTGGC 2

RESULT 50

US-09-949-041A-50/c
 ; Sequence 50, Application US/09949041A
 ; Publication No. US20030104387A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yang, Meng
 ; APPLICANT: Woo, Hok
 ; TITLE OF INVENTION: Mutation Detection of RNA Polymerase Beta Subunit Gene Having Rf
 ; FILE REFERENCE: Resistance
 ; CURRENT APPLICATION NUMBER: US/09/949,041A
 ; CURRENT FILING DATE: 2001-09-07
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 50
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR primer
 US-09-949-041A-50

Query Match 40.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 73;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GCGCTGTGGC 21
 Db 11 GCGCTGGGC 2

RESULT 51

US-10-403-232-144/c
 ; Sequence 144, Application US/10403232
 ; Publication No. US20030226164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Suttie, Janet Louise
 ; APPLICANT: Chilton, Mary-Bell
 ; APPLICANT: Que, Qiudeng
 ; APPLICANT: de Framond, Anic
 ; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
 ; FILE REFERENCE: 700050USPS
 ; CURRENT APPLICATION NUMBER: US/10/403,232
 ; CURRENT FILING DATE: 2003-03-28
 ; NUMBER OF SEQ ID NOS: 185
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 144
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide
 US-10-403-232-144

Query Match 40.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 73;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCGCGCTGT 18
 Db 12 GCGCGCGCGT 3

RESULT 52

US-10-257-017B-284862/c
 ; Sequence 284862, Application US/10257017B
 ; Publication No. US20040241651A1

; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
 ; FILE REFERENCE: E01/1193/WO
 ; CURRENT APPLICATION NUMBER: US/10/257,017B
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 382046
 ; SEQ ID NO 284862
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012030
 US-10-257-017B-284862

Query Match 40.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 73;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GCGCTGTGGC 21
 Db 11 GCGCGGTGGC 2

RESULT 53

US-10-257-017B-322854/c
 ; Sequence 322854, Application US/10257017B
 ; Publication No. US20040241651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
 ; FILE REFERENCE: E01/1193/WO
 ; CURRENT APPLICATION NUMBER: US/10/257,017B
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 382046
 ; SEQ ID NO 322854
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
 US-10-257-017B-322854

Query Match 40.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 73;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGCGCGCG 14
 Db 10 GCGCGCGCG 1

RESULT 54

US-10-257-017B-322859/c
 ; Sequence 322859, Application US/10257017B
 ; Publication No. US20040241651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; APPLICANT: Christian Piepenbrock
 ; APPLICANT: Kurt Berlin
 ; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
 ; FILE REFERENCE: E01/1193/WO

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322859
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322859

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 14
Db 10 GCCCGCGCGC 1

RESULT 55
US-10-257-017B-359284/c
; Sequence 359284, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359284
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008283
US-10-257-017B-359284

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 CGCGCTGTGG 20
Db 12 CGCGTTGTGG 3

RESULT 56
US-10-257-017B-376667/c
; Sequence 376667, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 376667
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007696
US-10-257-017B-376667

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGTG 19
Db 10 GCGCGATGTG 1

RESULT 57
US-10-732-620-110/c
; Sequence 110, Application US/10732620
; Publication No. US20050032186A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Shin, Hyun-Sun
; APPLICANT: Kwon, Heung-Sun
; TITLE OF INVENTION: REGULATORY ZINC FINGER PROTEINS
; FILE REFERENCE: 12279-009001
; CURRENT APPLICATION NUMBER: US/10/732,620
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: US 60/431,892
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-732-620-110

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCGCGCGCGC 15
Db 12 CCGCGCCCGC 3

RESULT 58
US-10-033-145-273
; Sequence 273, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-033-145-273

Query Match          38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTGG 20
```

```
Db      1  CGCTGTGG 8
|||||||
RESULT 59
US-10-033-145-1876/c
; Sequence 1876, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1876
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1876

Query Match      38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 51;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTGGCCC 8
|||||||
RESULT 60
US-10-713-381-17/c
; Sequence 17, Application US/10713381
; Publication No. US2004022131A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-17

Query Match      38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 51;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4  GGCCCGGC 11
|||||||
RESULT 61
US-10-487-934-173
; Sequence 173, Application US/10487934
; Publication No. US2004026582A1

Db      9  GGCCCGGC 2
|||||||
RESULT 62
US-09-984-292-42/c
; Sequence 42, Application US/09984292
; Patent No. US2002012843A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-09-984-292-42

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8  CGCGCGGC 15
|||||||
Db      9  CGCGCGGC 2
|||||||
RESULT 63
US-09-989-497-42/c
; Sequence 42, Application US/09989497
; Patent No. US2002014315A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE

; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-173

Query Match      38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 51;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CGCTGTGG 20
|||||||
Db      1  CGCTGTGG 8
|||||||
```

```
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-09-989-497-42

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGCGGCGC 15
Db      9 CGGCGGCGC 2

RESULT 64
US-09-249-155-6
; Sequence 6, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-6

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGGCC 8
Db      1 GCTGGGCC 8

RESULT 65
US-09-249-155-170
; Sequence 170, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
```

```
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-170

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGGCC 8
Db      1 GCTGGGCC 8

RESULT 66
US-10-318-031-13/G
; Sequence 13, Application US/10318031
; Publication No. US20030220479A1
; GENERAL INFORMATION:
; APPLICANT: LI, XIAODONG
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: ADLER, JON ELLIOTT
; TITLE OF INVENTION: CHIMERIC GALS VARIANTS AND THEIR USE IN THE ANALYSIS AND
; FILE REFERENCE: 100337.54104US
; CURRENT APPLICATION NUMBER: US/10/318,031
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 09/989,497
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/339,466
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: AscI site oligonucleotide
US-10-318-031-13

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGCGGCGC 15
Db      9 CGGCGGCGC 2

RESULT 67
US-10-314-322-6
; Sequence 6, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
```



```

; TITLE OF INVENTION: Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-6

```

```

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GCTGGCCC 8
        |||||
DB      1 GCTGGCCC 8

```

```

RESULT 68
US-10-314-322-170
; Sequence 170, Application US/10314322
; Publication No. US2003022991A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-170

```

```

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GCTGGCCC 8
        |||||
DB      1 GCTGGCCC 8

```

```

RESULT 69
US-10-314-322-305
; Sequence 305, Application US/10314322
; Publication No. US2003022991A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 000486.00016

```

```

; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-305

```

```

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      14 GCTGTGGC 21
        |||||
DB      1 GCTGTGGC 8

```

```

RESULT 70
US-10-450-797-1415
; Sequence 1415, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1415
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1415

```

```

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GCTGGCCC 8
        |||||
DB      4 GCTGGCCC 11

```

```

RESULT 71
US-10-633-531-13/c
; Sequence 13, Application US/10633531
; Publication No. US20050033021A1
; GENERAL INFORMATION:
; APPLICANT: LI, XIAODONG
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: ADLER, JON ELLIOTT
; TITLE OF INVENTION: CHIMERIC Gal5 VARIANTS AND THEIR USE IN THE ANALYSIS AND
; TITLE OF INVENTION: DISCOVERY OF MODULATORS OF G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 100337.54270US

```

```

; CURRENT APPLICATION NUMBER: US/10/633,531
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 09/989,497
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/339,466
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: Ascii site oligonucleotide
US-10-633-531-13

```

```

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 CGCGCGGC 15
         |||||
Db       9 CGCGCGGC 2

```

```

RESULT 72
US-10-952-773-42/c
; Sequence 42, Application US/10952773
; Publication No. US20050136512A1
; GENERAL INFORMATION:
; APPLICANT: XU, HONG
; APPLICANT: YAO, YONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/10/952,773
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-10-952-773-42

```

```

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 CGCGCGGC 15
         |||||
Db       9 CGCGCGGC 2

```

```

RESULT 73
US-10-403-232-144
; Sequence 144, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Qiudeng

```

```

; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 144
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-403-232-144

```

```

Query Match      38.1%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 CGCGCGGC 15
         |||||
Db       4 CGCGCGGC 11

```

```

RESULT 74
US-09-291-129-16/c
; Sequence 16, Application US/09291129
; Patent No. US20010014449A1
; GENERAL INFORMATION:
; APPLICANT: Nerenberg, Michael I.
; APPLICANT: Canter, David M.
; APPLICANT: Radtkey, Ray R.
; TITLE OF INVENTION: METHODS FOR DETERMINATION OF SINGLE
; TITLE OF INVENTION: NUCLEIC ACID POLYMORPHISMS USING A
; TITLE OF INVENTION: BIOELECTRIC MICROCHIP
; FILE REFERENCE: 240/240
; CURRENT APPLICATION NUMBER: US/09/291,129
; CURRENT FILING DATE: 1999-04-12
; EARLIER APPLICATION NUMBER: US 09/030,156
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: US 08/986,065
; EARLIER FILING DATE: 1997-12-05
; EARLIER APPLICATION NUMBER: US 08/859,644
; EARLIER FILING DATE: 1997-05-20
; EARLIER APPLICATION NUMBER: US 08/725,976
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: US 08/708,362
; EARLIER FILING DATE: 1996-09-06
; EARLIER APPLICATION NUMBER: US 08/534,454
; EARLIER FILING DATE: 1995-09-27
; EARLIER APPLICATION NUMBER: US 08/304,657
; EARLIER FILING DATE: 1994-09-09
; EARLIER APPLICATION NUMBER: US 08/271,882
; EARLIER FILING DATE: 1994-07-07
; EARLIER APPLICATION NUMBER: US 08/146,504
; EARLIER FILING DATE: 1993-11-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: DNA
; ORGANISM: human
US-09-291-129-16

```

```

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 CTGGCCCGCGC 12
         |||||
Db      11 CTGGACAGCGC 1

```

```

RESULT 75
US-10-245-206-16/c
; Sequence 16, Application US/10245206
; Publication No. US20030073122A1
; GENERAL INFORMATION:
; APPLICANT: Nerenberg, Michael I.
; APPLICANT: Canter, David M.
; APPLICANT: Radtkey, Ray R.
; TITLE OF INVENTION: METHODS FOR DETERMINATION OF SINGLE
; TITLE OF INVENTION: NUCLEIC ACID POLYMORPHISMS USING A
; TITLE OF INVENTION: BIOELECTRIC MICROCHIP
; FILE REFERENCE: 240/240
; CURRENT APPLICATION NUMBER: US/10/245,206
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/09/291,129
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US/09/030,156
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: US/08/986,065
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: US/08/859,644
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US/08/725,976
; PRIOR FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: US/08/708,262
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: US/08/534,454
; PRIOR FILING DATE: 1995-09-27
; PRIOR APPLICATION NUMBER: US/08/304,657
; PRIOR FILING DATE: 1994-09-09
; PRIOR APPLICATION NUMBER: US/08/271,882
; PRIOR FILING DATE: 1994-07-07
; PRIOR APPLICATION NUMBER: US/08/146,504
; PRIOR FILING DATE: 1993-11-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: DNA
; ORGANISM: human
US-10-245-206-16

```

```

Query Match          37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2  CTGGCCCGCG 12
          |||||
Db      11  CTGGACAGCG 1

```

```

RESULT 76
US-10-266-138B-11
; Sequence 11, Application US/10266138B
; Publication No. US20030152964A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: J6664US(ED:EP/JVT)seq1s13Sep'02;51-84
; CURRENT APPLICATION NUMBER: US/10/266,138B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/338,272
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq.# 61 of
; OTHER INFORMATION: Table I
US-10-266-138B-11

```

```

Query Match          37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      6  CCGCGCGCGCT 16
          ||| |||||
Db      1  CCCAACGCGCT 11

```

```

RESULT 77
US-10-265-509B-11
; Sequence 11, Application US/10265509B
; Publication No. US20030170739A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: GENE EXPRESSION FOR ANALYZING PHOTODAMAGE
; FILE REFERENCE: J6663US(ED:EP/JVT)seq1s13Sep'02;51-84
; CURRENT APPLICATION NUMBER: US/10/265,509B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/337,856
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq.# 61 of
; OTHER INFORMATION: Table I
US-10-265-509B-11

```

```

Query Match          37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      6  CCGCGCGCGCT 16
          ||| |||||
Db      1  CCCAACGCGCT 11

```

```

RESULT 78
US-10-084-839-3364/c
; Sequence 3364, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.

```

```
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tserska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3364
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3364
```

```
Query Match          37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5  GCCCGGGCGGC 15
         ||||| |||
Db       11  GCCCGGGGTGC 1
```

RESULT 79

```
US-10-450-797-76
; Sequence 76, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-76
```

```
Query Match          37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      6  CCCGGCGCGCT 16
         || ||| |||
Db       1  CCAGGCACGCT 11
```

RESULT 80

```
US-10-450-797-124/c
; Sequence 124, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
```

```
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-124
```

```
Query Match          37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      10  GCGCGCTGTGG 20
          ||||| |||
Db       11  GAGCGCAGTGG 1
```

RESULT 81

```
US-10-450-797-579
; Sequence 579, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 579
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-579
```

```
Query Match          37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4  GGCCCGGCGCG 14
          ||||| |||
Db       1  GGCCCTGAGCG 11
```

RESULT 82

```
US-10-450-797-851/c
; Sequence 851, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 851
```

; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-851

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CGCGCTGTGGC 21
| | | | | | | | | |
Db 11 CTCGCTGGGCG 1

RESULT 83

US-10-450-797-1173/c
; Sequence 1173, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1173
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1173

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
| | | | | | | | | |
Db 11 GCGTGCAGTGG 1

RESULT 84

US-10-754-408-8
; Sequence 8, Application US/10754408
; Publication No. US20040203035A1
; GENERAL INFORMATION:
; APPLICANT: Mast, Andrea L.
; APPLICANT: Dorn, Erin
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Accolla, Molly
; APPLICANT: Wigdal, Susan S.
; TITLE OF INVENTION: Connexin Allele Detection Assays
; FILE REFERENCE: FORS-08724
; CURRENT APPLICATION NUMBER: US/10/754,408
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-754-408-8

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CGCGCTGTGGC 21
| | | | | | | | | |
Db 1 CGGCGCGAGGC 11

RESULT 85

US-10-754-408-8/c
; Sequence 8, Application US/10754408
; Publication No. US20040203035A1
; GENERAL INFORMATION:
; APPLICANT: Mast, Andrea L.
; APPLICANT: Dorn, Erin
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Accolla, Molly
; APPLICANT: Wigdal, Susan S.
; TITLE OF INVENTION: Connexin Allele Detection Assays
; FILE REFERENCE: FORS-08724
; CURRENT APPLICATION NUMBER: US/10/754,408
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-754-408-8

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGCGCGCGCG 14
| | | | | | | | | |
Db 11 GCCTCGCGCGC 1

RESULT 86

US-09-827-395A-739
; Sequence 739, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 739
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-739

Query Match 37.1%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCGCGCGCG 15
| | | | | | | | | |
Db 5 GCGCGCGCGCG 15

QY 5 GCCCGCGCGC 15
 ||||| |||
 Db 7 GCCCGCGCGC 17

RESULT 91
 US-10-430-882-443
 ; Sequence 443, Application US/10430882
 ; Publication No. US20030203870A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lawrence Pharmaceuticals, Inc.
 ; APPLICANT: James McSwiggen
 ; APPLICANT: Bharat Chowhira
 ; APPLICANT: Peter Haeblerl
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
 ; FILE REFERENCE: MBH00-878-H (400/112)
 ; CURRENT APPLICATION NUMBER: US/10/430,882
 ; CURRENT FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: 09/827,395
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 09/780,533
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: PCT/US01/04273
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: PCT/US02/10512
 ; PRIOR FILING DATE: 2002-04-03
 ; NUMBER OF SEQ ID NOS: 2617
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 443
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-10-430-882-443

Query Match 37.1%; Score 7.8; DB 1; Length 17;
 Best Local Similarity 81.8%; Pred. No. 2.1e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 15
 ||||| |||
 Db 6 GCCCGCGCGC 16

RESULT 92
 US-09-154-750A-12
 ; Sequence 12, Application US/09154750A
 ; Publication No. US20020055097A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogelstein, Bert
 ; APPLICANT: Kinzler, Kenneth
 ; APPLICANT: Polyak, Kornelia
 ; TITLE OF INVENTION: p53-Induced Apoptosis
 ; FILE REFERENCE: 1107.75357
 ; CURRENT APPLICATION NUMBER: US/09/154,750A
 ; CURRENT FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/059,153
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/079817
 ; PRIOR FILING DATE: 1998-03-30
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-154-750A-12

Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 76;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGC 13
 ||||| |||
 Db 2 GCCCGCGC 10

RESULT 93
 US-09-154-750A-12/c
 ; Sequence 12, Application US/09154750A
 ; Publication No. US20020055097A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogelstein, Bert
 ; APPLICANT: Kinzler, Kenneth
 ; APPLICANT: Polyak, Kornelia
 ; TITLE OF INVENTION: p53-Induced Apoptosis
 ; FILE REFERENCE: 1107.75357
 ; CURRENT APPLICATION NUMBER: US/09/154,750A
 ; CURRENT FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/059,153
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/079817
 ; PRIOR FILING DATE: 1998-03-30
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-154-750A-12

Query Match 35.2%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 76;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCGCGCT 16
 ||||| |||
 Db 9 CGCGCGCT 1

RESULT 94

US-09-538-456-3/c
 ; Sequence 3, Application US/09538456
 ; Patent No. US20020076802A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alam, Mansoor
 ; APPLICANT: Sattar, Abdul
 ; APPLICANT: Kumar, Sushil
 ; APPLICANT: Samad, Abdul
 ; APPLICANT: Dhawan, Om Prakash
 ; APPLICANT: Khanuja, Suman Preet Singh
 ; APPLICANT: Shasany, Ajit Kumar
 ; APPLICANT: Singh, Seema
 ; APPLICANT: Kumar, Poovappallivadakethil Viswanathan Nair Ajay
 ; APPLICANT: Khaliq, Abdul
 ; APPLICANT: Zaim, Mohammad
 ; APPLICANT: Shahabuddin, Saba
 ; APPLICANT: Trivedi, Mala
 ; TITLE OF INVENTION: A novel Streptomyces strain with potential anti-microbial
 ; FILE REFERENCE: 148920.00003
 ; CURRENT APPLICATION NUMBER: US/09/538,456
 ; CURRENT FILING DATE: 2000-03-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Microsoft Word-97
 ; SEQ ID NO 3
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: primer
 US-09-538-456-3

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
|||||||
Db 9 CCGGCGTGC 1

RESULT 95
US-09-785-716A-6/c
; Sequence 6, Application US/09785716A
; Publication No. US20020184676P1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; APPLICANT: Dwivedi, Sanresh
; APPLICANT: Singh, Maneesha
; APPLICANT: Singh, Ajay Pratap
; APPLICANT: Singh, Vandana
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Kuman, Sushil
; TITLE OF INVENTION: New Peppermint Plant Named 'PRANJAL'
; FILE REFERENCE: 41799/VGG/K375
; CURRENT APPLICATION NUMBER: US/09/785,716A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for RAPD profile
US-09-785-716A-6

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
|||||||
Db 9 CCGGCGTGC 1

RESULT 96
US-09-799-880-6/c
; Sequence 6, Application US/09799880
; Publication No. US20030014799P1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Gupta, Ritika
; APPLICANT: Sastry, Kakaraparthi
; APPLICANT: Banerjee, Suchitra
; APPLICANT: Mallavarapu, Gopal
; APPLICANT: Ramesh, Srinivas
; APPLICANT: Shasany, Ajit
; APPLICANT: Darokar, Mahendra
; APPLICANT: Khanuja, Suman
; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAFAL'
; FILE REFERENCE: 2734-102
; CURRENT APPLICATION NUMBER: US/09/799,880
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-799-880-6

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
|||||||
Db 9 CCGGCGTGC 1

RESULT 97
US-09-915-063-1/c
; Sequence 1, Application US/09915063
; Publication No. US20030082544A1
; GENERAL INFORMATION:
; APPLICANT: Fors, Lance
; APPLICANT: Ganske, Rocky
; TITLE OF INVENTION: Methods and Systems for Validating Detection Assays, Developing
; TITLE OF INVENTION: Diagnostic DNA or RNA Analysis Products, and Increasing Revenue
; TITLE OF INVENTION: Margins from In-Vitro Diagnostic DNA or RNA Analysis Assays
; FILE REFERENCE: FORS-06467
; CURRENT APPLICATION NUMBER: US/09/915,063
; CURRENT FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: 60/304,521
; PRIOR FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-915-063-1

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCGGCGCGC 14
|||||||
Db 9 CTCGGCGCG 1

RESULT 98
US-09-929-135-1/c
; Sequence 1, Application US/09929135
; Publication No. US20030104470A1
; GENERAL INFORMATION:
; APPLICANT: Fors, Lance
; APPLICANT: Ganske, Rocky
; APPLICANT: Brower, Amy M.
; APPLICANT: Ziarno, Witold M.
; TITLE OF INVENTION: Electronic Medical Record, Library of Electronic Medical Records
; TITLE OF INVENTION: Polymorphism Data, and Computer Systems and Methods for Use Ther
; FILE REFERENCE: FORS-06443
; CURRENT APPLICATION NUMBER: US/09/929,135
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-929-135-1

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCGGCGCGC 14
|||||||
Db 9 CTCGGCGCG 1


```

; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2103
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2103

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GGCCTGTGG 20
Db      |||||
        2 GGCCTGTGG 10

RESULT 102
US-10-390-045-63/c
; Sequence 63, Application US/10390045
; Publication No. US20030170713A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/10/390,045
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US/09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-390-045-63

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
Db      |||||
        10 TGGCCCGGC 2

RESULT 103
US-10-330-627-279
; Sequence 279, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627

```

```

US-10-033-145-11/c
; Sequence 11, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-11

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 6 CCCGGCGCG 14
Db      |||||
        10 CCCGGCGCG 2

RESULT 100
US-10-033-145-1458/c
; Sequence 1458, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1458
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1458

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GCTGGCCGC 9
Db      |||||
        9 GCTGGCCGC 1

RESULT 101
US-10-033-145-2103
; Sequence 2103, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

```

```
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-279
```

```
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 12 GCGCTGTGG 20
Db 2 GGGCTGTGG 10
| | | | |
```

RESULT 104

```
US-10-330-627-280
; Sequence 280, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-280
```

```
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 12 GCGCTGTGG 20
Db 2 GGGCTGTGG 10
| | | | |
```

RESULT 105

```
US-10-330-627-447/c
; Sequence 447, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-447
```

```
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 13 CGCTGTGGC 21
Db 9 CGCTGGGC 1
| | | | |
```

RESULT 106

```
US-10-330-627-586/c
; Sequence 586, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 586
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-586
```

```
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 13 CGCTGTGGC 21
Db 10 CGCAGTGGC 2
| | | | |
```

RESULT 107

```
US-10-330-627-1214/c
; Sequence 1214, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcripts
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1214
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1214
```

```
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 TGGCCCGGC 11
Db 9 TGGCCAGGC 1
| | | | |
```

RESULT 108

```
US-10-330-627-1215/c
```

; Sequence 1215, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1215
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1215

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
|||||
DB 9 TGGCCAGGC 1

RESULT 109

US-10-330-627-1228
; Sequence 1228, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1228
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1228

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
|||||
DB 2 TGGCCAGGC 10

RESULT 110

US-10-330-627-1229
; Sequence 1229, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480

; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1229
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1229

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
|||||
DB 2 TGGCCAGGC 10

RESULT 111

US-10-330-627-1230
; Sequence 1230, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1230
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1230

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
|||||
DB 2 TGGCCAGGC 10

RESULT 112

US-10-330-627-1231
; Sequence 1231, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1231
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1231

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
||||| |||
Db 2 TGGCCAGGC 10

RESULT 113

US-10-330-627-1232
; Sequence 1232, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1232
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1232

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
||||| |||
Db 2 TGGCCAGGC 10

RESULT 114

US-10-330-627-1233
; Sequence 1233, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1233
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1233

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
||||| |||
Db 2 TGGCCAGGC 10

RESULT 115

US-10-330-627-1234
; Sequence 1234, Application US/10330627
; Publication No. US20030175771A1

; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1234
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1234

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
||||| |||
Db 2 TGGCCAGGC 10

RESULT 116

US-10-353-751-1/c
; Sequence 1, Application US/10353751
; Publication No. US20030219784A1
; GENERAL INFORMATION:
; APPLICANT: Ip, Hon S.
; APPLICANT: Ziarno, Witold A.
; APPLICANT: Donald, Glen
; TITLE OF INVENTION: Systems and Methods for Analysis of Agricultural Products
; FILE REFERENCE: FORS-07809
; CURRENT APPLICATION NUMBER: US/10/353,751
; CURRENT FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-353-751-1

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGCCGCG 14
||||| |||
Db 9 CTCGCCGCG 1

RESULT 117

US-10-321-039-753/c
; Sequence 753, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30

;; PRIOR APPLICATION NUMBER: 60/329,113
;; PRIOR FILING DATE: 2001-10-12
;; PRIOR APPLICATION NUMBER: 60/360,489
;; PRIOR FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 759
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 753
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-321-039-753

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCGGGCGG 14
DB 9 CTCGGCGG 1

RESULT 118

US-10-418-414-21/c
; Sequence 21, Application US/10418414
; Publication No. US20040072202A1

GENERAL INFORMATION:

;; APPLICANT: McGall, Glenn Hugh
;; Miyada, Charles Garrett
;; Cronin, Maureen T.
;; Tan, Jennifer Dee
;; Chee, Mark

TITLE OF INVENTION: Modified Nucleic Acid Probes

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew
;; STREET: One Market Plaza, Steuart Street Tower
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94105-1492

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/418,414
;; FILING DATE: 22-Aug-2003
;; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/09/608,691
;; FILING DATE: 29-Jun-2000
;; APPLICATION NUMBER: US/08/630,427
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/440,742
;; FILING DATE: 10-MAY-1995
;; APPLICATION NUMBER: WO PCT/US94/12305
;; APPLICATION NUMBER: US 08/284,064
;; FILING DATE: 02-AUG-1994
;; APPLICATION NUMBER: US 08/143,312
;; FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

;; NAME: Weber, Kenneth A.
;; REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 16528X-012510

TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 543-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:

;; NAME/KEY: modified_base
;; LOCATION: 10

;; OTHER INFORMATION: /note= "N = cytosine covalently modified

;; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-418-414-21

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCGGGCGG 14
DB 9 CGCGGCGG 1

RESULT 119

US-10-418-414-27
; Sequence 27, Application US/10418414
; Publication No. US20040072202A1

GENERAL INFORMATION:

;; APPLICANT: McGall, Glenn Hugh
;; Miyada, Charles Garrett
;; Cronin, Maureen T.
;; Tan, Jennifer Dee
;; Chee, Mark

TITLE OF INVENTION: Modified Nucleic Acid Probes

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew
;; STREET: One Market Plaza, Steuart Street Tower
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94105-1492

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/418,414
;; FILING DATE: 22-Aug-2003
;; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/09/608,691
;; FILING DATE: 29-Jun-2000
;; APPLICATION NUMBER: US/08/630,427
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/440,742
;; FILING DATE: 10-MAY-1995
;; APPLICATION NUMBER: WO PCT/US94/12305
;; APPLICATION NUMBER: US 08/284,064
;; FILING DATE: 02-AUG-1994
;; APPLICATION NUMBER: US 08/143,312
;; FILING DATE: 26-OCT-1993

ATTORNEY/AGENT INFORMATION:

;; NAME: Weber, Kenneth A.
;; REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 16528X-012510

TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 543-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid

```
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: 1
/ OTHER INFORMATION: /note= "N = guanine covalently modified
US-10-418-414-27
```

```
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 CCGGCGCG 14
| | | | |
DB 2 CCGGCGCG 10
```

```
RESULT 120
US-10-434-479-63/c
; Sequence 63, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-434-479-63
```

```
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 TGGCCCGCG 11
| | | | |
DB 10 TGGCCCGCG 2
```

```
RESULT 121
US-10-401-753-5/c
; Sequence 5, Application US/10401753
; Publication No. US20040194175P1
; GENERAL INFORMATION:
; APPLICANT: LAL, Raj K et al
; TITLE OF INVENTION: A CITRAL RICH HIGH YIELDING LEMONGRASS PLANT 'NIMA' OF CYMBOPOGON
; FILE REFERENCE: FLEXUOSUS
; CURRENT APPLICATION NUMBER: US/10/401,753
; CURRENT FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
```

```
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Random MAP primer
US-10-401-753-5
```

```
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 CCGGCGCG 15
| | | | |
DB 9 CCGGCGTG 1
```

```
RESULT 122
US-10-401-691-6/c
; Sequence 6, Application US/10401691
; Publication No. US20040194176P1
; GENERAL INFORMATION:
; APPLICANT: KHANUUA, SUMAN PREET SINGH
; APPLICANT: SHASANY, AJIT KUMAR
; APPLICANT: YADAV, USHA
; APPLICANT: DHAWAN, SUNITA
; APPLICANT: DAROKAR, MAHENDRA PANDURANG
; APPLICANT: BAL, JANEK RAJ
; APPLICANT: GUPTA, SONI
; APPLICANT: PANDEY, SWETA
; APPLICANT: SINGH, ANIL KUMAR
; APPLICANT: BANSAL, RAVI PRAKASH
; APPLICANT: LAL, RAJ KISHORI
; APPLICANT: DHAWAN, OM PARKESH
; APPLICANT: NAQVI, ALI ARIF
; APPLICANT: KALRA, ALOK
; APPLICANT: KRISHNA, ALOK
; APPLICANT: TOMAR, VIRENDRA KUMAR SINGH
; TITLE OF INVENTION: MINT PLANT 'KUSHAL' FOR LATE TRANSPLANTING
; FILE REFERENCE: 056859-0184
; CURRENT APPLICATION NUMBER: US/10/401,691
; CURRENT FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-401-691-6
```

```
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 CCGGCGCG 15
| | | | |
DB 9 CCGGCGTG 1
```

```
RESULT 123
US-10-404-304-5/c
; Sequence 5, Application US/10404304
; Publication No. US20040199969P1
; GENERAL INFORMATION:
; APPLICANT: Lal, Raj Kishori
; APPLICANT: Singh, Nilakshi
; APPLICANT: Mishra, Hari Om
; APPLICANT: Sharma, Jawahar Ram
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Kharuja, Suman Preet Singh
```

; TITLE OF INVENTION: EARLY MATURING, HIGH YIELDING PSYLLIUM (PLANTAGO OVATA F.)
; FILE OF INVENTION: VARIETY 'MAYURI' WITH MATURITY MARKER
; FILE REFERENCE: 11378.48US01
; CURRENT APPLICATION NUMBER: US/10/404,304
; CURRENT FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primers
US-10-404-304-5

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGGC 15
||| ||| ||
Db 9 CCGGCGTGC 1

RESULT 124

US-10-713-381-13
; Sequence 13, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-13

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 9
||| ||| |||
Db 1 GCGGGCCCG 9

RESULT 125

US-10-713-381-13/c
; Sequence 13, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-13

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 9
||| ||| |||
Db 10 GCGGGCCCG 2

RESULT 126

US-10-713-381-15
; Sequence 15, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-15

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 9
||| ||| |||
Db 2 GCGGGCCCG 10

RESULT 127

US-10-713-381-19
; Sequence 19, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-19

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCG 9
      ||| |||||
Db      1 GCGGGCCCG 9

RESULT 128
US-10-713-381-19/c
; Sequence 19, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-19

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCG 9
      ||| |||||
Db      10 GCGGGCCCG 2

RESULT 129
US-10-713-381-20
; Sequence 20, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-20

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCG 9
      ||| |||||
Db      10 GCGGGCCCG 2

RESULT 130
US-10-713-381-20/c
; Sequence 20, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-20

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCG 9
      ||| |||||
Db      10 GCGGGCCCG 2

RESULT 131
US-10-713-381-21
; Sequence 21, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-21

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCG 9
      ||| |||||
Db      4 GCGGGCCCG 12

RESULT 132
US-10-713-381-22
; Sequence 22, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-22

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCG 9
      ||| |||||
Db      4 GCGGGCCCG 12
```



```
Db      2  GGCGGCCCG 10
||||| ||
RESULT 132
US-10-713-381-22/c
; Sequence 22, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-22

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTGGGCCCG 9
||| |||||
Db      9  GCGGGCCCG 1

RESULT 133
US-10-713-381-23/c
; Sequence 23, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-23

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTGGGCCCG 9
||| |||||
Db      9  GCGGGCCCG 1

RESULT 134
US-10-713-381-22/c
; Sequence 22, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-22

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTGGGCCCG 9
||| |||||
Db      9  GCGGGCCCG 1

RESULT 135
US-10-478-014-32/c
; Sequence 32, Application US/10478014
; Publication No. US20040248083A1
; GENERAL INFORMATION:
; APPLICANT: Aarhus Universitet
; APPLICANT: Finn Skou Pedersen
; APPLICANT: Jacob Giehm Mikkelsen
; APPLICANT: Soren Vestergaards Rasmussen
; APPLICANT: Mogens Ouch
; APPLICANT: Lars Asgaard
; TITLE OF INVENTION: Improved Vectors for Gene Therapy
; FILE REFERENCE: P32171 PC 01
; CURRENT APPLICATION NUMBER: US/10/478,014
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: PA 2001 00789
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: palindrome at position 209-218 in Akv/AkvB
US-10-478-014-32

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTGGGCCCG 9
||| |||||
Db      1  GCTGGGCCAG 9

RESULT 136
US-10-487-934-236/c
; Sequence 32, Application US/10478014
; Publication No. US20040248083A1
; GENERAL INFORMATION:
; APPLICANT: Aarhus Universitet
; APPLICANT: Finn Skou Pedersen
; APPLICANT: Jacob Giehm Mikkelsen
; APPLICANT: Soren Vestergaards Rasmussen
; APPLICANT: Mogens Ouch
; APPLICANT: Lars Asgaard
; TITLE OF INVENTION: Improved Vectors for Gene Therapy
; FILE REFERENCE: P32171 PC 01
; CURRENT APPLICATION NUMBER: US/10/478,014
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: PA 2001 00789
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: palindrome at position 209-218 in Akv/AkvB
US-10-478-014-32

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTGGGCCCG 9
||| |||||
Db      10 GCTGGCCAG 2

RESULT 136
US-10-487-934-236/c
```

```

; Sequence 236, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-487-934-236

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
Db 9 TGGCCAGGC 1

RESULT 137
US-10-487-934-237/c
; Sequence 237, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-487-934-237

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
Db 9 TGGCCAGGC 1

RESULT 138
US-10-626-832-234/c
; Sequence 234, Application US/10626832
; Publication No. US2005000342A1
; GENERAL INFORMATION:
; APPLICANT: Davis Poynter, Nick
; APPLICANT: Nugent, Josephine
; APPLICANT: Birch-Machin, Ian
; APPLICANT: Allen, George P
; TITLE OF INVENTION: Viral Marker
; FILE REFERENCE: 620-262
; CURRENT APPLICATION NUMBER: US/10/626,832
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,576
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Equine herpesvirus 1
; US-10-626-832-234

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
Db 10 CTGGCTCGG 2

RESULT 139
US-10-647-114-13/c
; Sequence 13, Application US/10647114
; Publication No. US20050050593A1
; GENERAL INFORMATION:
; APPLICANT: GUPTA, ANIL KUMAR
; APPLICANT: KHANUJA, SUMAN PREET SINGH
; APPLICANT: GUPTA, MADHAN MOHAN
; APPLICANT: SHASANY, AJIT KUMAR
; APPLICANT: JAIN, NEERAJ
; APPLICANT: VERMA, RAM KISHOR
; APPLICANT: DAROKAR, MAHENDRA PANDURANG
; APPLICANT: BAGCHI, GURU DAS
; APPLICANT: KUMAR, SUSHIL
; TITLE OF INVENTION: HIGH HERB, PHYLLANTHIN AND HYPOPHYLLANTHIN YIELDING
; TITLE OF INVENTION: CULTIVAR OF PHYLLANTHUS AMARUS 'CIM-JEEVAN'
; FILE REFERENCE: 056859-0188
; CURRENT APPLICATION NUMBER: US/10/647,114
; CURRENT FILING DATE: 2003-08-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer
; US-10-647-114-13

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
Db 9 CCGGCGTGC 1

RESULT 140
US-10-639-682-6/c
; Sequence 6, Application US/10639682
; Publication No. US20050091705A1
; GENERAL INFORMATION:
; APPLICANT: LAL, RAJ KISHORI
; APPLICANT: KHANUJA, SUMAN PREET SINGH
; APPLICANT: AGNIHOTRI, ARUN KUMAR
; APPLICANT: MISRA, HARI OM

```

```

; APPLICANT: SHASANY, AJIT KUMAR
; APPLICANT: NAOVI, ALI ARIF
; APPLICANT: DHAWAN, OM PRAKASH
; APPLICANT: KALARA, ALOK
; APPLICANT: BAHL, JANAK RAJ
; APPLICANT: DAROKAR, MAHENDRA PANDURANG
; TITLE OF INVENTION: A HIGH ESSENTIAL OIL AND EUGENOL YIELDING CULTIVAR OF
; TITLE OF INVENTION: OCIMUM SANTUM 'CIM-AYU'
; FILE REFERENCE: 056859-0187
; CURRENT APPLICATION NUMBER: US/10/639,682
; CURRENT FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-639-682-6

```

```

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 7 CCGGCGCGC 15
    |||||
Db 9 CCGGCGTGC 1

```

RESULT 141

```

US-10-813-160-9/c
; Sequence 9, Application US/10813160
; Publication No. US20050142564A1
; GENERAL INFORMATION:
; APPLICANT: COUNCIL OF SCIENTIFIC & INDUSTRIAL RESEARCH
; APPLICANT: KHANUJA, Suman Preet Singh
; APPLICANT: PAUL, Shilpi
; APPLICANT: SHASANY, Ajit Kumar
; APPLICANT: DAROKAR, Mahendra Pandurang
; APPLICANT: SHUKLA, Ashutosh Kumar
; APPLICANT: GUPTA, Madan Mohan
; APPLICANT: KUMAR, Anuruddha
; TITLE OF INVENTION: PRIMERS AND A SCREENING METHOD FOR IDENTIFICATION OF ARTEMISININ
; FILE REFERENCE: Q80746
; CURRENT APPLICATION NUMBER: US/10/813,160
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: PCT/IN03/00404
; PRIOR FILING DATE: 2003-09-29
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer MAP06
US-10-813-160-9

```

```

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 7 CCGGCGCGC 15
    |||||
Db 9 CCGGCGTGC 1

```

RESULT 142

```

US-10-967-711-11/c
; Sequence 11, Application US/10967711

```

```

; Publication No. US20050186588A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Jarvis, Nancy
; APPLICANT: Roeven, Robert
; APPLICANT: Hall, Jeff G.
; APPLICANT: Allawi, Hatim T.
; TITLE OF INVENTION: Direct Nucleic Acid Detection in Bodily Fluids
; FILE REFERENCE: FORS-09661
; CURRENT APPLICATION NUMBER: US/10/967,711
; CURRENT FILING DATE: 2004-10-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-967-711-11

```

```

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 6 CCGGCGCGC 14
    |||||
Db 9 CTCGCGCGC 1

```

RESULT 143

```

US-10-811-244B-6/c
; Sequence 6, Application US/10811244B
; Publication No. US20050223447P1
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Paul, Shilpi
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Gupta, Anil Kumar
; APPLICANT: Darokar, Mahendra Pandurang
; TITLE OF INVENTION: HIGH ARTEMISININ YIELDING PLANT GENOTYPE 'CIM-AROGYA'
; FILE REFERENCE: U 015108-9
; CURRENT APPLICATION NUMBER: US/10/811,244B
; CURRENT FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: MAP Primer
US-10-811-244B-6

```

```

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 7 CCGGCGCGC 15
    |||||
Db 9 CCGGCGTGC 1

```

RESULT 144

```

US-11-035-899-386/c
; Sequence 386, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe

```

David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/035,899
FILING DATE: 14-Jan-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/477,464
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z-I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 386:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 386:
US-11-035-899-386

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
|||||||
Db 10 CTGGCCCTG 2

RESULT 145
US-11-035-899-387/c
; Sequence 387, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/035,899
FILING DATE: 14-Jan-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/477,464
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z-I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 387:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 387:
US-11-035-899-387

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
|||||||
Db 9 CTGGCCCTG 1

RESULT 146
US-09-984-292-42
; Sequence 42, Application US/09984292
; Patent No. US20020128433A1
; GENERAL INFORMATION:
; APPLICANT: XU, HONG
; APPLICANT: YAO, YONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-09-984-292-42

Query Match 35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCGCGCTG 17
|||||||
Db 1 GCGCGCGG 9

RESULT 147

US-09-989-497-42
 ; Sequence 42, Application US/09989497
 ; Patent No. US20020143151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YAO, YONG
 ; APPLICANT: XU, HONG
 ; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
 ; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
 ; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
 ; FILE REFERENCE: 078003-0280735
 ; CURRENT APPLICATION NUMBER: US/09/989,497
 ; CURRENT FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 09/984,292
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: 60/243,770
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 42
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
 ; OTHER INFORMATION: oligonucleotide
 US-09-989-497-42

Query Match 35.2%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
 DB 1 GGCGCGCCG 9

RESULT 148

US-10-318-031-13
 ; Sequence 13, Application US/10318031
 ; Publication No. US20030220479A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, XIAODONG
 ; APPLICANT: XU, HONG
 ; APPLICANT: STASZEWSKI, LENA
 ; APPLICANT: ADLER, JON ELLIOTT
 ; TITLE OF INVENTION: CHIMERIC Gal5 VARIANTS AND THEIR USE IN THE ANALYSIS AND
 ; TITLE OF INVENTION: DISCOVERY OF MODULATORS OF G-PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: 100337 54104US
 ; CURRENT APPLICATION NUMBER: US/10/318,031
 ; CURRENT FILING DATE: 2002-12-13
 ; PRIOR APPLICATION NUMBER: 09/989,497
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 09/984,292
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: 60/339,466
 ; PRIOR FILING DATE: 2001-12-14
 ; PRIOR APPLICATION NUMBER: 60/243,770
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
 ; OTHER INFORMATION: Ascii site oligonucleotide
 US-10-318-031-13

Query Match 35.2%; Score 7.4; DB 1; Length 11;

Best Local Similarity 88.9%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 GGCGCGCTG 17
 DB 1 GGCGCGCCG 9

RESULT 149

US-10-633-531-13
 ; Sequence 13, Application US/10633531
 ; Publication No. US20050033021A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, XIAODONG
 ; APPLICANT: XU, HONG
 ; APPLICANT: STASZEWSKI, LENA
 ; APPLICANT: ADLER, JON ELLIOTT
 ; TITLE OF INVENTION: CHIMERIC Gal5 VARIANTS AND THEIR USE IN THE ANALYSIS AND
 ; TITLE OF INVENTION: DISCOVERY OF MODULATORS OF G-PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: 100337 54270US
 ; CURRENT APPLICATION NUMBER: US/10/633,531
 ; CURRENT FILING DATE: 2003-08-05
 ; PRIOR APPLICATION NUMBER: 09/989,497
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 09/984,292
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: 60/339,466
 ; PRIOR FILING DATE: 2001-12-14
 ; PRIOR APPLICATION NUMBER: 60/243,770
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
 ; OTHER INFORMATION: Ascii site oligonucleotide
 US-10-633-531-13

Query Match 35.2%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 1e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
 DB 1 GGCGCGCCG 9

RESULT 150

US-10-952-773-42
 ; Sequence 42, Application US/10952773
 ; Publication No. US20050136512A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YAO, YONG
 ; APPLICANT: XU, HONG
 ; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
 ; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
 ; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
 ; FILE REFERENCE: 078003-0280649
 ; CURRENT APPLICATION NUMBER: US/10/952,773
 ; CURRENT FILING DATE: 2004-09-30
 ; PRIOR APPLICATION NUMBER: 60/243,770
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 42
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
 ; OTHER INFORMATION: Ascii site oligonucleotide
 US-10-952-773-42

```
; OTHER INFORMATION: oligonucleotide
US-10-952-773-42

Query Match      35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 GCGCGCGCTG 17
Db   1 GCGCGCGCG 9

RESULT 151
US-09-923-517-40
; Sequence 40, Application US/09923517
; Publication No. US20020039741A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; Compositions and Methods for the Modulation of
; Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,517
; FILING DATE: 07-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,517A
; FILING DATE: 07-Aug-2001
; APPLICATION NUMBER: 09/364,416
; FILING DATE: 1999-07-30
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-430-196-40

Query Match      34.3%; Score 7.2; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  8 CGCGCGCGCTGTG 19
Db   5 CAGCGCGCGCGG 16

RESULT 153
US-09-942-487-3
; Sequence 3, Application US/09942487
; Publication No. US20020086310A1
; GENERAL INFORMATION:
; APPLICANT: FAN, FRANK
; APPLICANT: HE, YIPING
; APPLICANT: HUANG, JIANZHONG
; APPLICANT: JIANG, XINHE
; APPLICANT: McDEVITT, DAMIEN
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: ST. JOHN, ANNEMARIE
; TITLE OF INVENTION: IDENTIFICATION OF TARGETS OF
; FILE REFERENCE: P51167
; CURRENT APPLICATION NUMBER: US/09/942,487
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/229,965
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 11

; OTHER INFORMATION: oligonucleotide
US-10-952-773-42

Query Match      35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9 GCGCGCGCTG 17
Db   1 GCGCGCGCG 9

RESULT 151
US-09-923-517-40
; Sequence 40, Application US/09923517
; Publication No. US20020039741A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; Compositions and Methods for the Modulation of
; Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,517
; FILING DATE: 07-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/364,416
; FILING DATE: 1999-07-30
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-923-517-40

Query Match      34.3%; Score 7.2; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  8 CGCGCGCGCTGTG 19
Db   5 CAGCGCGCGCGG 16

RESULT 152
US-10-430-196-40
; Sequence 40, Application US/10430196
; Publication No. US20030194738A1
; GENERAL INFORMATION:
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-942-487-3

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
Db 1 GCGCGGC 7

RESULT 154
US-09-942-487-3/c
; Sequence 3, Application US/09942487
; Publication No. US20020086310A1
; GENERAL INFORMATION:
; APPLICANT: FAN, FRANK
; APPLICANT: HE, YIPING
; APPLICANT: HUANG, JIANZHONG
; APPLICANT: JIANG, XINHE
; APPLICANT: McDEVITT, DAMIEN
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: ST. JOHN, ANNEMARIE
; TITLE OF INVENTION: IDENTIFICATION OF TARGETS OF
; TITLE OF INVENTION: ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: P51167
; CURRENT APPLICATION NUMBER: US/09/942,487
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/229,965
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-942-487-3

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
Db 8 GCGCGGC 2

RESULT 155
US-09-942-487-5
; Sequence 5, Application US/09942487
; Publication No. US20020086310A1
; GENERAL INFORMATION:
; APPLICANT: FAN, FRANK
; APPLICANT: HE, YIPING
; APPLICANT: HUANG, JIANZHONG
; APPLICANT: JIANG, XINHE
; APPLICANT: McDEVITT, DAMIEN
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: ST. JOHN, ANNEMARIE
; TITLE OF INVENTION: IDENTIFICATION OF TARGETS OF
; TITLE OF INVENTION: ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: P51167
; CURRENT APPLICATION NUMBER: US/09/942,487
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/229,965
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-942-487-5

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
Db 8 GCGCGGC 2

RESULT 156
US-09-942-487-5/c
; Sequence 5, Application US/09942487
; Publication No. US20020086310A1
; GENERAL INFORMATION:
; APPLICANT: FAN, FRANK
; APPLICANT: HE, YIPING
; APPLICANT: HUANG, JIANZHONG
; APPLICANT: JIANG, XINHE
; APPLICANT: McDEVITT, DAMIEN
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: ST. JOHN, ANNEMARIE
; TITLE OF INVENTION: IDENTIFICATION OF TARGETS OF
; TITLE OF INVENTION: ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: P51167
; CURRENT APPLICATION NUMBER: US/09/942,487
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/229,965
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-942-487-5

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
Db 10 GCGCGGC 4

RESULT 157
US-09-867-262-5
; Sequence 5, Application US/09867262
; Patent No. US20020119457A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
; FILE REFERENCE: DEVER1460-17
; CURRENT APPLICATION NUMBER: US/09/867,262
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-12-07
```

; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-867-262-5

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
|||||
Db 1 CGCGCTG 7

RESULT 158

US-09-885-551A-6
; Sequence 6, Application US/09885551A
; Patent No. US20020146762A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHTSHILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/09/885,551A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-885-551A-6

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
|||||
Db 1 CGCGCTG 7

RESULT 159

US-09-990-186-1278
; Sequence 1278, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3

; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1278

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
|||||
Db 4 GCTGTGG 10

RESULT 160

US-09-989-994-1278
; Sequence 1278, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1278

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
|||||
Db 4 GCTGTGG 10

RESULT 161

US-10-087-426-6
; Sequence 6, Application US/10087426
; Publication No. US20020142394A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-23
; CURRENT APPLICATION NUMBER: US/10/087,426
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489


```

; PRIOR FILING DATE: 1996-11-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-11-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-087-426-6

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 11 CGCGCTG 17
    |||||
Db 1 CGCGCTG 7

```

RESULT 162

```

US-10-033-145-36
; Sequence 36, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-36

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GCTGGCC 7
    |||||
Db 3 GCTGGCC 9

```

RESULT 163

```

US-10-033-145-299
; Sequence 299, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05

```

```

; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 299
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-299

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 13 CGCTGTG 19
    |||||
Db 1 CGCTGTG 7

```

RESULT 164

```

US-10-033-145-527/c
; Sequence 527, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 527
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-527

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 15 CTGTGCG 21
    |||||
Db 9 CTGTGCG 3

```

RESULT 165

```

US-10-033-145-702
; Sequence 702, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 702
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-702

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;

```

Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCCCGGC 11
|||||
Db 4 GCCCGGC 10

RESULT 166

US-10-033-145-771
; Sequence 771, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 771
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-771

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCCCGGC 11
|||||
Db 1 GCCCGGC 7

RESULT 167

US-10-033-145-1178/c
; Sequence 1178, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1178
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1178

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
|||||
Db 8 GCGCGGC 2

RESULT 168

US-10-033-145-1502/c
; Sequence 1502, Application US/10033145

Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1502
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1502

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
|||||
Db 10 GCTGTGG 4

RESULT 169

US-10-033-145-1540/c
; Sequence 1540, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1540
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1540

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
|||||
Db 7 GCTGGCC 1

RESULT 170

US-10-033-145-1855/c
; Sequence 1855, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18

```
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1855
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1855

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 GCTGTGG 20
        |||||
Db       9 GCTGTGG 3

RESULT 171
US-10-033-145-1872
; Sequence 1872, Application US/10033145
; Publication No. US200201515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1872
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1872

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCCCGGC 11
        |||||
Db       2 GCCCGGC 8

RESULT 172
US-10-033-145-1908
; Sequence 1908, Application US/10033145
; Publication No. US200201515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1908
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1908

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 GCTGTGG 20
        |||||
Db       9 GCTGTGG 3

RESULT 173
US-10-033-145-2019
; Sequence 2019, Application US/10033145
; Publication No. US200201515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2019
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2019

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 GCTGTGG 20
        |||||
Db       1 GCTGTGG 7

RESULT 174
US-10-150-509-1
; Sequence 1, Application US/10150509
; Publication No. US20020178460A1
; GENERAL INFORMATION:
; APPLICANT: Enikolopov, Grigori N.
; APPLICANT: Mignone, John
; TITLE OF INVENTION: TRANSGENIC MICE EXPRESSING FLUORESCENT
; FILE REFERENCE: 1314.1062-010
; CURRENT APPLICATION NUMBER: US/10/150,509
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: US 09/444,335
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: PCT/US00/31150
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Linker
US-10-150-509-1

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCGCGC 15
        |||||
Db       2 GCGCGC 8

RESULT 175
```

US-10-150-509-1/c
; Sequence 1, Application US/10150509
; Publication No. US20020178460A1
; GENERAL INFORMATION:
; APPLICANT: ENIKOLOPOV, Grigori N.
; APPLICANT: MIGNONE, John
; TITLE OF INVENTION: TRANSGENIC MICE EXPRESSING FLUORESCENT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 1314.1062-010
; CURRENT APPLICATION NUMBER: US/10/150,509
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: US 09/444,335
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: PCT/US00/31150
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Linker
US-10-150-509-1

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGC 15
|||
Db 9 GCGCGC 3

RESULT 176
US-10-094-146-21
; Sequence 21, Application US/10094146
; Publication No. US20020192755A1
; GENERAL INFORMATION:
; APPLICANT: FRANCIS, Kevin P.
; APPLICANT: DOYLE, Timothy C.
; APPLICANT: NAWOTKA, Kevin A.
; TITLE OF INVENTION: METHODS OF SCREENING FOR INTRODUCTION OF DNA INTO A
; TITLE OF INVENTION: TARGET CELL
; FILE REFERENCE: 9400-0015 / PXE-015.US
; CURRENT APPLICATION NUMBER: US/10/094,146
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/274,094
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/292,828
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Asc I linker
US-10-094-146-21

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGC 15
|||
Db 2 GCGCGC 8

RESULT 177
US-10-094-146-21/c
; Sequence 21, Application US/10094146

Publication No. US20020192755A1
; GENERAL INFORMATION:
; APPLICANT: FRANCIS, Kevin P.
; APPLICANT: DOYLE, Timothy C.
; APPLICANT: NAWOTKA, Kevin A.
; TITLE OF INVENTION: METHODS OF SCREENING FOR INTRODUCTION OF DNA INTO A
; TITLE OF INVENTION: TARGET CELL
; FILE REFERENCE: 9400-0015 / PXE-015.US
; CURRENT APPLICATION NUMBER: US/10/094,146
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/274,094
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/292,828
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Asc I linker
US-10-094-146-21

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGC 15
|||
Db 9 GCGCGC 3

RESULT 178
US-10-108-077-6
; Sequence 6, Application US/10108077
; Publication No. US20030036116A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsothe
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTI
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/10/108,077
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-108-077-6

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
|||
Db 1 CGCGCTG 7

RESULT 179
US-10-142-111-23/c
; Sequence 23, Application US/10142111
; Publication No. US20030101495A1

```

; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/142,111
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-142-111-23

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
Db 7 GCTGTGG 1

RESULT 180
US-10-390-045-54/c
; Sequence 54, Application US/10390045
; Publication No. US20030170713A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/10/390,045
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US/09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-390-045-54

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 7 GCTGGCC 1

RESULT 181
US-10-330-627-237
; Sequence 237, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-261/c
; Sequence 261, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-261

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 4 GCTGGCC 10

RESULT 182
US-10-330-627-261/c
; Sequence 261, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-261

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGGCC 13
Db 10 CCGGGCC 4

RESULT 183
US-10-330-627-307/c
; Sequence 307, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564

```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 307
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-307

    Query Match          33.3%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 98;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 7 GCTGGCC 1

RESULT 184
US-10-330-627-308/c
; Sequence 308, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-308

    Query Match          33.3%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 98;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 7 GCTGGCC 1

RESULT 185
US-10-330-627-524
; Sequence 524, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 524
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-524

    Query Match          33.3%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 98;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 7 GCTGGCC 1

RESULT 186
US-10-330-627-621/c
; Sequence 621, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 621
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-621

    Query Match          33.3%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 98;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTGGCCC 8
Db 7 CTTGGCCC 1

RESULT 187
US-10-330-627-1065/c
; Sequence 1065, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1065
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1065

    Query Match          33.3%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 98;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCCCGG 10
Db 7 GGCCCGG 1

RESULT 188
US-10-330-627-1071
; Sequence 1071, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
```

```

; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1071
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1071

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GCTGGGCC 7
        |||||
DB      4 GCTGGGCC 10

```

RESULT 189

```

US-10-330-627-1142
; Sequence 1142, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1142
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1142

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 CCGGGCGC 13
        |||||
DB      3 CCGGGCGC 9

```

RESULT 190

```

US-10-330-627-1149
; Sequence 1149, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1149

```

```

; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1149

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 GCCCGGCC 11
        |||||
DB      4 GCCCGGCC 10

```

RESULT 191

```

US-10-197-019-97/c
; Sequence 97, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MMH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-197-019-97

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GCTGGGCC 7
        |||||
DB      7 GCTGGGCC 1

```

RESULT 192

```

US-10-197-019-108/c
; Sequence 108, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MMH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-197-019-108

```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;

```

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCC 8
|||||
Db 8 CTGGCCC 2

RESULT 193

US-10-257-021-108
; Sequence 108, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Fizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-021-108

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
|||||
Db 3 CGCGCTG 9

RESULT 194

US-10-403-232-143
; Sequence 143, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Qiudeng
; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 143
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-403-232-143

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
|||||
Db 4 GGCGCGC 10

RESULT 195

US-10-422-523-28
; Sequence 28, Application US/10422523
; Publication No. US20040002103A1
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; TITLE OF INVENTION: SYNTHETIC LIGATION REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-15A US
; CURRENT APPLICATION NUMBER: US/10/422,523
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: 09/332,835
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-422-523-28

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
|||||
Db 1 CGCGCTG 7

RESULT 196

US-10-301-875A-10
; Sequence 10, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-10

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGCGC 13
|||||
Db 3 CCGGCGC 9

RESULT 197

US-10-301-875A-11
; Sequence 11, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION


```
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-11

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CCGCGCGC 13
Db      3 CCGCGCGC 9

RESULT 198
US-10-301-875A-19/c
; Sequence 19, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-19

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CCGCGCGC 14
Db      7 CCGCGCGC 1

RESULT 199
US-10-301-875A-20/c
; Sequence 20, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-20

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CCGCGCGC 14
Db      7 CCGCGCGC 1

RESULT 201
US-10-301-875A-27/c
; Sequence 27, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-21

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CCGCGCGC 14
Db      7 CCGCGCGC 1

RESULT 202
US-10-301-875A-21/c
; Sequence 21, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-21

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CCGCGCGC 14
Db      7 CCGCGCGC 1

RESULT 203
US-10-301-875A-27/c
; Sequence 27, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-27
```

US-10-301-875A-27

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGGCC 13
|||||
Db 9 CCGGGCC 3

RESULT 202

US-10-434-479-54/c
; Sequence 54, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMP2A1 GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-434-479-54

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
|||||
Db 7 GCTGGCC 1

RESULT 203

US-10-029-221C-5
; Sequence 5, Application US/10029221C
; Publication No. US20040152077A1
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; APPLICANT: DJAVAKHISHVILI, TSOTNE D.
; APPLICANT: FREY, GERHARD J.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-21
; CURRENT APPLICATION NUMBER: US/10/029,221C
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-029-221C-5

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCGGCTG 17
|||||
Db 1 CCGGCTG 7

RESULT 204

US-10-816-079-27/c
; Sequence 27, Application US/10816079
; Publication No. US20040166527A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Beaudry, Gary A
; APPLICANT: Madden, Stephen L
; APPLICANT: Bertelsen, Arthur H
; TITLE OF INVENTION: Composition and Methods for the Identification of Lung Tumor
; TITLE OF INVENTION: Cells
; FILE REFERENCE: GAO129C2
; CURRENT APPLICATION NUMBER: US/10/816,079
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: 09/663,516
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/080,037
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SAGE tag
US-10-816-079-27

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
|||||
Db 9 CTGTGGC 3

RESULT 205

US-10-631-544-6
; Sequence 6, Application US/10631544
; Publication No. US20040248143A1
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/10/631,544
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10

```
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-631-544-6

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  11 CGCGCTG 17
Db   1 CGCGCTG 7

RESULT 206
US-10-487-934-119
; Sequence 119, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-119

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15 CTGTGGC 21
Db   2 CTGTGGC 8

RESULT 207
US-10-487-934-185
; Sequence 185, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-185

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15 CTGTGGC 21
Db   2 CTGTGGC 8

RESULT 208
US-10-487-934-186
; Sequence 186, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-186

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 CTGGCCC 8
Db   1 CTGGCCC 7

RESULT 209
US-10-398-271-14
; Sequence 14, Application US/10398271
; Publication No. US20050124010A1
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Fu, Pengcheng
; APPLICANT: Latterich, Martin
; APPLICANT: Wei, Jing
; APPLICANT: Levin, Michael
; TITLE OF INVENTION: WHOLE CELL ENGINEERING BY MUTAGENIZING A
; TITLE OF INVENTION: SUBSTANTIAL PORTION OF A STARTING GENOME, COMBINING
; TITLE OF INVENTION: MUTATIONS, AND OPTIONALLY REPEATING
; FILE REFERENCE: 09010-060US1
; CURRENT APPLICATION NUMBER: US/10/398,271
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: PCT/US01/31004
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/US01/19367
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/279,702
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/677,584
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
US-10-398-271-14
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polynucleotide sequence of a restriction site
US-10-398-271-14

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  11  CGCGCTG 17
Db   1  CGCGCTG 7

RESULT 210
US-10-987-549-29/c
; Sequence 29, Application US/10987549
; Publication No. US20050191656A1
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/10/987,549
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/09/479,608
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-29

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15  CTGTGGC 21
Db   10 CTGTGGC 4

RESULT 211
US-10-987-549-30/c
; Sequence 30, Application US/10987549
; Publication No. US20050191656A1
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/10/987,549
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/09/479,608
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-30

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15  CTGTGGC 21
Db   10 CTGTGGC 4

RESULT 212
US-10-987-549-31/c
; Sequence 31, Application US/10987549
; Publication No. US20050191656A1
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/10/987,549
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/09/479,608
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-31

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15  CTGTGGC 21
Db   8  CTGTGGC 2

RESULT 213
US-10-987-549-32/c
; Sequence 32, Application US/10987549
; Publication No. US20050191656A1
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/10/987,549
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/09/479,608
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-32
```

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-32

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
Db 7 CTGTGGC 1

RESULT 214
US-10-727-780A-443
; Sequence 443, Application US/10727780A
; Publication No. US2005023329A1
; GENERAL INFORMATION:
; APPLICANT: Vaish, Narendra
; APPLICANT: Zinnen, Shawn
; APPLICANT: McSwiggen, James
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: Inhibition of Gene Expression Using Duplex Forming
; FILE REFERENCE: 03-1070 (400.139)
; CURRENT FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 772
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 443
; LENGTH: 10
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-727-780A-443

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCCCCG 10
Db 1 GGCCCCG 7

RESULT 215
US-10-727-780A-443/c
; Sequence 443, Application US/10727780A
; Publication No. US2005023329A1
; GENERAL INFORMATION:
; APPLICANT: Vaish, Narendra
; APPLICANT: Zinnen, Shawn
; APPLICANT: McSwiggen, James
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: Inhibition of Gene Expression Using Duplex Forming
; FILE REFERENCE: 03-1070 (400.139)
; CURRENT FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 772
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 443
; LENGTH: 10
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-727-780A-443
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```
Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCCCCG 10
Db 10 GGCCCCG 4

RESULT 216
US-11-035-899-388/c
; Sequence 388, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/11/035,899
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 388:
US-11-035-899-388

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCC 8
Db 8 CTGGCCC 2

RESULT 217
US-11-035-899-389/c
; Sequence 389, Application US/11035899
```

```

; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 389:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 389:
US-11-035-899-389

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCC 8
Db 7 CTGGCCC 1

RESULT 218
US-11-035-899-579
; Sequence 579, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA

```

```

; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 579:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 579:
US-11-035-899-579

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGCCCG 9
Db 4 TGGCCCG 10

RESULT 219
US-11-035-899-580
; Sequence 580, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005

```

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 580:
US-11-035-899-580

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TGGCCCG 9
        |||||
Db       3 TGGCCCG 9

RESULT 220
US-11-035-899-581
; Sequence 581, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
;             Jennifer C. Learmont
;             Dale A. McPhee
;             Suzanne Crowe
;             David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 582:
US-11-035-899-582

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 581:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 581:
US-11-035-899-581

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TGGCCCG 9
        |||||
Db       2 TGGCCCG 8

RESULT 221
US-11-035-899-582
; Sequence 582, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
;             Jennifer C. Learmont
;             Dale A. McPhee
;             Suzanne Crowe
;             David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 582:
US-11-035-899-582
```

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Fred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TGGCCCG 9
| | | | |
Db 1 TGGCCCG 7

Search completed: May 10, 2006, 10:47:25
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:49:30 ; Search time 0.001 Seconds
(without alignments)
19.992 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336
Perfect score: 21
Sequence: 1 gctggccgcgcgtgtggc 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 31 seqs, 476 residues

Total number of hits satisfying chosen parameters: 62

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 38 summaries

Database : pubnewdb1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
C 1	15	71.4	18	1	US-10-310-914A-552603	Sequence 552603,
C 2	14.8	70.5	20	1	US-10-310-914A-1289776	Sequence 1289776,
C 3	14	66.7	20	1	US-10-310-914A-539788	Sequence 539788,
C 4	13.8	65.7	19	1	US-10-310-914A-174538	Sequence 174538,
C 5	13.8	65.7	19	1	US-10-310-914A-490721	Sequence 490721,
C 6	13.8	65.7	19	1	US-10-310-914A-559227	Sequence 559227,
C 7	13.8	65.7	19	1	US-10-310-914A-710539	Sequence 710539,
C 8	13.4	63.8	18	1	US-10-310-914A-232524	Sequence 232524,
C 9	13.4	63.8	18	1	US-10-310-914A-708934	Sequence 708934,
C 10	13.2	62.9	18	1	US-10-310-914A-474217	Sequence 474217,
C 11	13.2	62.9	18	1	US-10-310-914A-1344026	Sequence 1344026,
C 12	12.8	61.0	18	1	US-10-310-914A-52923	Sequence 52923, A
C 13	12.8	61.0	18	1	US-10-310-914A-157006	Sequence 157006,
C 14	12.8	61.0	18	1	US-10-310-914A-388441	Sequence 388441,
C 15	12.8	61.0	18	1	US-10-310-914A-1179628	Sequence 1179628,
C 16	12.4	59.0	16	1	US-11-067-231-131	Sequence 131, App
C 17	11.4	54.3	16	1	US-10-517-151-91	Sequence 91, Appl
C 18	11.2	53.3	19	1	US-10-310-914A-490721	Sequence 490721,
C 19	10.8	51.4	15	1	US-10-858-341-274	Sequence 274, App
C 20	10.8	51.4	15	1	US-10-858-145-274	Sequence 274, App
C 21	10	47.6	11	1	US-10-766-560-14	Sequence 14, Appl
C 22	9.8	46.7	14	1	US-10-980-194-66	Sequence 66, Appl
C 23	9	42.9	11	1	US-11-158-209-473	Sequence 473, App
C 24	9	42.9	12	1	US-11-103-122-25	Sequence 25, Appl
C 25	9	42.9	12	1	US-11-103-122-29	Sequence 29, Appl
C 26	8.8	41.9	12	1	US-11-260-192-15	Sequence 15, Appl
C 27	8.4	40.0	11	1	US-11-158-209-829	Sequence 829, App
C 28	8.4	40.0	11	1	US-11-158-209-1161	Sequence 1161, App
C 29	8.4	40.0	18	1	US-10-310-914A-52923	Sequence 52923, A
C 30	8.2	39.0	15	1	US-10-858-341-274	Sequence 274, App
C 31	8.2	39.0	15	1	US-10-858-145-274	Sequence 274, App
C 32	8.2	39.0	19	1	US-10-310-914A-710539	Sequence 710539,
C 33	8	38.1	10	1	US-10-993-514-36	Sequence 36, Appl

C 34 8 38.1 11 1 US-11-227-086-42 Sequence 42, Appl
35 8 38.1 18 1 US-10-310-914A-388441 Sequence 388441,
36 7.8 37.1 11 1 US-11-158-209-841 Sequence 841, App
C 37 7.8 37.1 19 1 US-10-310-914A-559227 Sequence 559227,
C 38 7.4 35.2 10 1 US-10-913-792-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-310-914A-552603/c
; Sequence 552603, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 552603
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-552603

Query Match 71.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTGGCCCGCGCGC 15
DB 15 GCTGGCCCGCGCGC 1

RESULT 2
US-10-310-914A-1289776/c
; Sequence 1289776, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1289776
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1289776

Query Match 70.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GGCCTGGCGCGCTGTGGC 21
DB 20 GGCCTGGCGCGCTGTGGC 3

RESULT 3
US-10-310-914A-539788/c
; Sequence 539788, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

```
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 539788
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-539788

Query Match      66.7%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCCGCGCG 14
    |||||
Db 17 GCTGGCCCGCGCG 4
    |||||

RESULT 4
US-10-310-914A-174538/c
; Sequence 174538, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174538
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-174538

Query Match      65.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 3.2;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGGCGCGTGTGGC 21
    |||||
Db 18 GCCCGGCGCGTGTGGC 2
    |||||

RESULT 5
US-10-310-914A-490721
; Sequence 490721, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 490721
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-490721
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Query Match      65.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 3.2;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGGCGCGTGTGGC 21
    |||||
Db 3 GCCCGGCGCGCGGGC 19
    |||||

RESULT 6
US-10-310-914A-559227
; Sequence 559227, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 559227
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-559227

Query Match      65.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 3.2;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGGCGCGTGTGGC 21
    |||||
Db 1 GCCUGGCCCGCUGUGGC 17
    |||||

RESULT 7
US-10-310-914A-710539
; Sequence 710539, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 710539
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-710539

Query Match      65.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 3.2;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGGCGCGTGTGGC 21
    |||||
Db 3 GCCCGGCGCGCUCGGC 19
    |||||

RESULT 8
US-10-310-914A-232524/c
; Sequence 232524, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
```

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; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 232524
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-232524

Query Match 63.8%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 3.4;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 4 GGCCCGCGCGCTGT 18
Db 18 GGCCCGCGCGCTGT 4

RESULT 9
US-10-310-914A-708934/c
; Sequence 708934, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 708934
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-708934

Query Match 63.8%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 3.4;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 4 GGCCCGCGCGCTGT 18
Db 18 GGCCCGCGCGCTGT 4

RESULT 10
US-10-310-914A-474217
; Sequence 474217, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 474217
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-474217

Query Match 62.9%; Score 13.2; DB 1; Length 18;
```

```
Best Local Similarity 72.2%; Pred. No. 3.9;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCCCGCGCGCTGTGG 20
Db 1 UGGCCCGCGCGCGCGG 18

RESULT 11
US-10-310-914A-1344026/c
; Sequence 1344026, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1344026
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1344026

Query Match 62.9%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.9;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTGGCCCGCGCGCTGT 18
Db 18 GCGCCCGCGAGCGCAGT 1

RESULT 12
US-10-310-914A-52923/c
; Sequence 52923, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52923
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-52923

Query Match 61.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.8;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTGGCCCGCGCGCTG 17
Db 17 CTGGACCGCGCGCGG 2

RESULT 13
US-10-310-914A-157006/c
; Sequence 157006, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
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; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 157006
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-157006

Query Match          61.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.8;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGCCGGCGCGCTGTG 19
Db 18 GCGCCGGCGCGCTGAG 3

RESULT 14
US-10-310-914A-388441/c
; Sequence 388441, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 388441
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-388441

Query Match          61.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.8;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGCCGGCGCGCTGTG 19
Db 18 GCGCCGGCGCGCTGGG 3

RESULT 15
US-10-310-914A-1179628/c
; Sequence 1179628, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1179628
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1179628

Query Match          61.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.8;
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCCGGCGCGCTGTGG 20
Db 17 GCGCCGGCGCGCTTGG 2

RESULT 16
US-11-067-231-131
; Sequence 131, Application US/11067231
; Publication No. US20050272063A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Katagiri, Toyomasa
; APPLICANT: Fukukawa, Chikako
; TITLE OF INVENTION: METHOD FOR TREATING SYNOVIAL SARCOMA
; FILE REFERENCE: 1254-0272PUS1
; CURRENT APPLICATION NUMBER: US/11/067,231
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 60/407,506
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/486,195
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/JP03/10591
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: PCT/JP2004/002144
; PRIOR FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US 60/598,834
; PRIOR FILING DATE: 2004-08-05
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-11-067-231-131

Query Match          59.0%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 4.5;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGCGCGCGC 15
Db 3 CCGGCGCGCGCGCGC 16

RESULT 17
US-10-517-151-91
; Sequence 91, Application US/10517151
; Publication No. US20060019252A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Furukawa, Yoichi
; APPLICANT: Oncotherapy Science, Inc.
; APPLICANT: The University of Tokyo
; TITLE OF INVENTION: Genes and Polypeptides Relating to Hepatocellular or
; TITLE OF INVENTION: Colorectal Carcinoma
; FILE REFERENCE: 082379-000400US
; CURRENT APPLICATION NUMBER: US/10/517,151
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/386,985
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: WO PCT/JP03/07070
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial
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;
; FEATURE:
; OTHER INFORMATION: an artificially synthesized S-oligonucleotide
US-10-517-151-91

Query Match      54.3%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 7.8;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCGCGCGC 14
    ||||| |||||
Db 3 CTGGTCCGCGCGC 15

RESULT 18
US-10-310-914A-490721/c
; Sequence 490721, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 490721
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-490721

Query Match      53.3%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 13;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGCCCGCGCGCGTGTG 19
    ||||| |||||
Db 19 GCCCGCGCGCGCGG 4

RESULT 19
US-10-858-341-274/c
; Sequence 274, Application US/10858341
; Publication No. US20050287667A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnajad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-09053
; CURRENT APPLICATION NUMBER: US/10/858,341
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(3)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(7)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(13)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-145-274

Query Match      51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 9.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGGCCCGCGCGCGC 15
    ||||| |||||
Db 15 CCGGCCCGCGCGCGC 2

RESULT 20
US-10-858-145-274/c
; Sequence 274, Application US/10858145
; Publication No. US20060073596A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnajad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: PRONAI-09054
; CURRENT APPLICATION NUMBER: US/10/858,145
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(3)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(7)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(13)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-145-274

Query Match      51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 9.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGGCCCGCGCGCGC 15
    ||||| |||||
Db 15 CCGGCCCGCGCGCGC 2

RESULT 21
US-10-766-560-14
; Sequence 14, Application US/10766560
; Publication No. US20050281837A1
; GENERAL INFORMATION:
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Bartoloni, Antonella
```

```
;
; LOCATION: (7)..(7)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(13)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-341-274

Query Match      51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 9.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGGCCCGCGCGCGC 15
    ||||| |||||
Db 15 CCGGCCCGCGCGCGC 2

RESULT 20
US-10-858-145-274/c
; Sequence 274, Application US/10858145
; Publication No. US20060073596A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnajad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: PRONAI-09054
; CURRENT APPLICATION NUMBER: US/10/858,145
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(3)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(7)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(13)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-145-274

Query Match      51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 9.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGGCCCGCGCGCGC 15
    ||||| |||||
Db 15 CCGGCCCGCGCGCGC 2

RESULT 21
US-10-766-560-14
; Sequence 14, Application US/10766560
; Publication No. US20050281837A1
; GENERAL INFORMATION:
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Bartoloni, Antonella
```

; TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE POLYPEPTIDES WITH ALTERED TOXICITY USEFUL
; TITLE OF INVENTION: PREPARATION OF AN ANTIPERTUSSIS VACCINE

; FILE REFERENCE: 002441.00076
; CURRENT APPLICATION NUMBER: US/10/766,560
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/261,668
; PRIOR FILING DATE: 1994-06-17
; PRIOR APPLICATION NUMBER: US 08/012,243
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/265,742
; PRIOR FILING DATE: 1988-11-01
; PRIOR APPLICATION NUMBER: ITALY 22481 A/87
; PRIOR FILING DATE: 1987-11-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Bordetella pertussis
US-10-766-560-14

Query Match 47.6%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGCGCGCT 16
|||||
DB 2 CCGGCGCGCT 11

RESULT 22

US-10-980-194-66/c
; Sequence 66, Application US/10980194
; Publication No. US20050250120A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BUCHRIESEN-BROSCH, ROLAND
; APPLICANT: BILLIAULT, ALAIN
; APPLICANT: GARNIER, THIERRY
; TITLE OF INVENTION: DELETED SEQUENCES IN M. BOVIS BCG/M. BOVIS OR M.
; TITLE OF INVENTION: TUBERCULOSIS, METHOD FOR DETECTING MYCOBACTERIA USING
; TITLE OF INVENTION: THESE SEQUENCES AND VACCINES
; FILE REFERENCE: 05394.0013-01000
; CURRENT APPLICATION NUMBER: US/10/980,194
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 09/936,523
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: PCT/FR00/00637
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 66
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-980-194-66

Query Match 46.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 13;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTGCCCCCGCGC 14
|||||
DB 13 CCGCCCCCGCGT 1

RESULT 23

US-11-158-209-473/c
; Sequence 473, Application US/11158209
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn

; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 473
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-473

Query Match 42.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGCGCTG 17
|||||
DB 9 GCGCGCGCTG 1

RESULT 24

US-11-103-122-25/c
; Sequence 25, Application US/11103122
; Publication No. US20050282190A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Hua
; APPLICANT: Lis, John T.
; TITLE OF INVENTION: MODULAR DESIGN AND CONSTRUCTION OF NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES, APTAMER-DERIVED NUCLEIC ACID CONSTRUCTS, RNA
; TITLE OF INVENTION: SCAFFOLDS, THEIR EXPRESSION, AND METHODS OF USE
; FILE REFERENCE: 19603/4491
; CURRENT APPLICATION NUMBER: US/11/103,122
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: 60/560,895
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: functional
; OTHER INFORMATION: element N3
US-11-103-122-25

Query Match 42.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTGGC 21
|||||
DB 9 CGCTGTGGC 1

RESULT 25

US-11-103-122-29/c
; Sequence 29, Application US/11103122
; Publication No. US20050282190A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Hua
; APPLICANT: Lis, John T.
; TITLE OF INVENTION: MODULAR DESIGN AND CONSTRUCTION OF NUCLEIC ACID

```

; TITLE OF INVENTION: MOLECULES, APTAMER-DERIVED NUCLEIC ACID CONSTRUCTS, RNA
; FILE REFERENCE: 19603/4491
; CURRENT APPLICATION NUMBER: US/11/103,122
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: 60/560,895
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: functional
; OTHER INFORMATION: element N3
US-11-103-122-29

Query Match      42.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CGCTGTGGC 21
        |||||
DB       9 CGCTGTGGC 1

RESULT 26
US-11-260-192-15/c
; Sequence 15, Application US/11260192
; Publication No. US20060067934A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, Craig A.
; APPLICANT: GOODWIN, Raymond G.
; APPLICANT: BECKMANN, Patricia M.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND -BETA RECEPTORS
; FILE REFERENCE: A8466
; CURRENT APPLICATION NUMBER: US/11/260,192
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US/10/420,785
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 09/758,124
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 08/953,268
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: US 08/555,629
; PRIOR FILING DATE: 1995-11-09
; PRIOR APPLICATION NUMBER: US 08/468,453
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/038,765
; PRIOR FILING DATE: 1993-03-13
; PRIOR APPLICATION NUMBER: US 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: US 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: US 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: US 07/403,241
; PRIOR FILING DATE: 1989-09-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-Terminus of human TNF receptor including restriction
; OTHER INFORMATION: endonuclease cleavage sites
US-11-260-192-15

Query Match      41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

; TITLE OF INVENTION: MOLECULES, APTAMER-DERIVED NUCLEIC ACID CONSTRUCTS, RNA
; FILE REFERENCE: 19603/4491
; CURRENT APPLICATION NUMBER: US/11/103,122
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: 60/560,895
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: functional
; OTHER INFORMATION: element N3
US-11-103-122-29

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 CCGCGCGCTGT 18
        |||||
DB     12 CCGCGCGAGTTGT 1

RESULT 27
US-11-158-209-829
; Sequence 829, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 829
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-829

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 GCGCTGTGGC 21
        |||||
DB       2 GCGCTGTGGC 11

RESULT 28
US-11-158-209-1161
; Sequence 1161, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 1161
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-1161

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 GCTGGCCCGG 10
| | | | | | |
Db 1 GGTGGCCCGG 10

Query Match 39.0%; Score 8.2; DB 1; Length 15;
Best Local Similarity 76.9%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 3; Indels

```

RESULT 29
US-10-310-914A-52923
; Sequence 52923, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically d
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,9
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 52923
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-52923

```

Query Match 40.0%; Score 8.4; DB 1; Length 18;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CGGCGCGCTG 17
|||
Db 2 CGGCGCGCCG 11

```

? SEQ-NAME: Placentin version 3.2
? SEQ ID NO 274
? LENGTH: 15
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetic
? FEATURE:
? NAME/KEY: modified_base
? LOCATION: (3)..(3)
? OTHER INFORMATION: methylated C nucleotide
? FEATURE:
? NAME/KEY: modified_base
? LOCATION: (5)..(5)
? OTHER INFORMATION: methylated C nucleotide
? FEATURE:
? NAME/KEY: modified_base
? LOCATION: (7)..(7)
? OTHER INFORMATION: methylated C nucleotide
? FEATURE:
? NAME/KEY: modified_base
? LOCATION: (13)..(13)
? OTHER INFORMATION: methylated C nucleotide
? US-10-858-145-274

```

Query Match 39.0%; Score 8.2; DB 1; Length 15;
Best Local Similarity 76.9%; Pred. No. 33;
Matches 10: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

PROGRAM: ATTACCAAT_SEQUENCE
FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: modified_base
LOCATION: (3)..(3)
OTHER INFORMATION: methylated C nucleotide
FEATURE:
NAME/KEY: modified_base
LOCATION: (5)..(5)
OTHER INFORMATION: methylated C nucleotide
FEATURE:
NAME/KEY: modified_base
LOCATION: (7)..(7)
OTHER INFORMATION: methylated C nucleotide
FEATURE:
NAME/KEY: modified_base
LOCATION: (13)..(13)
OTHER INFORMATION: methylated C nucleotide
US-10-858-341-274

```

```

RESULT 32
US-10/310-914A-710539/c
: Sequence 710539, Application US/10310914A
: Publication No. US2006000332A1
: GENERAL INFORMATION:
: APPLICANT: Bentwich, Isaac
: APPLICANT: Shlier, Kvuzat
: TITLE OF INVENTION: Bioinformatically detected
: FILE OF INVENTION: uses thereof
: FILE REFERENCE: 06087.0200.CPUS01
: CURRENT APPLICATION NUMBER: US/10/310,914A
: CURRENT FILING DATE: 2002-12-06
: NUMBER OF SEQ ID NOS: 1389402
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 710539

```


; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-710539

Query Match 39.0%; Score 8.2; DB 1; Length 19;
Best Local Similarity 76.9%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTGGCGCGCGC 13
||| ||| ||| ||| |||
Db 13 GCGCGCGCGCGC 1

RESULT 33
US-10-993-514-36
; Sequence 36, Application US/10993514
; Publication No. US20050250122A1

; GENERAL INFORMATION:
; APPLICANT: Aerssens, Jeroen
; APPLICANT: Athanasidou, Maria
; APPLICANT: Brain, Carlos
; APPLICANT: Cohen, Nadine
; APPLICANT: Bain, Bradley
; APPLICANT: Denton, R. Rex
; APPLICANT: Judson, Richard S.
; APPLICANT: Ozdemir, Vural
; APPLICANT: Reed, Carol R.
; TITLE OF INVENTION: APO4 Genetic Markers Associated with Progression of Alzheimer's
; TITLE OF INVENTION: Disease
; FILE REFERENCE: 2300.0080001
; CURRENT APPLICATION NUMBER: US/10/993,514
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: US 60/524,467
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer Extension Oligo for Detecting Alleles at PSS in
; OTHER INFORMATION: Haplotypes Comprising Preferred Embodiments of Progression
; OTHER INFORMATION: Markers I and Progression Markers II
US-10-993-514-36

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGCTGTG 19
||| ||| ||| ||| |||
Db 3 GCGCTGTG 10

RESULT 34
US-11-227-086-42/c
; Sequence 42, Application US/11227086
; Publication No. US20060084117A1

; GENERAL INFORMATION:
; APPLICANT: XU, YONG
; APPLICANT: YAO, YONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: T1530-00214
; CURRENT APPLICATION NUMBER: US/11/227,086
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: 09/989,497
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29

; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-11-227-086-42

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGCGCGCGC 15
||| ||| ||| ||| |||
Db 9 CGCGCGCGC 2

RESULT 35

US-10-310-914A-388441
; Sequence 388441, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 388441
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-388441

Query Match 38.1%; Score 8; DB 1; Length 18;
Best Local Similarity 68.8%; Pred. No. 42;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CCCGCGCGCTGTGCGC 21
||| ||| ||| ||| ||| |||
Db 3 CCCAGCGCGCCGCGGC 18

RESULT 36
US-11-158-209-841
; Sequence 841, Application US/11158209
; Publication No. US2006008852A1

; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 841

```
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-841

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCGGGCGCGCT 16
   ||| |||||
Db 1 CCCAACGGCGCT 11

RESULT 37
US-10-310-914A-559227/c
; Sequence 559227, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 559227
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-559227

Query Match      37.1%; Score 7.8; DB 1; Length 19;
Best Local Similarity 81.8%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGGC 11
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Db 11 GCGGGCCAGGC 1

RESULT 38
US-10-913-792-6/c
; Sequence 6, Application US/10913792
; Publication No. US20060031957A1
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Lal, Raj Kishori
; APPLICANT: Agnihotri, Arun Kumar
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Dwivedi, Samresh
; APPLICANT: Misra, Hari Om
; APPLICANT: Dhawan, Om Parkash
; APPLICANT: Kakra, Alok
; APPLICANT: Singh, Aparbal
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Singh, Saudan
; APPLICANT: Patra, Dharani Dhar
; APPLICANT: Agarwal, Shilpi
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Gupta, Anil Kumar
; APPLICANT: Gupta, Moti Lal
; APPLICANT: Chandra, Ram
; TITLE OF INVENTION: DISTINCT TYPE CULTIVAR OF OCIMUM BASILICUM "CIM-SAUMYA"
; FILE REFERENCE: 11378.64US01
; CURRENT APPLICATION NUMBER: US/10/913,792
; CURRENT FILING DATE: 2004-08-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6

; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Operon Primer OPA 06
US-10-913-792-6

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGGCGGC 15
   ||||| ||
Db 9 CCGGGCTGC 1

Search completed: May 10, 2006, 10:49:31
Job time : 1 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:46:22 ; Search time 0.001 Seconds
(without alignments)
331.422 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336

Perfect score: 21

Sequence: 1 gctgcccgcgcgtgtggc 21

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 0.5

Searched: 741 segs, 7891 residues

Total number of hits satisfying chosen parameters: 1482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 813 summaries

Database : ngsdb1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	12.8	61.0	17	1	ADL47206
3	12.8	61.0	17	1	ADW54550
4	12.4	59.0	16	1	ADL91730
5	12.4	59.0	17	1	ADL46910
6	12.4	59.0	17	1	ADL46909
7	12.2	58.1	17	1	AA776338
8	12.2	58.1	17	1	AAW54140
9	12.2	58.1	17	1	AAW33584
10	12.2	58.1	17	1	AA719706
11	12.2	58.1	17	1	ADW02886
12	12.2	58.1	17	1	ABW71913
13	12.2	58.1	17	1	ABW295400
14	12.2	58.1	17	1	ABD19452
15	12	57.1	15	1	AA739559
16	12	57.1	15	1	ABW45841
17	11.8	56.2	15	1	AAW45245
18	11.4	54.3	16	1	ADW44902
19	11	52.4	15	1	AAQ57977
20	10.8	51.4	15	1	AAV02387
21	10.8	51.4	15	1	AAW46831
22	10.8	51.4	15	1	AAW46943
23	10.8	51.4	15	1	AAW45244
24	10.8	51.4	15	1	AAW46942
25	10.8	51.4	15	1	AAW45246
26	10.8	51.4	15	1	AAW46830
27	10.8	51.4	15	1	AAW97374
28	10.4	49.5	13	1	AAW76242
29	10.4	49.5	13	1	AAW54032
30	10.4	49.5	13	1	AAW33476
31	10.4	49.5	13	1	AAW19598
32	10.4	49.5	13	1	AAW95292
33	10.4	49.5	13	1	ABD19276

34	10.4	49.5	14	1	AAF88189	Murine CSF-1 speci
35	10.4	49.5	14	1	AAF88184	Human CSF-1 derive
36	10.4	49.5	14	1	ADH02741	B. anthracis ATR/h
37	10.2	48.6	15	1	AAW97374	PCR primer #1 for
38	10	47.6	12	1	AAW60901	Conjugate forming
39	9.8	46.7	14	1	AAW62477	M. tuberculosis alp
40	9.8	46.7	14	1	AAW24230	M. tuberculosis al
41	9.8	46.7	14	1	ADM68001	Asci reverse ligat
42	9.8	46.7	14	1	ADM67994	Oligonucleotide As
43	9.8	46.7	14	1	ADW85199	Alcohol dehydrogen
44	9.4	44.8	11	1	AAW54772	Endothelial nitric
45	9.4	44.8	11	1	AAW34219	Human adenosine re
46	9.4	44.8	11	1	AAW20341	Human endothelial
47	9.4	44.8	11	1	ABW69628	Human skin EST 741
48	9.4	44.8	11	1	ABW69375	Human skin EST 716
49	9.4	44.8	11	1	ABW68029	Human skin EST 581
50	9.4	44.8	11	1	ABW26035	Human endothelial
51	9.4	44.8	11	1	ABD19675	Human endothelial
52	9.4	44.8	11	1	ADQ33478	Human facial skin-
53	9.4	44.8	12	1	ABW21184	Oligonucleotide pr
54	9.4	44.8	12	1	ABW04204	Oligonucleotide pr
55	9.4	44.8	12	1	ABW90189	Oligonucleotide pr
56	9.4	44.8	12	1	ADM67995	Oligonucleotide As
57	9.4	44.8	12	1	ADW44241	Human melanoma dif
58	9.4	44.8	13	1	ABC66097	Oligonucleotide SE
59	9.4	44.8	13	1	ABC66096	Oligonucleotide SE
60	9.4	44.8	13	1	ADW63462	Human Her2 class I
61	9.4	44.8	13	1	ADR33857	Human nicking agen
62	9.4	44.8	13	1	ADR33858	Human nicking agen
63	9.4	44.8	13	1	ADR33855	Human nicking agen
64	9.4	44.8	13	1	ADR33856	Sequence of portio
65	9.2	43.8	15	1	AAQ57977	Human dendritic ce
66	9	42.9	10	1	AAZ85441	Metastatic breast
67	9	42.9	10	1	AAZ85441	Metastatic breast
68	9	42.9	10	1	AAZ84999	Metastatic breast
69	9	42.9	10	1	AAZ81584	Metastatic breast
70	9	42.9	10	1	AAH64571	Human ubiquitously
71	9	42.9	10	1	AAH64570	Human ubiquitously
72	9	42.9	10	1	AAH64063	Human ubiquitously
73	9	42.9	10	1	ABW78444	Human Th1 cell pre
74	9	42.9	10	1	ABW30052	Vancomycin-resista
75	9	42.9	11	1	ABW69619	Human skin EST 740
76	9	42.9	11	1	ADQ35656	Human hair-bearing
77	9	42.9	12	1	ABW29997	Hepatitis B virus
78	9	42.9	12	1	AEA14698	Immunostimulatory
79	8.8	41.9	12	1	AAW55523	Primer PBS 777-23
80	8.8	41.9	12	1	ABW14022	DNA adaptor sequen
81	8.8	41.9	12	1	ABW14028	DNA sequence of a
82	8.8	41.9	12	1	ADW47248	Oligonucleotide us
83	8.8	41.9	12	1	ADU73707	Connective tissue
84	8.8	41.9	12	1	ADW92309	E. coli RNA RT-PC
85	8.8	41.9	12	1	ADW92172	Universal bacteria
86	8.8	41.9	12	1	ADW223854	Human SNP detectio
87	8.8	41.9	12	1	ADW223918	Human SNP detectio
88	8.8	41.9	12	1	ADW223906	IGFBP2 oligonucleo
89	8.8	41.9	15	1	AAW45246	IGFBP2 oligonucleo
90	8.4	40.0	10	1	AAQ88580	Human mitochondria
91	8.4	40.0	10	1	AAW32927	Sequence of first
92	8.4	40.0	10	1	AAW32911	Sequence of a targ
93	8.4	40.0	10	1	AAW32930	5'-fluorescein-lab
94	8.4	40.0	10	1	AAW207924	8-oxo-dGTPase onco
95	8.4	40.0	10	1	AAW54917	C/EBP-beta antisen
96	8.4	40.0	10	1	AAW28340	Lung cancer indica
97	8.4	40.0	10	1	AAW34364	Human adenosine re
98	8.4	40.0	10	1	AAW77611	Human dendritic ce
99	8.4	40.0	10	1	AAW285164	Metastatic breast
100	8.4	40.0	10	1	AAW285539	Metastatic breast
101	8.4	40.0	10	1	AAW281510	Metastatic breast
102	8.4	40.0	10	1	AAW285260	Metastatic breast
103	8.4	40.0	10	1	AAW283876	Metastatic breast
104	8.4	40.0	10	1	AAW281514	Metastatic breast
105	8.4	40.0	10	1	AAW741184	Human monocyte and
106	8.4	40.0	10	1	AAW20486	Human C/EBP polynu

C 253	8	38.1	10	1	ABK30053	Vancomycin-resista	C 326	7.8	37.1	11	1	ABV71986	Human skin EST 977
C 254	8	38.1	10	1	AAL39799	SMOH polymorphism	327	7.8	37.1	11	1	ABV66078	Human skin EST 386
C 255	8	38.1	10	1	ADG28253	Human Myo/V1 prote	328	7.8	37.1	11	1	ABV68518	Human skin EST 630
C 256	8	38.1	10	1	ADG28195	Human Myo/V1 prote	329	7.8	37.1	11	1	ABV68764	Human skin EST 655
C 257	8	38.1	10	1	ADG28266	Human Myo/V1 prote	330	7.8	37.1	11	1	ABV69433	Human skin EST 821
C 258	8	38.1	10	1	ADG28042	Human Myo/V1 prote	331	7.8	37.1	11	1	ABV70501	Human skin EST 728
C 259	8	38.1	10	1	AAD47803	Human GNB3 gene po	332	7.8	37.1	11	1	ABV71731	Human skin EST 821
C 260	8	38.1	10	1	ACA94569	DNA tag from human	333	7.8	37.1	11	1	ABV63204	Human skin EST 951
C 261	8	38.1	10	1	ABD296226	Human C/EBP antise	334	7.8	37.1	11	1	ABV65901	Human skin EST 990
C 262	8	38.1	10	1	ABD20135	Human C/EBPN DNA f	335	7.8	37.1	11	1	ABV65801	Human skin EST 358
C 263	8	38.1	10	1	ADK13021	Human glioma endot	336	7.8	37.1	11	1	ABV69385	Human skin EST 717
C 264	8	38.1	10	1	ADK13021	Breast cancer deta	337	7.8	37.1	11	1	ABV69394	Human skin EST 718
C 265	8	38.1	11	1	AZ18995	Murine MRL SAGE ta	338	7.8	37.1	11	1	ABV69452	Human skin EST 723
C 266	8	38.1	11	1	AZ18995	Murine MRL SAGE ta	339	7.8	37.1	11	1	ABV70625	Human skin EST 841
C 267	8	38.1	11	1	AZ18995	Murine MRL SAGE ta	340	7.8	37.1	11	1	ABV62244	Human skin EST 30
C 268	8	38.1	11	1	AZ18995	Murine C57BL/6 SAG	341	7.8	37.1	11	1	ABV62740	Human skin EST 526
C 269	8	38.1	11	1	AAX54962	C/EBP-beta antisen	342	7.8	37.1	11	1	ABV63080	Human skin EST 866
C 270	8	38.1	11	1	AAX23380	HLA-A, HLA-B, HLA-	343	7.8	37.1	11	1	ABV63395	Human skin EST 174
C 271	8	38.1	11	1	AAX34409	Human adenosine re	344	7.8	37.1	11	1	ABV66320	Human skin EST 410
C 272	8	38.1	11	1	ABQ87660	Human C/EBP polyu	345	7.8	37.1	11	1	ABV66933	Human skin EST 594
C 273	8	38.1	11	1	ABV69823	Human skin stress/	346	7.8	37.1	11	1	ABV668596	Human skin EST 471
C 274	8	38.1	11	1	ABV62316	Human skin EST 760	347	7.8	37.1	11	1	ABV70229	Human skin EST 638
C 275	8	38.1	11	1	ABV67208	Human skin EST 102	348	7.8	37.1	11	1	ABV63481	Human skin EST 801
C 276	8	38.1	11	1	ABV69737	Human skin EST 499	349	7.8	37.1	11	1	ABV63732	Human skin EST 126
C 277	8	38.1	11	1	ABV68966	Human skin EST 752	350	7.8	37.1	11	1	ABV65830	Human skin EST 151
C 278	8	38.1	11	1	ABV68820	Human skin EST 675	351	7.8	37.1	11	1	ABV62808	Human skin EST 361
C 279	8	38.1	11	1	ABV62402	Human skin EST 188	352	7.8	37.1	11	1	ABV70161	Human skin EST 594
C 280	8	38.1	11	1	ABV65601	Human skin EST 338	353	7.8	37.1	11	1	ABV67671	Human skin EST 794
C 281	8	38.1	11	1	ABV68097	Human skin EST 588	354	7.8	37.1	11	1	ABV68707	Human skin EST 545
C 282	8	38.1	11	1	ABV70503	Human skin EST 828	355	7.8	37.1	11	1	ABV66603	Human skin EST 649
C 283	8	38.1	11	1	ABV33082	Human skin EST 828	356	7.8	37.1	11	1	ADA25627	Human skin EST 438
C 284	8	38.1	11	1	ABV7604	Human skin EST 868	357	7.8	37.1	11	1	ADH77004	Allele-specific hu
C 285	8	38.1	11	1	ABZ96225	Human C/EBP antise	358	7.8	37.1	11	1	ADQ36024	Photodamage detect
C 286	8	38.1	11	1	ABD20134	Human C/EBPN DNA f	359	7.8	37.1	11	1	ADQ36024	Human photodamage
C 287	8	38.1	11	1	ADQ35029	Human facial skin-	360	7.8	37.1	11	1	ADQ32015	Human hair-bearing
C 288	8	38.1	11	1	ADQ31967	Human facial skin-	361	7.8	37.1	11	1	ADQ32041	Human facial skin-
C 289	8	38.1	11	1	ADQ33912	Human facial skin-	362	7.8	37.1	11	1	ADQ32145	Human facial skin-
C 290	8	38.1	11	1	ADP25610	5' Aesci site oligo	363	7.8	37.1	11	1	ADQ32145	Human facial skin-
C 291	8	38.1	12	1	ADP42386	Oligonucleotide SE	364	7.8	37.1	11	1	ADQ34751	Human facial skin-
C 292	8	38.1	17	1	AAT76338	Human fibronectin	365	7.8	37.1	11	1	ADQ34112	Human facial skin-
C 293	8	38.1	17	1	AAX54140	Human fibronectin	366	7.8	37.1	11	1	ADQ34112	Oligonucleotide #1
C 294	8	38.1	17	1	AAX33584	Low adenosine anti	367	7.8	37.1	11	1	ADT79188	Oligonucleotide #1
C 295	8	38.1	17	1	AAF19706	Human fibronectin	368	7.8	37.1	12	1	AAK55033	C/EBP-beta antisen
C 296	8	38.1	17	1	ABZ95400	Human fibronectin	369	7.8	37.1	12	1	AAA34480	Human adenosine re
C 297	8	38.1	17	1	ABD19452	Human fibronectin	370	7.8	37.1	12	1	AAZ20602	Human C/EBP polyu
C 298	7.8	37.1	11	1	AAX54772	Endothelial nitric	371	7.8	37.1	12	1	ABZ96296	Human C/EBP antise
C 299	7.8	37.1	11	1	AAK34219	Human adenosine re	372	7.8	37.1	12	1	ABD20205	Human C/EBPN DNA f
C 300	7.8	37.1	11	1	AAF20341	Human endothelial	373	7.8	37.1	15	1	ABL45841	Human EDG6 gene al
C 301	7.8	37.1	11	1	ABV68029	Human skin EST 581	374	7.8	37.1	15	1	AAF45245	Human EDG6 gene al
C 302	7.8	37.1	11	1	ABZ96035	Human endothelial	375	7.8	37.1	17	1	ADL47206	Human EDG6 gene al
C 303	7.8	37.1	11	1	ABD19675	Human endothelial	376	7.8	37.1	17	1	ADL46910	Human EDG6 gene al
C 304	7.8	37.1	11	1	ADQ33478	Human facial skin-	377	7.8	37.1	17	1	ADL46909	Human EDG6 gene al
C 305	7.8	37.1	11	1	ABV68955	Human skin EST 674	378	7.4	35.2	10	1	AAZ52054	Human EDG6 gene al
C 306	7.8	37.1	11	1	ADQ34850	Human facial skin-	379	7.4	35.2	10	1	AAZ52054	Human EDG6 gene al
C 307	7.8	37.1	11	1	AAV61050	Nucleotide sequenc	380	7.4	35.2	10	1	AAQ96790	Human EDG6 gene al
C 308	7.8	37.1	11	1	AAV58720	Nucleotide sequenc	381	7.4	35.2	10	1	AAQ96790	Human EDG6 gene al
C 309	7.8	37.1	11	1	AAZ38076	Human FKHL7 DNA fr	382	7.4	35.2	10	1	AAZ29308	HIV-1 NL4-3 nef ge
C 310	7.8	37.1	11	1	AAZ65615	Multiplex analysis	383	7.4	35.2	10	1	AAV38304	5'-primer for mam
C 311	7.8	37.1	11	1	ADL15332	Human allele speci	384	7.4	35.2	10	1	AAV35965	MDR Spt junction s
C 312	7.8	37.1	11	1	ABQ15764	Allele-specific fa	385	7.4	35.2	10	1	AAV35965	Primer used in RAP
C 313	7.8	37.1	11	1	ABQ87418	Human skin stress/	386	7.4	35.2	10	1	AAV35949	Primer used in RAP
C 314	7.8	37.1	11	1	ABQ86369	Human skin stress/	387	7.4	35.2	10	1	AAV18606	p53 serial analysi
C 315	7.8	37.1	11	1	ABQ87096	Human skin stress/	388	7.4	35.2	10	1	AAV77471	US5912147 primer 1
C 316	7.8	37.1	11	1	ABQ86824	Human skin stress/	389	7.4	35.2	10	1	AAV77472	US5912147 primer 1
C 317	7.8	37.1	11	1	ABQ86321	Human skin stress/	390	7.4	35.2	10	1	AAV77472	US5912147 primer 1
C 318	7.8	37.1	11	1	ABV69665	Human skin EST 745	391	7.4	35.2	10	1	AAV54874	C/EBP-beta antisen
C 319	7.8	37.1	11	1	ABV67742	Human skin EST 552	392	7.4	35.2	10	1	AAV54874	Leukotriene C4 syn
C 320	7.8	37.1	11	1	ABV64310	Human skin EST 209	393	7.4	35.2	10	1	AAV86209	SAGE tag used to i
C 321	7.8	37.1	11	1	ABV64565	Human skin EST 235	394	7.4	35.2	10	1	AAV86209	SAGE tag used to i
C 322	7.8	37.1	11	1	ABV71376	Human skin EST 916	395	7.4	35.2	10	1	AAV34321	Human adenosine re
C 323	7.8	37.1	11	1	ABV66441	Human skin EST 422	396	7.4	35.2	10	1	AAZ77583	Human dendritic ce
C 324	7.8	37.1	11	1	ABV70902	Human skin EST 868	397	7.4	35.2	10	1	AAZ79675	Human dendritic ce
C 325	7.8	37.1	11	1	ABV71153	Human skin EST 893	398	7.4	35.2	10	1	AAZ85628	Human dendritic ce

545	7.4	35.2	10	1	ADR27909	Human VE-statin ex	618	7	33.3	10	1	AA278274	Human dendritic ce
546	7.4	35.2	10	1	AD576996	Breast cancer dete	c 619	7	33.3	10	1	AA279074	Human dendritic ce
547	7.4	35.2	10	1	AD576954	Breast cancer dete	c 620	7	33.3	10	1	AA278343	Human dendritic ce
548	7.4	35.2	10	1	AD577203	Breast cancer dete	c 621	7	33.3	10	1	AA277871	Human dendritic ce
549	7.4	35.2	10	1	AD578056	Breast cancer dete	c 622	7	33.3	10	1	AA279427	Human dendritic ce
550	7.4	35.2	10	1	AD577992	Breast cancer dete	c 623	7	33.3	10	1	AA279444	Human dendritic ce
551	7.4	35.2	10	1	AD577293	Breast cancer dete	c 624	7	33.3	10	1	AA278099	Human dendritic ce
552	7.4	35.2	10	1	AD577023	Breast cancer dete	c 625	7	33.3	10	1	AA279480	Human dendritic ce
553	7.4	35.2	10	1	AD576953	Breast cancer dete	c 626	7	33.3	10	1	AA277608	Human dendritic ce
554	7.4	35.2	10	1	AD576221	Breast cancer dete	c 627	7	33.3	10	1	AA282905	Metastatic breast
555	7.4	35.2	10	1	AD578162	Breast cancer dete	c 628	7	33.3	10	1	AA283064	Metastatic breast
556	7.4	35.2	10	1	AD576799	Breast cancer dete	c 629	7	33.3	10	1	AA283387	Metastatic breast
557	7.4	35.2	10	1	AD577335	Breast cancer dete	c 630	7	33.3	10	1	AA285889	Metastatic breast
558	7.4	35.2	10	1	AD576995	Breast cancer dete	c 631	7	33.3	10	1	AA282125	Metastatic breast
559	7.4	35.2	10	1	AD576366	Breast cancer dete	c 632	7	33.3	10	1	AA282631	Metastatic breast
560	7.4	35.2	10	1	AD578102	Breast cancer dete	c 633	7	33.3	10	1	AA282867	Metastatic breast
561	7.4	35.2	10	1	AD577022	Breast cancer dete	c 634	7	33.3	10	1	AA281312	Metastatic breast
562	7.4	35.2	10	1	AD577202	Breast cancer dete	c 635	7	33.3	10	1	AA280814	Metastatic breast
563	7.4	35.2	10	1	ADU18767	Hypoxia-related tu	c 636	7	33.3	10	1	AA281489	Metastatic breast
564	7.4	35.2	10	1	ADU19573	Hypoxia-related tu	c 637	7	33.3	10	1	AA285240	Metastatic breast
565	7.4	35.2	10	1	ADU19354	Hypoxia-related tu	c 638	7	33.3	10	1	AA285596	Metastatic breast
566	7.4	35.2	10	1	ADU19103	Hypoxia-related tu	c 639	7	33.3	10	1	AA282633	Metastatic breast
567	7.4	35.2	10	1	ADU19820	Hypoxia-related tu	c 640	7	33.3	10	1	AA285912	Metastatic breast
568	7.4	35.2	10	1	ADU18946	Hypoxia-related tu	c 641	7	33.3	10	1	AA282082	Metastatic breast
569	7.4	35.2	10	1	ADU78581	Rice oligonucleoti	c 642	7	33.3	10	1	AA283360	Metastatic breast
570	7.4	35.2	10	1	ADW73862	Arm 1 oligo includ	c 643	7	33.3	10	1	AA284570	Metastatic breast
571	7.4	35.2	10	1	ADY54310	Phyllanthus amarus	c 644	7	33.3	10	1	AA284917	Metastatic breast
572	7.4	35.2	10	1	ADZ231138	Human SNP detectio	c 645	7	33.3	10	1	AA286247	Metastatic breast
573	7.4	35.2	10	1	ADZ24419	Human SNP detectio	c 646	7	33.3	10	1	AA281044	Metastatic breast
574	7.4	35.2	10	1	ADZ23793	Human SNP detectio	c 647	7	33.3	10	1	AA281638	Metastatic breast
575	7.4	35.2	10	1	ADZ24430	Human SNP detectio	c 648	7	33.3	10	1	AA281933	Metastatic breast
576	7.4	35.2	10	1	ADZ67686	INVADER oligonucle	c 649	7	33.3	10	1	AA284040	Metastatic breast
577	7.4	35.2	10	1	ADZ76869	Krishna tulsi DNA	c 650	7	33.3	10	1	AA286609	Metastatic breast
578	7.4	35.2	10	1	AEA90141	Artemisia annua ar	c 651	7	33.3	10	1	AA282698	Metastatic breast
579	7.4	35.2	11	1	ABV69801	Human skin EST 758	c 652	7	33.3	10	1	AA284042	Metastatic breast
580	7.4	35.2	11	1	ABV62380	Human skin EST 166	c 653	7	33.3	10	1	AA284284	Metastatic breast
581	7.4	35.2	11	1	ADZ56110	5' AscI site oligo	c 654	7	33.3	10	1	AA285585	Metastatic breast
582	7.2	34.3	12	1	AAZ54938	C/EBP-beta antisen	c 655	7	33.3	10	1	AA285958	Metastatic breast
583	7.2	34.3	12	1	AAZ34385	Human adenosine re	c 656	7	33.3	10	1	AA282293	Metastatic breast
584	7.2	34.3	12	1	AAF20507	Human C/EBP polynu	c 657	7	33.3	10	1	AA282945	Metastatic breast
585	7.2	34.3	12	1	ABZ96201	Human C/EBP antise	c 658	7	33.3	10	1	AA283312	Metastatic breast
586	7.2	34.3	12	1	AE331299	Mouse 18S rDNA com	c 659	7	33.3	10	1	AA283464	Metastatic breast
587	7.2	34.3	12	1	AE331301	Human 18S rDNA com	c 660	7	33.3	10	1	AA282560	Metastatic breast
588	7.2	34.3	12	1	AE331300	Rat 18S rDNA compl	c 661	7	33.3	10	1	AA282992	Metastatic breast
589	7.2	34.3	15	1	AAF46831	IGFBP3 oligonucleo	c 662	7	33.3	10	1	AA279752	Human colon prefer
590	7.2	34.3	15	1	AAF46830	IGFBP3 oligonucleo	c 663	7	33.3	10	1	AA279859	Human dendritic ce
591	7.2	34.3	16	1	ADL91730	Collagen type IX a	c 664	7	33.3	10	1	AA279807	Human prostate pre
592	7.2	34.3	20	1	AAV69995	Mouse c-jun protei	c 665	7	33.3	10	1	AA279746	Human colon prefer
593	7	33.3	10	1	ABA06199	Human normal hepat	c 666	7	33.3	10	1	AA279746	Human colon prefer
594	7	33.3	10	1	ABL45887	Human EDG6 gene al	c 667	7	33.3	10	1	AA279746	Human colon prefer
595	7	33.3	10	1	AAZ85815	Metastatic breast	c 668	7	33.3	10	1	AA279746	Human colon prefer
596	7	33.3	10	1	AAO71095	Merlin exon 10 spl	c 669	7	33.3	10	1	AA279746	Human colon prefer
597	7	33.3	10	1	AAQ87111	Nael substrate Oli	c 670	7	33.3	10	1	AA279746	Human colon prefer
598	7	33.3	10	1	AAQ96792	HIV-1 NL4-3 nef ge	c 671	7	33.3	10	1	AA279746	Human colon prefer
599	7	33.3	10	1	AAQ96984	HIV-1 NL4-3 nef ge	c 672	7	33.3	10	1	AA279746	Human colon prefer
600	7	33.3	10	1	AAQ96983	HIV-1 NL4-3 nef ge	c 673	7	33.3	10	1	AA279746	Human colon prefer
601	7	33.3	10	1	AAQ96985	HIV-1 NL4-3 nef ge	c 674	7	33.3	10	1	AA279746	Human colon prefer
602	7	33.3	10	1	AAQ96793	HIV-1 NL4-3 nef ge	c 675	7	33.3	10	1	AA279746	Human colon prefer
603	7	33.3	10	1	AAQ96986	HIV-1 NL4-3 nef ge	c 676	7	33.3	10	1	AA279746	Human colon prefer
604	7	33.3	10	1	AAQ90121	PCR primer for the	c 677	7	33.3	10	1	AA279746	Human colon prefer
605	7	33.3	10	1	AAT29334	5'-primer for mam	c 678	7	33.3	10	1	AA279746	Human colon prefer
606	7	33.3	10	1	AAT29313	5'-primer for mam	c 679	7	33.3	10	1	AA279746	Human colon prefer
607	7	33.3	10	1	AAT29293	5'-primer for mam	c 680	7	33.3	10	1	AA279746	Human colon prefer
608	7	33.3	10	1	AAT10090	Hammerhead ribozym	c 681	7	33.3	10	1	AA279746	Human colon prefer
609	7	33.3	10	1	AAV50187	Yeast tag for addi	c 682	7	33.3	10	1	AA279746	Human colon prefer
610	7	33.3	10	1	AAZ77475	US5912147 primer 1	c 683	7	33.3	10	1	AA279746	Human colon prefer
611	7	33.3	10	1	AAZ77476	US5912147 primer 2	c 684	7	33.3	10	1	AA279746	Human colon prefer
612	7	33.3	10	1	AAZ77477	US5912147 primer 2	c 685	7	33.3	10	1	AA279746	Human colon prefer
613	7	33.3	10	1	AAZ28347	Lung cancer indica	c 686	7	33.3	10	1	AA279746	Human colon prefer
614	7	33.3	10	1	AAZ61441	Primer SP4A5 for 9	c 687	7	33.3	10	1	AA279746	Human colon prefer
615	7	33.3	10	1	AAZ78750	Human dendritic ce	c 688	7	33.3	10	1	AA279746	Human colon prefer
616	7	33.3	10	1	AAZ79591	Human dendritic ce	c 689	7	33.3	10	1	AA279746	Human colon prefer
617	7	33.3	10	1	AAZ79112	Human dendritic ce	c 690	7	33.3	10	1	AA279746	Human colon prefer

691	7	33.3	10	1	AAF70446	Human DRD2 polymor
692	7	33.3	10	1	AA91467	Human CHRM5 gene,
693	7	33.3	10	1	AB383148	Claudin 2 ovarian
694	7	33.3	10	1	AAF38910	Yeast NORF gene SA
695	7	33.3	10	1	AAF33704	Yeast NORF gene SA
696	7	33.3	10	1	AAF36509	Yeast NORF gene SA
697	7	33.3	10	1	AAF33404	Yeast NORF gene SA
698	7	33.3	10	1	AAF36625	Yeast NORF gene SA
699	7	33.3	10	1	AAF37397	Yeast NORF gene SA
700	7	33.3	10	1	AAF40108	Yeast NORF gene SA
701	7	33.3	10	1	AAF43351	Yeast NORF gene SA
702	7	33.3	10	1	AAF33705	Yeast NORF gene SA
703	7	33.3	10	1	AAF36000	Yeast NORF gene SA
704	7	33.3	10	1	AAF42397	Yeast NORF gene SA
705	7	33.3	10	1	AAF43632	Yeast NORF gene SA
706	7	33.3	10	1	AA595650	Human NP1R gene a
707	7	33.3	10	1	AA225081	Primer #8 used to
708	7	33.3	10	1	AA226712	Human GPR31 gene p
709	7	33.3	10	1	AA226031	Primer #33 to dete
710	7	33.3	10	1	ABL42059	C-terminal tail of
711	7	33.3	10	1	ABL42059	C-terminal tail of
712	7	33.3	10	1	ABL42060	Fragment of a reve
713	7	33.3	10	1	ABL42060	Fragment of a reve
714	7	33.3	10	1	ABL52166	Human PER1 prefer
715	7	33.3	10	1	ABL01195	Human AKR1B1 gene
716	7	33.3	10	1	AA598854	Colony stimulating
717	7	33.3	10	1	AA598814	Colony stimulating
718	7	33.3	10	1	ABL42674	Human maturation/a
719	7	33.3	10	1	ABL42776	Human maturation/a
720	7	33.3	10	1	ABL42840	Human maturation/a
721	7	33.3	10	1	ABL57664	Human SCYA24 prime
722	7	33.3	10	1	AA225385	Human primer #2 to
723	7	33.3	10	1	ABN81466	Human HTATIP PCR p
724	7	33.3	10	1	ABN81466	Human HTATIP PCR p
725	7	33.3	10	1	ABN81466	Human HTATIP PCR p
726	7	33.3	10	1	AA226186	Human L1PE gene po
727	7	33.3	10	1	AA226186	Human endothelin 2
728	7	33.3	10	1	AA226186	Human CSF3 gene al
729	7	33.3	10	1	AB071544	Zinc finger protei
730	7	33.3	10	1	ABQ88698	Human CFL1 primer
731	7	33.3	10	1	ABA99350	Human IL8 gene
732	7	33.3	10	1	ABN80659	Human P450(cytochr
733	7	33.3	10	1	ABV78586	Human Th2 cell pre
734	7	33.3	10	1	ABV78572	Human Th2 cell pre
735	7	33.3	10	1	ABV78572	Human Th2 cell pre
736	7	33.3	10	1	ABV78578	Human Th2 cell pre
737	7	33.3	10	1	ABV84533	Human liver phosph
738	7	33.3	10	1	ABV84789	Human gamma-glutam
739	7	33.3	10	1	ABV84679	Human HCC/chronic
740	7	33.3	10	1	ABV84371	Human MHC class II
741	7	33.3	10	1	ABV84732	Human liver phosph
742	7	33.3	10	1	ABL52041	Human SLC18A2 pref
743	7	33.3	10	1	ABQ81583	Asci linker. Synt
744	7	33.3	10	1	ABQ81583	Asci linker. Synt
745	7	33.3	10	1	ABA93362	Human ACAAI gene p
746	7	33.3	10	1	ABK72402	Human HTR5A gene a
747	7	33.3	10	1	AA597348	Human CYBB1 gene
748	7	33.3	10	1	ABL45895	Human EDG6 gene al
749	7	33.3	10	1	ABL45880	Human EDG6 gene al
750	7	33.3	10	1	AA595576	Human IL8RB gene a
751	7	33.3	10	1	ABK54355	Human SCYA26 gene
752	7	33.3	10	1	ABK72641	Leukotriene B4 rec
753	7	33.3	10	1	AA599404	Aldehyde dehydroge
754	7	33.3	10	1	AA599416	Aldehyde dehydroge
755	7	33.3	10	1	AA226806	Primer #13 to dete
756	7	33.3	10	1	ABK30056	Vancomycin-resista
757	7	33.3	10	1	ABK30050	Human CALM1 gene a
758	7	33.3	10	1	AA595997	Human CHRM5 gene p
759	7	33.3	10	1	ABK61807	Human Myo/V1 prote
760	7	33.3	10	1	ADG28070	Human Myo/V1 prote
761	7	33.3	10	1	ADG28070	Human Myo/V1 prote
762	7	33.3	10	1	ADG28259	Human Myo/V1 prote
763	7	33.3	10	1	ADH22188	Primer extension D
764	7	33.3	10	1	AA47787	Human GNB3 gene po
765	7	33.3	10	1	ACA94583	DNA tag from human
766	7	33.3	10	1	ACA94582	DNA tag from human
767	7	33.3	10	1	ACA94581	DNA tag from human
768	7	33.3	10	1	ACA94515	DNA tag from human
769	7	33.3	10	1	ABT14391	Nucleic acid PCR a
770	7	33.3	10	1	ADA63307	Zinc finger target
771	7	33.3	10	1	ADA60153	Human ARG energy m
772	7	33.3	10	1	ADC55425	Oligomer #11 which
773	7	33.3	10	1	ADC55425	Oligomer #11 which
774	7	33.3	10	1	ADF42385	Oligonucleotide SE
775	7	33.3	10	1	ADG98581	Human CBTP gene al
776	7	33.3	10	1	ADH62262	Human energy metab
777	7	33.3	10	1	AD48191	6784-1-G-Tam PNA p
778	7	33.3	10	1	ADJ93959	Azotobacter bacter
779	7	33.3	10	1	ADM21511	Synthetic zinc fin
780	7	33.3	10	1	ADG65501	UCP2 primer extens
781	7	33.3	10	1	ADG65512	UCP2 primer extens
782	7	33.3	10	1	ADH57554	Extendable oligo E
783	7	33.3	10	1	ADH13646	Extracellular tumo
784	7	33.3	10	1	ADH13679	Extracellular tumo
785	7	33.3	10	1	ADO39879	Androgen-regulated
786	7	33.3	10	1	ADR27959	Murine VE-statin e
787	7	33.3	10	1	AD577172	Breast cancer dete
788	7	33.3	10	1	AD576595	Breast cancer dete
789	7	33.3	10	1	AD578142	Breast cancer dete
790	7	33.3	10	1	AD578064	Breast cancer dete
791	7	33.3	10	1	AD576596	Breast cancer dete
792	7	33.3	10	1	AD578054	Breast cancer dete
793	7	33.3	10	1	AD576240	Breast cancer dete
794	7	33.3	10	1	AD577171	Breast cancer dete
795	7	33.3	10	1	AD576513	Breast cancer dete
796	7	33.3	10	1	AD578031	Breast cancer dete
797	7	33.3	10	1	AD578152	Breast cancer dete
798	7	33.3	10	1	AD576514	Breast cancer dete
799	7	33.3	10	1	ADU18287	Hypoxia-related tu
800	7	33.3	10	1	ADU19179	Hypoxia-related tu
801	7	33.3	10	1	ADU19612	Hypoxia-related tu
802	7	33.3	10	1	ADU19600	Hypoxia-related tu
803	7	33.3	10	1	ADU18248	Hypoxia-related tu
804	7	33.3	10	1	ADU18578	Hypoxia-related tu
805	7	33.3	10	1	ADU19243	Hypoxia-related tu
806	7	33.3	10	1	ADU18636	Hypoxia-related tu
807	7	33.3	10	1	ADU19803	Hypoxia-related tu
808	7	33.3	10	1	ADU18717	Hypoxia-related tu
809	7	33.3	10	1	AEA15026	Asi DNA linker se
810	7	33.3	10	1	AEA15026	Asi DNA linker se
811	7	33.3	10	1	AD267940	NTRK1 gene polymor
812	7	33.3	10	1	AD285561	Human BACE455 cDNA
813	7	33.3	10	1	AEA62005	NTRK1 gene polymor

ALIGNMENTS

RESULT 1

AAV69995/c
ID AAV69995 standard; DNA; 20 BP.XX
AC AAV69995;XX
DT 04-FEB-1999 (first entry)XX
DE Mouse c-jun protein antisense oligonucleotide #40.XX
KW Mouse; c-fos; c-jun; activating protein 1; AP-1; diagnosis; metastasis;
KW antisense oligonucleotide; phosphorothioate; regulation;
KW malignant tumour; cell cycle expression; hyperproliferative disease; ss.XX
OS Synthetic.

OS Mus sp.

XX
FH Key

Location/Qualifiers

FT modified_base 1. 20
 FT /*tag= a
 FT /note= "phosphorothioate linkages"
 PN WO9846272-A1.
 PD 22-OCT-1998.
 XX 14-APR-1998; 98WO-US0007386.
 PF 14-APR-1997; 97US-00837201.
 PR (ISIS-) ISIS PHARM INC.
 PA Dean NM, McKay R, Miraglia L, Baker B;
 PI WPI; 1998-609906/51.
 XX Antisense oligonucleotides regulating Activating Protein 1 subunits -
 PT hybridise with c-fos and c-jun mRNA, used for regulating metastasis, cell
 PT cycle expression and hyperproliferative disease.
 XX Example 7; Page 52; 120pp; English.
 PS AAV69993 to AAV70008 represent antisense oligonucleotides which are
 CC specifically hybridisable with a region of a nucleic acid encoding mouse
 CC c-Jun protein. The antisense compound regulates the expression of the c-
 CC Jun protein. The present invention also describes antisense
 CC oligonucleotides which regulate the c-Fos protein. The antisense
 CC oligonucleotides are used for the diagnosis and treatment of diseases or
 CC disorders associated with Activating Protein 1 expression, of which c-Fos
 CC and c-Jun are subunits. The antisense oligonucleotides are used in
 CC compositions as c-Fos and/or c-Jun together with a carrier and a
 CC chemotherapeutic agent. They are used to regulate the expression of c-Fos
 CC or c-Jun in cells or tissues, preferably by inhibiting metastasis. They
 CC also regulate cell cycle expression and can be used to treat an animal
 CC with, or being prone to, a hyperproliferative disease
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 8 G; 0 T; 0 U; 0 Other;
 Query Match 68.6%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 24;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 CCGCGCGCGCTGTGGC 21 (C)nt 3631-44 w/tdel
 DB 16 CCGCGCGCGCTGTGC 1 , subst idon' to 3631-47
 RESULT 2
 ADL47206/c
 ID ADL47206 standard; RNA; 17 BP.
 XX ADL47206;
 AC ADL47206;
 XX 20-MAY-2004 (first entry)
 DT Human NOGO receptor zinzyme substrate sequence #193.
 DE antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; ikappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; diabetes; obesity;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis;
 KW NOGO receptor zinzyme; substrate; ds.
 XX Unidentified.
 OS WO200281628-A2.
 PN

XX 17-OCT-2002.
 XX 03-APR-2002; 2002WO-US010512.
 XX 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Blatt L, Chowira B, Haerberli P, Meswigen J, Poenaugh K;
 PI WPI; 2003-058513/05.
 XX Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, ikappaB kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX Claim 9; SEQ ID NO 739; 317pp; English.
 PS The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC ikappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human NOGO
 CC receptor zinzyme substrate sequence.
 XX
 SQ Sequence 17 BP; 4 A; 7 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 61.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 41;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TGGCCCGCGCGCTGT 18
 DB 17 TTGCCCGCGCGCTGT 2
 RESULT 3
 ADM54550
 ID ADM54550 standard; mRNA; 17 BP.
 XX ADM54550;
 AC ADM54550;
 XX 03-JUN-2004 (first entry)
 DT Human GRID mRNA substrate sequence #860.
 DE Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
 KW NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNazyme; amberzyme; Inozyme;
 KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
 XX Homo sapiens.
 OS US2003134806-A1.
 PN 17-JUL-2003.
 PD 23-FEB-2001; 2001US-00792818.
 PF 10-FEB-2000; 2000US-0181594P.
 XX

PA (JARV/) JARVIS T.
PA (CARL/) CARLOWITZ I V.
PA (MCSW/) MCSWIGGEN J.
PA (HAMB/) HAMBELIN P A.
PA (ELLIS/) ELLIS J H.
XX
XX Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
PI
XX
XX
XX WPI; 2003-829646/77.
DR
XX
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
PT
XX
XX Claim 4; SEQ ID NO 862; 74pp; English.
PS
XX
XX The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyne, DNzyme,
CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule,
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequences (encoding at least the novel
CC nucleic acid molecule in a manner that allows its expression), a
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX
SQ Sequence 17 BP; 0 A; 8 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 41;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGCCCGCGCGCGTGT 18
:||||| ||||| :|:
Db 2 UGGCCCGCGCCUGU 17

RESULT 4
ADL91730
ID ADL91730 standard; DNA; 16 BP.
XX
XX ADL91730;
AC
XX
XX 03-JUN-2004 (first entry)
DT
DE
XX
XX Collagen type IX alpha 3 (SYX 4) control S-oligo, SEQ ID NO:131.
KW
KW Synovial sarcoma; SYX; sarcoma-associated gene; drug screening;
KW Frizzled homologue 10; FZD10-associated disease; colorectal cancer;
KW gastric cancer; chronic myeloid leukaemia; acute myeloid leukaemia.;
KW FZD10 antibody; diagnosis; prognosis; prevention; cytostatic;
KW gene therapy; control oligonucleotide; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2004020669-A2.
PN
XX
XX 11-MAR-2004.
PD
XX
XX 21-AUG-2003; 2003WO-JP010591.
PF
XX
XX 30-AUG-2002; 2002US-0407506P.
PR
XX 11-JUL-2003; 2003US-0486195P.
PR
XX

PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
XX Nakamura Y, Katagiri T;
PI
XX WPI; 2004-239208/22.
DR
XX
XX Use of a compound or composition for diagnosing, treating or preventing
PT synovial sarcoma or a disease associated with Frizzled homologue 10, e.g.
PT colorectal cancer, gastric cancer, chronic myeloid leukemia or acute
PT myeloid leukemia.
XX
XX Example 4; SEQ ID NO 131; 143pp; English.
PS
XX
XX The invention relates to the use of a compound or composition for
CC diagnosing, prognosing, treating or preventing synovial sarcoma or a
CC Frizzled homologue 10 (FZD10)-associated disease in a patient. The
CC invention encompasses the use of sarcoma-associated genes designated SYX
CC 1-26 or their encoded proteins in diagnosing of synovial sarcoma and in
CC screening for compounds for treating or preventing this condition; and
CC the use of antibodies specific for FZD10 (FZD10 is also referred to as
CC SYX 1 in the specification) for diagnosing, treating or preventing FZD10-
CC associated diseases. The compound, composition and methods of the
CC invention are useful for diagnosing, treating or preventing synovial
CC sarcoma or FZD10-associated diseases, such as colorectal cancer, gastric
CC cancer, chronic myeloid leukaemia or acute myeloid leukaemia. Sequences
CC ADL91688-Ad91751 represent antisense and control S-oligonucleotides used
CC in a study of antisense-mediated inhibition of the expression of synovial
CC sarcoma-associated genes.
XX
SQ Sequence 16 BP; 1 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 59.0%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 43;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGCGCGCGC 15
| ||||| |||||
Db 3 CCGGCCCGCGCGCGC 16

RESULT 5
ADL46910/C
ID ADL46910 standard; RNA; 17 BP.
XX
XX ADL46910;
AC
XX
XX 20-MAY-2004 (first entry)
DT
DE
XX
XX Human NOGO receptor inozyme substrate sequence #343.
KW
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW NOGO receptor inozyme; substrate; ds.
XX
XX Unidentified.
OS
XX
XX WO200281628-A2.
PN
XX
XX 17-OCT-2002.
PD
XX
XX 03-APR-2002; 2002WO-US010512.
PF
XX
XX 05-APR-2001; 2001US-00827395.
PR
XX 29-MAY-2001; 2001US-0294412P.
PR
XX 28-AUG-2001; 2001US-0315315P.
PR
XX

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:14:10 ; Search time 79.9111 Seconds
(without alignments)
645.083 Million cell updates/sec

Title: US-09-904-968A-3

Perfect score: 29

Sequence: 1 ccatacactgctgtgacctgtaaat 29

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
- 7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/prodata/1/ina/baGfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	31571	2	US-08-323-443B-1
2	29	100.0	53526	3	US-08-658-136-2
3	29	100.0	53577	3	US-08-658-136-1
4	29	100.0	53577	3	US-08-460-215A-1
5	20.2	69.7	601	3	US-09-949-016-142117
6	20.2	69.7	601	3	US-09-949-016-142118
7	20.2	69.7	44064	3	US-09-949-016-12015
8	20.2	69.7	44072	3	US-09-949-016-15757
9	20	69.0	24546	3	US-09-949-016-16538
10	19.8	68.3	105045	3	US-09-949-002-663
11	19.6	67.6	378	3	US-09-621-976-10243
12	19.6	67.6	8930	3	US-09-814-915A-91
13	19.6	67.6	47787	3	US-09-949-016-11969
14	19.6	67.6	97423	3	US-09-949-016-12742
15	19.6	67.6	97424	3	US-09-949-016-15576
16	19.4	66.9	601	3	US-09-949-016-51876
17	19.4	66.9	22104	3	US-09-949-016-12745
18	19.4	66.9	22104	3	US-09-949-016-12763
19	19.4	66.9	47493	3	US-09-949-016-13241
20	19.4	66.9	105679	3	US-09-949-016-12360
21	19.4	66.9	150032	3	US-09-949-016-14321
22	19.4	66.9	387902	3	US-09-949-016-14543
23	19.4	66.9	421883	3	US-09-949-016-12557
24	19.2	66.2	1683	3	US-09-902-540-4280

C 25	19.2	66.2	20250	3	US-09-902-540-1213	Sequence 1213, Ap
C 26	19.2	66.2	95750	3	US-09-949-016-11926	Sequence 11926, A
C 27	19	65.5	601	3	US-09-949-016-95981	Sequence 95981, A
C 28	19	65.5	843	3	US-09-252-991A-5079	Sequence 5079, Ap
C 29	19	65.5	1530	3	US-09-252-991A-5138	Sequence 5138, Ap
C 30	19	65.5	1581	3	US-09-252-991A-5015	Sequence 5015, Ap
C 31	19	65.5	66175	3	US-09-949-016-12293	Sequence 12293, A
C 32	19	65.5	95122	3	US-09-949-016-17235	Sequence 17235, A
C 33	19	65.5	97376	3	US-09-949-016-16093	Sequence 16093, A
C 34	18.8	64.8	601	3	US-09-949-016-15692	Sequence 15692, A
C 35	18.8	64.8	36611	3	US-09-949-016-17287	Sequence 17287, A
C 36	18.8	64.8	107679	3	US-09-949-016-16409	Sequence 16409, A
C 37	18.6	64.1	601	3	US-09-949-016-160801	Sequence 160801, A
C 38	18.6	64.1	45427	3	US-09-949-016-16243	Sequence 16243, A
C 39	18.6	64.1	50186	3	US-09-949-016-14066	Sequence 14066, A
C 40	18.6	64.1	92581	3	US-09-949-016-12182	Sequence 12182, A
C 41	18.6	64.1	92581	3	US-09-949-016-15442	Sequence 15442, A
C 42	18.6	64.1	767677	3	US-09-949-016-12147	Sequence 12147, A
C 43	18.6	64.1	767677	3	US-09-949-016-17361	Sequence 17361, A
C 44	18.4	63.4	495	3	US-09-621-976-11554	Sequence 11554, A
C 45	18.4	63.4	601	3	US-09-949-016-19572	Sequence 19572, A

ALIGNMENTS

RESULT 1
US-08-323-443B-1
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323.443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0372/0A462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

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; IMMEDIATE SOURCE:
; CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match      100.0%; Score 29; DB 2; Length 31571;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
    |||||
Db 1448 CCATCCACCTGCTGTGTGACCTGGTAAAT 1476

RESULT 2
US-08-658-136-2
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match      100.0%; Score 29; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
    |||||
Db 2043 CCATCCACCTGCTGTGTGACCTGGTAAAT 2071

RESULT 4
US-08-460-215A-1
; Sequence 1, Application US/08460215A
; Patent No. 6867288
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,215A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DUGAN, DEBORAH
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-17.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-460-215A-1

Query Match 100.0%; Score 29; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
|||||
DB 2043 CCATCCACCTGCTGTGTGACCTGGTAAAT 2071

RESULT 5

US-09-949-016-142117
; Sequence 142117, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142117
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142117

Query Match 69.7%; Score 20.2; DB 3; Length 601;
Best Local Similarity 88.0%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGT 25
|||||
DB 410 CCATCCACCTGCTGTGTGACCTGGT 434

RESULT 6

US-09-949-016-142118
; Sequence 142118, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142118
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142118

Query Match 69.7%; Score 20.2; DB 3; Length 601;
Best Local Similarity 88.0%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGT 25
|||||
DB 442 CCATCCACCTGCTGTGTGACCTGGT 466

RESULT 7

US-09-949-016-12015/c
; Sequence 12015, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12015
; LENGTH: 44064
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12015

Query Match 69.7%; Score 20.2; DB 3; Length 44064;
Best Local Similarity 88.0%; Pred. No. 65;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGT 25
|||||
DB 34189 CCATCCACCTGCTGTGTGACCTGGT 34165

RESULT 8

US-09-949-016-15757/c
; Sequence 15757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

Query Match 67.6%; Score 19.6; DB 3; Length 8930;
Best Local Similarity 84.6%; Pred. No. 97;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TCACCTGCTGTGTGACCTGGTAAAT 29
DB 8850 TGCATCTGTATGTGACGTGTAAT 8875

RESULT 13
US-09-949-016-11969
; Sequence 11969, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11969
; LENGTH: 47787
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11969

Query Match 67.6%; Score 19.6; DB 3; Length 47787;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGTGACCTGGTAAA 28
DB 12984 ATTACCTCTGTGTGACCTGGAAAA 13009

RESULT 14
US-09-949-016-12742
; Sequence 12742, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12742
; LENGTH: 97423
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12742

Query Match 67.6%; Score 19.6; DB 3; Length 97423;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTA 26

DB 39563 CCTGCCGCTGCTGTGTGACCTGGCA 39588

RESULT 15
US-09-949-016-15576
; Sequence 15576, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15576
; LENGTH: 97424
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15576

Query Match 67.6%; Score 19.6; DB 3; Length 97424;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTA 26
DB 39563 CCTGCCGCTGCTGTGTGACCTGGCA 39588

Search completed: May 9, 2006, 05:56:12
Job time : 82.9111 secs

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